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(54) Title: NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

(57) Abstract

The invention provides proteins from *Neisseria meningitidis*, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics.

919 (46 kDa)**A) PURIFICATION****M1 919**

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NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

This application is a continuation-in-part of the following U.S. Provisional Patent applications, from each of which priority is claimed, and each of which is incorporated by reference in its entirety: 60/083,758 (filed May 1, 1998); 60/094,869 (filed July 31, 1998); 60/098,994 (filed September 2, 1998); 60/099,062 (filed September 2, 1998); 60/103,749 (filed October 9, 1998); 60/103,794 (filed October 9, 1998); 60/103,796 (filed October 9, 1998); and 60/121,528 (filed February 25, 1999).

This invention relates to antigens from the bacterial species: *Neisseria meningitidis* and *Neisseria gonorrhoeae*.

BACKGROUND

Neisseria meningitidis is a non-motile, gram negative diplococcus human pathogen. It colonizes the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. It is closely related to *N. gonorrhoea*, although one feature that clearly differentiates meningococcus from gonococcus is the presence of a polysaccharide capsule that is present in all pathogenic meningococci.

N. meningitidis causes both endemic and epidemic disease. In the United States the attack rate is 0.6-1 per 100,000 persons per year, and it can be much greater during outbreaks. (see Lieberman *et al.* (1996) Safety and Immunogenicity of a Serogroups A/C *Neisseria meningitidis* Oligosaccharide-Protein Conjugate Vaccine in Young Children. *JAMA* 275(19):1499-1503; Schuchat *et al* (1997) Bacterial Meningitis in the United States in 1995. *N Engl J Med* 337(14):970-976). In developing countries, endemic disease rates are much higher and during epidemics incidence rates can reach 500 cases per 100,000 persons per year. Mortality is extremely high, at 10-20% in the United States, and much higher in developing countries. Following the introduction of the conjugate vaccine against *Haemophilus influenzae*, *N. meningitidis* is the major cause of bacterial meningitis at all ages in the United States (Schuchat *et al* (1997) *supra*).

Based on the organism's capsular polysaccharide, 12 serogroups of *N. meningitidis* have been identified. Group A is the pathogen most often implicated in epidemic disease in sub-Saharan Africa. Serogroups B and C are responsible for the vast majority of cases in the

United States and in most developed countries. Serogroups W135 and Y are responsible for the rest of the cases in the United States and developed countries. The meningococcal vaccine currently in use is a tetravalent polysaccharide vaccine composed of serogroups A, C, Y and W135. Although efficacious in adolescents and adults, it induces a poor immune response and short duration of protection, and cannot be used in infants [eg. Morbidity and Mortality weekly report, Vol.46, No. RR-5 (1997)]. This is because polysaccharides are T-cell independent antigens that induce a weak immune response that cannot be boosted by repeated immunization. Following the success of the vaccination against *H.influenzae*, conjugate vaccines against serogroups A and C have been developed and are at the final stage of clinical testing (Zollinger WD "New and Improved Vaccines Against Meningococcal Disease". In: *New Generation Vaccines, supra*, pp. 469-488; Lieberman *et al* (1996) *supra*; Costantino *et al* (1992) Development and phase I clinical testing of a conjugate vaccine against meningococcus A and C. *Vaccine* 10:691-698).

Meningococcus B (menB) remains a problem, however. This serotype currently is responsible for approximately 50% of total meningitis in the United States, Europe, and South America. The polysaccharide approach cannot be used because the menB capsular polysaccharide is a polymer of $\alpha(2-8)$ -linked *N*-acetyl neuraminic acid that is also present in mammalian tissue. This results in tolerance to the antigen; indeed, if an immune response were elicited, it would be anti-self, and therefore undesirable. In order to avoid induction of autoimmunity and to induce a protective immune response, the capsular polysaccharide has, for instance, been chemically modified substituting the *N*-acetyl groups with *N*-propionyl groups, leaving the specific antigenicity unaltered (Romero & Outschoorn (1994) Current status of Meningococcal group B vaccine candidates: capsular or non-capsular? *Clin Microbiol Rev* 7(4):559-575).

Alternative approaches to menB vaccines have used complex mixtures of outer membrane proteins (OMPs), containing either the OMPs alone, or OMPs enriched in porins, or deleted of the class 4 OMPs that are believed to induce antibodies that block bactericidal activity. This approach produces vaccines that are not well characterized. They are able to protect against the homologous strain, but are not effective at large where there are many antigenic variants of the outer membrane proteins. To overcome the antigenic variability, multivalent vaccines containing up to nine different porins have been constructed (eg. Poolman JT (1992) Development of a meningococcal vaccine. *Infect. Agents Dis.* 4:13-28).

Additional proteins to be used in outer membrane vaccines have been the opa and opc proteins, but none of these approaches have been able to overcome the antigenic variability (eg. Ala'Aldeen & Borriello (1996) The meningococcal transferrin-binding proteins 1 and 2 are both surface exposed and generate bactericidal antibodies capable of killing homologous and heterologous strains. *Vaccine* 14(1):49-53).

A certain amount of sequence data is available for meningococcal and gonococcal genes and proteins (e.g. EP-A-0467714, WO96/29412), but this is by no means complete. Other men B proteins may include those listed in WO 97/28273, WO 96/29412, WO 95/03413, US 5,439,808, and US 5,879,686.

The provision of further sequences could provide an opportunity to identify secreted or surface-exposed proteins that are presumed targets for the immune system and which are not antigenically variable. For instance, some of the identified proteins could be components of efficacious vaccines against meningococcus B, some could be components of vaccines against all meningococcal serotypes, and others could be components of vaccines against all pathogenic *Neisseriae* including *Neisseria meningitidis* or *Neisseria gonorrhoeae*. Those sequences specific to *N. meningitidis* or *N. gonorrhoeae* that are more highly conserved are further preferred sequences.

It is thus an object of the invention is to provide Neisserial DNA sequences which encode proteins that are antigenic or immunogenic.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 illustrates the products of protein expression and purification of the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 2 illustrates the products of protein expression and purification of the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 3 illustrates the products of protein expression and purification of the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 4 illustrates the products of protein expression and purification of the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 5 illustrates the products of protein expression and purification of the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 6 illustrates the products of protein expression and purification of the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 7 illustrates the products of protein expression and purification of the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 8 illustrates the products of protein expression and purification of the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 9 illustrates the products of protein expression and purification of the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 10 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 11 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 12 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 13 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 14 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 15 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 16 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 17 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 18 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 19 shows an alignment comparison of amino acid sequences for ORF 225 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 20 shows an alignment comparison of amino acid sequences for ORF 235 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 21 shows an alignment comparison of amino acid sequences for ORF 287 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 22 shows an alignment comparison of amino acid sequences for ORF 519 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 23 shows an alignment comparison of amino acid sequences for ORF 919 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

THE INVENTION

The invention provides proteins comprising the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples.

It also provides proteins comprising sequences homologous (i.e., those having sequence identity) to the *N. meningitidis* amino acid sequences disclosed in the examples. Depending on the particular sequence, the degree of homology (sequence identity) is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more). These proteins include mutants and allelic variants of the sequences disclosed in the examples. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman

homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with parameters: gap penalty 12, gap extension penalty 1.

The invention further provides proteins comprising fragments of the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples. The fragments should comprise at least n consecutive amino acids from the sequences and, depending on the particular sequence, n is 7 or more (eg. 8, 10, 12, 14, 16, 18, 20 or more). Preferably the fragments comprise an epitope from the sequence.

The proteins of the invention can, of course, be prepared by various means (eg. recombinant expression, purification from cell culture, chemical synthesis *etc.*) and in various forms (eg. native, fusions *etc.*). They are preferably prepared in substantially pure or isolated form (ie. substantially free from other *N. meningitidis* or *N. gonorrhoeae* host cell proteins)

According to a further aspect, the invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means.

According to a further aspect, the invention provides nucleic acid comprising the *N. meningitidis* nucleotide sequences and *N. gonorrhoeae* nucleotide sequences disclosed in the examples.

According to a further aspect, the invention comprises nucleic acids having sequence identity of greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) to the nucleic acid sequences herein. Sequence identity is determined as above-discussed.

According to a further aspect, the invention comprises nucleic acid that hybridizes to the sequences provided herein. Conditions for hybridization are set forth herein.

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least n consecutive nucleotides from the *N. meningitidis* sequences or *N. gonorrhoeae* sequences and depending on the particular sequence, n is 10 or more (eg 12, 14, 15, 18, 20, 25, 30, 35, 40 or more).

According to a further aspect, the invention provides nucleic acid encoding the proteins and protein fragments of the invention.

It should also be appreciated that the invention provides nucleic acid comprising sequences complementary to those described above (eg. for antisense or probing purposes).

Nucleic acid according to the invention can, of course, be prepared in many ways (eg. by chemical synthesis, in part or in whole, from genomic or cDNA libraries, from the

organism itself *etc.*) and can take various forms (*eg.* single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also protein nucleic acids (PNA) *etc.*

According to a further aspect, the invention provides vectors comprising nucleotide sequences of the invention (*eg.* expression vectors) and host cells transformed with such vectors.

According to a further aspect, the invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as vaccines, for instance, or as diagnostic reagents or as immunogenic compositions.

The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (*eg.* as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of (I) a medicament for treating or preventing infection due to Neisserial bacteria (ii) a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria or (iii) for raising antibodies. Said Neisserial bacteria may be any species or strain (such as *N. gonorrhoeae*) but are preferably *N. meningitidis*, especially strain B or strain C.

The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody according to the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell according to the invention under conditions which induce protein expression.

A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridizing conditions to form duplexes; and (b) detecting said duplexes.

A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody according to the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Methodology - Summary of standard procedures and techniques.

General

This invention provides *Neisseria meningitidis* menB nucleotide sequences, amino acid sequences encoded therein. With these disclosed sequences, nucleic acid probe assays and expression cassettes and vectors can be produced. The expression vectors can be transformed into host cells to produce proteins. The purified or isolated polypeptides (which may also be chemically synthesized) can be used to produce antibodies to detect menB proteins. Also, the host cells or extracts can be utilized for biological assays to isolate agonists or antagonists. In addition, with these sequences one can search to identify open reading frames and identify amino acid sequences. The proteins may also be used in immunogenic compositions, antigenic compositions and as vaccine components.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature e.g., Sambrook *Molecular Cloning; A Laboratory Manual, Second Edition* (1989); *DNA Cloning, Volumes I and ii* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C.C. Blackwell eds 1986).

Standard abbreviations for nucleotides and amino acids are used in this specification.

All publications, patents, and patent applications cited herein are incorporated in full by reference.

Expression systems

The *Neisseria* menB nucleotide sequences can be expressed in a variety of different expression systems; for example those used with mammalian cells, plant cells, baculoviruses, bacteria, and yeast.

i. Mammalian Systems

Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation (Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells." In *Molecular Cloning: A Laboratory Manual*, 2nd ed.).

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, also provide useful promoter sequences. Expression may be either constitutive or regulated (inducible). Depending on the promoter selected, many promoters may be inducible using known substrates, such as the use of the mouse mammary tumor virus (MMTV) promoter with the glucocorticoid responsive element (GRE) that is induced by glucocorticoid in hormone-responsive transformed cells (see for example, U.S. Patent 5,783,681).

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a

regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter (Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.). Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer (Dijkema et al (1985) *EMBO J.* 4:761) and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus (Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777) and from human cytomegalovirus (Boshart et al. (1985) *Cell* 41:521). Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion (Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237).

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus tripartite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation (Birnstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M.

Glover); Proudfoot (1989) *Trends Biochem. Sci.* 14:105). These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator/polyadenylation signals include those derived from SV40 (Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*).

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 (Gluzman (1981) *Cell* 23:175) or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replication systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 (Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946) and pHEBO (Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074).

The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), and a number of other cell lines.

ii. Plant Cellular Expression Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: U.S. 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987); Whittier et al., *Nucleic Acids Research* 15:2515-2535 (1987); Wirsal et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, Gibberellins: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987)

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Repr.* 11(2):165-185.

Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet*, 202:179-185, 1985. The genetic material may also be transferred into the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension.

These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

iii. Baculovirus Systems

The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit). These techniques are generally known to

those skilled in the art and fully described in Summers and Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) (hereinafter "Summers and Smith").

Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This construct may contain a single gene and operably linked regulatory elements; multiple genes, each with its own set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31).

The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, 42:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli*.

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO

Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* 69:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human (alpha) α -interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacqz-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

A recombinant polypeptide or polyprotein may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with cyanogen bromide.

Alternatively, recombinant polyproteins or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See

Summers and Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91. The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15 μm in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant virus) of occlusion bodies. *Current Protocols in Microbiology* Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers and Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (PCT Pub. No. WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, et al. (1989) *In Vitro Cell. Dev. Biol.* 25:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. See, e.g., Summers and Smith *supra*.

The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, e.g., HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, or the like. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also secreted in the medium or result from lysis of insect cells, so as to provide a product which is at least substantially free of host debris, e.g., proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

iv. Bacterial Systems

Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps

initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) (Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173). Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) (Chang *et al.* (1977) *Nature* 198:1056), and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) (Goeddel *et al.* (1980) *Nuc. Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucl. Acids Res.* 9:731; U.S. Patent 4,738,921; EPO Publ. Nos. 036 776 and 121 775). The beta-lactamase (*bla*) promoter system (Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)), bacteriophage lambda PL (Shimatake *et al.* (1981) *Nature* 292:128) and T5 (U.S. Patent 4,689,406) promoter systems also provide useful promoter sequences.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter (U.S. Patent 4,551,433). For example, the *tac* promoter is a hybrid *trp-lac* promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor (Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21). Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system (Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci.* 82:1074). In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO Publ. No. 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon

(Shine *et al.* (1975) *Nature* 254:34). The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA (Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R.F. Goldberger)). To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site, it is often necessary to optimize the distance between the SD sequence and the ATG of the eukaryotic gene (Sambrook *et al.* (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*).

A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* or *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO Publ. No. 219 237).

Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene (Nagai *et al.* (1984) *Nature* 309:810). Fusion proteins can also be made with sequences from the *lacZ* (Jia *et al.* (1987) *Gene* 60:197), *trpE* (Allen *et al.* (1987) *J. Biotechnol.* 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol.* 135:11), and *Chey* (EPO Publ. No. 324 647) genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated (Miller *et al.* (1989) *Bio/Technology* 7:698).

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in bacteria (U.S. Patent 4,336,336). The

signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) (Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghrayeb *et al.* (1984) *EMBO J.* 3:2437) and the *E. coli* alkaline phosphatase signal sequence (*phoA*) (Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212). As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. No. 244 042).

Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number

vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EPO Publ. No. 127 328). Integrating vectors may also be comprised of bacteriophage or transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline (Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469). Selectable markers may also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: *Bacillus subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541), *Escherichia coli* (Shimatake *et al.* (1981) *Nature* 292:128; Amann *et al.* (1985) *Gene* 40:183; Studier *et al.* (1986) *J. Mol. Biol.* 189:113; EPO Publ. Nos. 036 776, 136 829 and 136 907), *Streptococcus cremoris* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655); *Streptococcus lividans* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655), *Streptomyces lividans* (U.S. Patent 4,745,056).

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with CaCl_2 or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by

electroporation. Transformation procedures usually vary with the bacterial species to be transformed. (See e.g., use of *Bacillus*: Masson *et al.* (1989) *FEMS Microbiol. Lett.* 60:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541; use of *Campylobacter*: Miller *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:856; and Wang *et al.* (1990) *J. Bacteriol.* 172:949; use of *Escherichia coli*: Cohen *et al.* (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower *et al.* (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim. Biophys. Acta* 949:318; use of *Lactobacillus*: Chassy *et al.* (1987) *FEMS Microbiol. Lett.* 44:173; use of *Pseudomonas*: Fiedler *et al.* (1988) *Anal. Biochem* 170:38; use of *Staphylococcus*: Augustin *et al.* (1990) *FEMS Microbiol. Lett.* 66:203; use of *Streptococcus*: Barany *et al.* (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun.* 32:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti *et al.* (1987) *Proc. 4th Evr. Cong. Biotechnology* 1:412.

v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences.

Examples include alcohol dehydrogenase (ADH) (EPO Publ. No. 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO Publ. No. 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences (Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1).

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (U.S. Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EPO Publ. No. 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, (Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA* 77:1078; Henikoff *et al.* (1981) *Nature* 283:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene* 11:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;).

A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, plant, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human

superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See e.g., EPO Publ. No. 196056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (e.g., WO88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EPO Publ. No. 012 873; JPO Publ. No. 62:096,086) and the A-factor gene (U.S. Patent 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EPO Publ. No. 060 057).

A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (U.S. Patent Nos. 4,546,083 and 4,870,008; EPO Publ. No. 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alphafactor. (See e.g., PCT Publ. No. WO 89/02463.)

Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator

sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 (Botstein *et al.* (1979) *Gene* 8:17-24), pCI/1 (Brake *et al.* (1984) *Proc. Natl. Acad. Sci. USA* 81:4642-4646), and YRp17 (Stinchcomb *et al.* (1982) *J. Mol. Biol.* 158:157). In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See e.g., Brake *et al.*, *supra*.

Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome (Orr-Weaver *et al.* (1983) *Methods in Enzymol.* 101:228-245). An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, *supra*. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced (Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:6750). The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions (Butt *et al.* (1987) *Microbiol. Rev.* 51:351).

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors and methods of introducing exogenous DNA into yeast hosts have been developed for, *inter alia*, the following yeasts: *Candida albicans* (Kurtz, *et al.* (1986) *Mol. Cell. Biol.* 6:142); *Candida maltosa* (Kunze, *et al.* (1985) *J. Basic Microbiol.* 25:141); *Hansenula polymorpha* (Gleeson, *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302); *Kluyveromyces fragilis* (Das, *et al.* (1984) *J. Bacteriol.* 158:1165); *Kluyveromyces lactis* (De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:737; Van den Berg *et al.* (1990) *Bio/Technology* 8:135); *Pichia guilliermondii* (Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141); *Pichia pastoris* (Cregg, *et al.* (1985) *Mol. Cell. Biol.* 5:3376; U.S. Patent Nos. 4,837,148 and 4,929,555); *Saccharomyces cerevisiae* (Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163); *Schizosaccharomyces pombe* (Beach and Nurse (1981) *Nature* 300:706); and *Yarrowia lipolytica* (Davidow, *et al.* (1985) *Curr. Genet.* 10:380471 Gaillardin, *et al.* (1985) *Curr. Genet.* 10:49).

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See e.g., [Kurtz *et al.* (1986) *Mol. Cell. Biol.* 6:142; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das *et al.* (1984) *J.*

Bacteriol. 158:1165; De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:1165; Van den Berg *et al.* (1990) *Bio/Technology* 8:135; Kluyveromyces]; [Cregg *et al.* (1985) *Mol. Cell. Biol.* 5:3376; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; U.S. Patent Nos. 4,837,148 and 4,929,555; *Pichia*]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163 *Saccharomyces*]; [Beach and Nurse (1981) *Nature* 300:706; *Schizosaccharomyces*]; [Davidow *et al.* (1985) *Curr. Genet.* 10:39; Gaillardin *et al.* (1985) *Curr. Genet.* 10:49; *Yarrowia*].

Definitions

A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

A "conserved" *Neisseria* amino acid fragment or protein is one that is present in a particular *Neisserial* protein in at least x% of *Neisseria*. The value of x may be 50% or more, e.g., 66%, 75%, 80%, 90%, 95% or even 100% (i.e. the amino acid is found in the protein in question in all *Neisseria*). In order to determine whether an amino acid is "conserved" in a particular *Neisserial* protein, it is necessary to compare that amino acid residue in the sequences of the protein in question from a plurality of different *Neisseria* (a reference population). The reference population may include a number of different *Neisseria* species or may include a single species. The reference population may include a number of different serogroups of a particular species or a single serogroup. A preferred reference population consists of the 5 most common *Neisseria* strains.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a *Neisserial* sequence is heterologous to a mouse host cell.

"Epitope" means antigenic determinant, and may elicit a cellular and/or humoral response.

Conditions for "high stringency" are 65 degrees C in 0.1 xSSC 0.5% SDS solution.

An "origin of replication" is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A "mutant" sequence is defined as a DNA, RNA or amino acid sequence differing from but having homology with the native or disclosed sequence. Depending on the particular sequence, the degree of homology (sequence identity) between the native or disclosed sequence and the mutant sequence is preferably greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) which is calculated as described above. As used herein, an "allelic variant" of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs at essentially the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions. (see, for example, U.S. Patent 5,753,235).

Antibodies

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An "antibody combining site" is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. "Antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanized antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying *Neisseria menB* proteins.

Antibodies elicited against the proteins of the present invention bind to antigenic polypeptides or proteins or protein fragments that are present and specifically associated with strains of *Neisseria meningitidis* menB. In some instances, these antigens may be associated with specific strains, such as those antigens specific for the menB strains. The antibodies of the invention may be immobilized to a matrix and utilized in an immunoassay or on an affinity chromatography column, to enable the detection and/or separation of polypeptides, proteins or protein fragments or cells comprising such polypeptides, proteins or protein fragments. Alternatively, such polypeptides, proteins or protein fragments may be immobilized so as to detect antibodies bindably specific thereto.

Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 µg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating at 4°C for 2-18 hours. The serum is recovered by centrifugation (e.g., 1,000g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the standard method of Kohler & Milstein (*Nature* (1975) 256:495-96), or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells that express membrane-bound immunoglobulin specific for the antigen bind to the plate, and

are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (e.g., hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for the production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either *in vitro* (e.g., in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly ^{32}P and ^{125}I), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example, ^{125}I may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with ^{125}I , or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

Antigens, immunogens, polypeptides, proteins or protein fragments of the present invention elicit formation of specific binding partner antibodies. These antigens, immunogens, polypeptides, proteins or protein fragments of the present invention comprise immunogenic compositions of the present invention. Such immunogenic compositions may further comprise or include adjuvants, carriers, or other compositions that promote or enhance

or stabilize the antigens, polypeptides, proteins or protein fragments of the present invention. Such adjuvants and carriers will be readily apparent to those of ordinary skill in the art.

Pharmaceutical Compositions

Pharmaceutical compositions can comprise (include) either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature, when given to a patient that is febrile. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgment of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of

organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal and transcutaneous applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Vaccines

Vaccines according to the invention may either be prophylactic (i.e., to prevent infection) or therapeutic (i.e., to treat disease after infection).

Such vaccines comprise immunizing antigen(s) or immunogen(s), immunogenic polypeptide, protein(s) or protein fragments, or nucleic acids (e.g., ribonucleic acid or deoxyribonucleic acid), usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or

liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the immunogen or antigen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (PCT Publ. No. WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalene, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) RibiTM adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (DetoxTM); (3) saponin adjuvants, such as StimulonTM (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (e.g., IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (e.g., gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc; (6) detoxified mutants of a bacterial ADP-ribosylating toxin such as a cholera toxin (CT), a pertussis toxin (PT), or an *E. coli* heat-labile toxin (LT), particularly LT-K63, LT-R72, CT-S109, PT-K9/G129; see, e.g., WO 93/13302 and WO 92/19265; and (7) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59 are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

The vaccine compositions comprising immunogenic compositions (e.g., which may include the antigen, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Alternatively, vaccine compositions comprising immunogenic compositions may comprise an antigen, polypeptide, protein, protein fragment or nucleic acid in a pharmaceutically acceptable carrier.

More specifically, vaccines comprising immunogenic compositions comprise an immunologically effective amount of the immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (e.g., nonhuman primate, primate, *etc.*), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

Typically, the vaccine compositions or immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

The immunogenic compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal and transcutaneous applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

As an alternative to protein-based vaccines, DNA vaccination may be employed (e.g., Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly *et al.* (1997) *Annu Rev Immunol* 15:617-648).

Gene Delivery Vehicles

Gene therapy vehicles for delivery of constructs, including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence *in vivo* can be either constitutive or regulated.

The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses e.g., MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines are made from human parent cells (e.g., HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC No. VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102,

WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (i.e., there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors comprising sequences of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ

described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC as accession numbers ATCC VR-977 and ATCC VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in U.S. Serial No. 08/405,627, filed March 15, 1995, WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, *Nature* 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human

immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus, for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Trinita virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No.08/240,030, filed May 9, 1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu &

Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed to transform a host cell. Exemplary naked DNA introduction methods are described in WO 90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in U.S. 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. 5,206,152 and WO92/11033.

Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP-0524968; and in Stryer, *Biochemistry*, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

Delivery Methods

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for expression of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hypodermic sprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in *eg.* WO93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Polynucleotide and polypeptide pharmaceutical compositions

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

A. Polypeptides

One example are polypeptides which include, without limitation: asialoglycoprotein (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF),

granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of plasmodium falciparum known as RII.

B.Hormones, Vitamins, Etc.

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

C.Polyalkylenes, Polysaccharides, etc.

Also, polyalkylene glycol can be included with the desired polynucleotides or polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

D.Lipids, and Liposomes

The desired polynucleotide or polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide or polypeptide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and

DOTAP/DOPE (Boehringer). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, eg. Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See eg. Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77; Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348; Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

E.Lipoproteins

In addition, lipoproteins can be included with the polynucleotide or polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been

isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C, and E, over time these lipoproteins lose A and acquire C and E apoproteins. VLDL comprises A, B, C, and E apoproteins, LDL comprises apoprotein B; and HDL comprises apoproteins A, C, and E.

The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) *Annu Rev. Biochem* 54:699; Law (1986) *Adv. Exp Med. Biol.* 151:162; Chen (1986) *J Biol Chem* 261:12918; Kane (1980) *Proc Natl Acad Sci USA* 77:2465; and Utermann (1984) *Hum Genet* 65:232.

Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol.* (*supra*); Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750.

Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443.

Lipoproteins can also be purchased from commercial suppliers, such as Biomedical Technologies, Inc., Stoughton, Massachusetts, USA.

Further description of lipoproteins can be found in Zuckermann et al., PCT. Appln. No. US97/14465.

F. Polycationic Agents

Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide or polypeptide to be delivered.

Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both in vitro, ex vivo, and in vivo applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, etc.

The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine, and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic acid condensing agents. Briefly, transcriptional factors such as C/CEBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

Organic polycationic agents include: spermine, spermidine, and putrescine.

The dimensions and of the physical properties of a polycationic agent can be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

Synthetic Polycationic Agents

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin[®], and lipofectAMINE[®] are monomers that form polycationic complexes when combined with polynucleotides or polypeptides.

Immunodiagnostic Assays

Neisserial antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisserial antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisserial proteins within biological samples, including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are

assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt solutions, *etc.*) required for the conduct of the assay, as well as suitable set of assay instructions.

Nucleic Acid Hybridisation

"Hybridization" refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor hydrogen bonding. Factors that affect this bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.* [*supra*] Volume 2, chapter 9, pages 9.47 to 9.57.

"Stringency" refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated T_m of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1 µg for a plasmid or phage digest to 10^{-9} to 10^{-8} g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting, hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes can be used. For example, a single-copy

yeast gene can be detected with an exposure time of only 1 hour starting with 1 μg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of 10^8 cpm/ μg . For a single-copy mammalian gene a conservative approach would start with 10 μg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than 10^8 cpm/ μg , resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature (T_m) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$T_m = 81 + 16.6(\log_{10} C_i) + 0.4[\%(G + C)] - 0.6(\%\text{formamide}) - 600/n - 1.5(\%\text{mismatch}).$$

where C_i is the salt concentration (monovalent ions) and n is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are 42°C for a probe which is 95% to 100% homologous to the target fragment, 37°C for 90% to 95% homology, and 32°C for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be

washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

Nucleic Acid Probe Assays

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

The nucleic acid probes will hybridize to the Neisserial nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native Neisserial sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the Neisserial sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisserial sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisserial sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisserial sequence in order to hybridize therewith and thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions, such as temperature, salt condition and the like. For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated *eg.* backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance *etc.* [*eg.* see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [*eg.* see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

One example of a nucleotide hybridization assay is described by Urdea *et al.* in international patent application WO92/02526 [see also US patent 5,124,246].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acids. The assay is described in: Mullis *et al.* [*Meth. Enzymol.* (1987) 155: 335-350]; US patent 4,683,195; and US patent 4,683,202. Two "primer" nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisserial sequence.

A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisserial sequence (or its complement).

Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al.* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes

containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

EXAMPLES

The examples describe nucleic acid sequences which have been identified in *N. meningitidis*, and *N. gonorrhoeae* along with their respective and putative translation products. Not all of the nucleic acid sequences are complete *ie.* they encode less than the full-length wild-type protein.

The examples are generally in the following format:

- a nucleotide sequence which has been identified in *N. meningitidis*
- the putative translation product of said *N. meningitidis* sequence
- a computer analysis of said translation product based on database comparisons
- a corresponding nucleotide sequence identified from *N. gonorrhoeae*
- the putative translation product of said *N. gonorrhoeae* sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a corresponding nucleotide sequence identified from strain A of *N. meningitidis*
- the putative translation product of said *N. meningitidis* strain A sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a description of the characteristics of the protein which indicates that it might be suitably antigenic or immunogenic.

Sequence comparisons were performed at NCBI (<http://www.ncbi.nlm.nih.gov>) using the algorithms BLAST, BLAST2, BLASTn, BLASTp, tBLASTn, BLASTx, & tBLASTx [eg. see also Altschul *et al.* (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25:2289-3402]. Searches were performed against the following databases: non-redundant GenBank+EMBL+DDBJ+PDB sequences and non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR sequences.

Dots within nucleotide sequences represent nucleotides which have been arbitrarily introduced in order to maintain a reading frame. In the same way, double-underlined nucleotides were removed. Lower case letters represent ambiguities which arose during

alignment of independent sequencing reactions (some of the nucleotide sequences in the examples are derived from combining the results of two or more experiments).

Nucleotide sequences were scanned in all six reading frames to predict the presence of hydrophobic domains using an algorithm based on the statistical studies of Esposti *et al.* [Critical evaluation of the hydropathy of membrane proteins (1990) *Eur J Biochem* 190:207-219]. These domains represent potential transmembrane regions or hydrophobic leader sequences.

Open reading frames were predicted from fragmented nucleotide sequences using the program ORFFINDER (NCBI).

Underlined amino acid sequences indicate possible transmembrane domains or leader sequences in the ORFs, as predicted by the PSORT algorithm (<http://www.psort.nibb.ac.jp>). Functional domains were also predicted using the MOTIFS program (GCG Wisconsin & PROSITE).

For each of the following examples: based on the presence of a putative leader sequence and/or several putative transmembrane domains (single-underlined) in the gonococcal protein, it is predicted that the proteins from *N. meningitidis* and *N. gonorrhoeae*, and their respective epitopes, could be useful antigens or immunogenic compositions for vaccines or diagnostics.

The standard techniques and procedures which may be employed in order to perform the invention (*e.g.* to utilize the disclosed sequences for vaccination or diagnostic purposes) were summarized above. This summary is not a limitation on the invention but, rather, gives examples that may be used, but are not required.

In particular, the following methods were used to express, purify and biochemically characterize the proteins of the invention.

Chromosomal DNA Preparation

N.meningitidis strain 2996 was grown to exponential phase in 100ml of GC medium, harvested by centrifugation, and resuspended in 5ml buffer (20%(w/v) Sucrose, 50mM Tris-HCl, 50mM EDTA, pH8). After 10 minutes incubation on ice, the bacteria were lysed by adding 10ml of lysis solution (50mM NaCl, 1% Na-Sarkosyl, 50µg/ml Proteinase K), and the suspension incubated at 37°C for 2 hours. Two phenol extractions (equilibrated to pH 8) and one CHCl₃/isoamylalcohol (24:1) extraction were performed. DNA was precipitated by addition of 0.3M sodium acetate and 2 volumes of ethanol, and collected by centrifugation.

The pellet was washed once with 70%(v/v) ethanol and redissolved in 4.0ml TE buffer (10mM Tris-HCl, 1mM EDTA, pH 8.0). The DNA concentration was measured by reading the OD at 260 nm.

Oligonucleotide design

Synthetic oligonucleotide primers were designed on the basis of the coding sequence of each ORF, using (a) the meningococcus B sequence when available, or (b) the gonococcus/meningococcus A sequence, adapted to the codon preference usage of meningococcus as necessary. Any predicted signal peptides were omitted, by designing the 5' primers to sequence immediately downstream from the predicted leader sequence.

For most ORFs, the 5' primers included two restriction enzyme recognition sites (*Bam*HI-*Nde*I, *Bam*HI-*Nhe*I, *Eco*RI-*Nde*I or *Eco*RI-*Nhe*I), depending on the restriction pattern of the gene of interest. The 3' primers included a *Xho*I or a *Hind*III restriction site (table 1). This procedure was established in order to direct the cloning of each amplification product (corresponding to each ORF) into two different expression systems: pGEX-KG (using *Bam*HI-*Xho*I, *Bam*HI-*Hind*III, *Eco*RI-*Xho*I or *Eco*RI-*Hind*III), and pET21b+ (using *Nde*I-*Xho*I, *Nhe*I-*Xho*I, *Nde*I-*Hind*III or *Nhe*I-*Hind*III).

5'-end primer tail:	<u>CGCGGATCCCATATG</u>	(<i>Bam</i> HI- <i>Nde</i> I)
	<u>CGCGGATCCGCTAGC</u>	(<i>Bam</i> HI- <i>Nhe</i> I)
	<u>CCGGAATTCTACATATG</u>	(<i>Eco</i> RI- <i>Nde</i> I)
	<u>CCGGAATTCTAGCTAGC</u>	(<i>Eco</i> RI- <i>Nhe</i> I)
3'-end primer tail:	<u>CCCGCTCGAG</u>	(<i>Xho</i> I)
	<u>CCCGCTCGAG</u>	(<i>Hind</i> III)

For cloning ORFs into the pGEX-His vector, the 5' and 3' primers contained only one restriction enzyme site (*Eco*RI, *Kpn*I or *Sal*I for the 5' primers and *Pst*I, *Xba*I, *Sph*I or *Sal*I for the 3' primers). Again restriction sites were chosen according to the particular restriction pattern of the gene (table 1).

5'-end primer tail:	(AAA) <u>AAAGAATTC</u>	(<i>Eco</i> RI)
	(AAA) <u>AAAGGTACC</u>	(<i>Kpn</i> I)
3'-end primer tail:	(AAA) <u>AAACTGCAG</u>	(<i>Pst</i> I)
	(AAA) <u>AAATCTAGA</u>	(<i>Xba</i> I)

5' or 3'-end primer tail: AAAGCATGC (*Sph*I)
AAAAAAGTCGAC (*Sal*I)

As well as containing the restriction enzyme recognition sequences, the primers included nucleotides which hybridized to the sequence to be amplified. The melting temperature depended on the number and type of hybridising nucleotides in the whole primer, and was determined for each primer using the formulae:

$$T_m = 4 (G+C) + 2 (A+T) \quad (\text{tail excluded})$$

$$T_m = 64.9 + 0.41 (\% \text{ GC}) - 600/N \quad (\text{whole primer})$$

The melting temperatures of the selected oligonucleotides were usually 65-70°C for the whole oligo and 50-55°C for the hybridising region alone.

Table 1 shows the forward and reverse primers used for each amplification. In certain cases, the sequence of the primer does not exactly match the sequence of the predicted ORF. This is because when initial amplifications were performed, the complete 5' and/or 3' sequences for some meningococcal B ORFs were not known. However the corresponding sequences had been identified in *Gonococcus* or in *Meningococcus A*. Hence, when the *Meningococcus B* sequence was incomplete or uncertain, *Gonococcal* or *Meningococcal A* sequences were used as the basis for primer design. These sequences were altered to take account of codon preference. It can be appreciated that, once the complete sequence is identified, this approach will no longer be necessary.

Oligonucleotides were synthesized using a Perkin Elmer 394 DNA/RNA Synthesizer, eluted from the columns in 2.0ml NH_4OH , and deprotected by 5 hours incubation at 56°C . The oligos were precipitated by addition of 0.3M Na-Acetate and 2 volumes ethanol. The samples were centrifuged and the pellets resuspended in either 100 μl or 1.0ml of water. The OD_{260} was determined using a Perkin Elmer Lambda Bio spectrophotometer and the concentration adjusted to 2-10pmol/ μl .

Amplification

The standard PCR protocol was as follows: 50-200ng of genomic DNA was used as a template in the presence of 20-40μM of each oligonucleotide primer, 400-800μM dNTPs solution, 1x PCR buffer (including 1.5mM MgCl₂), 2.5 units *TaqI* DNA polymerase (using

Perkin-Elmer AmpliTaq, GIBCO Platinum, Pwo DNA polymerase, or Tahara Shuzo Taq polymerase). In some cases, PCR was optimised by the addition of 10µl DMSO or 50µl 2M Betaine.

After a hot start (adding the polymerase during a preliminary 3 minute incubation of the whole mix at 95°C), each sample underwent a two-step amplification. The first 5 cycles were performed using the hybridization temperature that excluded the restriction enzyme tail of the primer (see above). This was followed by 30 cycles using the hybridization temperature calculated for the whole length oligos. The cycles were completed with a 10 minute extension step at 72°C. The standard cycles were as follows:

	Denaturation	Hybridisation	Elongation
First 5 cycles	30 seconds 95°C	30 seconds 50-55°C	30-60 seconds 72°C
Last 30 cycles	30 seconds 95°C	30 seconds 65-70°C	30-60 seconds 72°C

Elongation times varied according to the length of the ORF to be amplified. Amplifications were performed using either a 9600 or a 2400 Perkin Elmer GeneAmp PCR System. To check the results, 1/10 of the amplification volume was loaded onto a 1-1.5% (w/v) agarose gel and the size of each amplified fragment compared with a DNA molecular weight marker.

The amplified DNA was either loaded directly on a 1% agarose gel or first precipitated with ethanol and resuspended in a volume suitable to be loaded on a 1.0% agarose gel. The DNA fragment corresponding to the band of correct size was purified using the Qiagen Gel Extraction Kit, following the manufacturer's protocol. DNA fragments were eluted in a volume of 30µl or 50µl with either H₂O or 10mM Tris, pH 8.5.

Digestion of PCR fragments

The purified DNA corresponding to the amplified fragment was doubly-digested with the appropriate restriction enzymes for; cloning into pET-21b+ and expressing the protein as a C-terminus His-tagged fusion, for cloning into pGEX-KG and expressing the protein as a N-

terminus GST-fusion, and for cloning into pGEX-His and expressing the protein as a N-terminus GST-His tagged fusion.

Each purified DNA fragment was incubated at 37°C for 3 hours to overnight with 20 units of appropriate restriction enzyme (New England Biolabs) in a volume of either 30 or 40 µl in the presence of suitable digestion buffer. Digested fragments were purified using the QIAquick PCR purification kit (following the manufacturer's instructions) and eluted in a volume of 30 µl or 50 µl with either H₂O or 10mM Tris, pH 8.5. The DNA concentration was determined by quantitative agarose gel electrophoresis (1.0% gel) in the presence of a titrated molecular weight marker.

Digestion of the cloning vectors (pET22B, pGEX-KG, pTRC-His A, pET21b+, pGEX-KG, and pGEX-His)

The vector pGEX-His is a modified pGEX-2T vector carrying a region encoding six histidine residues upstream of the thrombin cleavage site and containing the multiple cloning site of the vector pTRC99 (Pharmacia). 10 µg plasmid was double-digested with 50 units of each restriction enzyme in 200 µl reaction volume in the presence of appropriate buffer by overnight incubation at 37°C. After loading the whole digestion on a 1% agarose gel, the band corresponding to the digested vector was purified from the gel using the Qiagen QIAquick Gel Extraction Kit and the DNA was eluted in 50 µl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD₂₆₀ of the sample, and adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

10 µg of plasmid vector was doubly-digested with 50 units of each restriction enzyme in a volume of 200 µl with the appropriate buffer overnight at 37°C. The digest was loaded onto a 1.0% agarose gel and the band corresponding to the digested vector purified using the Qiagen QIAquick Gel Extraction Kit. DNA was eluted in 50 µl of 10mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD_{260nm} and the concentration adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

Cloning

For some ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated in both pET22b and pGEX-KG. In a final volume of 20 µl, a molar

ratio of 3:1 fragment/vector was ligated using 0.5 µl of NEB T4 DNA ligase (400 units/µl), in the presence of the buffer supplied by the manufacturer. The reaction was incubated at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit", following the manufacturer's instructions.

In order to introduce the recombinant plasmid in a suitable strain, 100 µl *E. coli* DH5 competent cells were incubated with the ligase reaction solution for 40 minutes on ice, then at 37°C for 3 minutes, then, after adding 800 µl LB broth, again at 37°C for 20 minutes. The cells were then centrifuged at maximum speed in an Eppendorf microfuge and resuspended in approximately 200 µl of the supernatant. The suspension was then plated on LB ampicillin (100 mg/ml).

The screening of the recombinant clones was performed by growing 5 randomly-chosen colonies overnight at 37 °C in either 2 ml (pGEX or pTC clones) or 5ml (pET clones) LB broth + 100 µg/ml ampicillin. The cells were then pelleted and the DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions, to a final volume of 30 µl. 5 µl of each individual miniprep (approximately 1g) were digested with either *NdeI/XhoI* or *BamHI/XhoI* and the whole digestion loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1Kb DNA Ladder, GIBCO). The screening of the positive clones was made on the base of the correct insert size.

For other ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated into both pET21b+ and pGEX-KG. A molar ratio of of 3:1 fragment/vector was used in a final volume of 20µl, that included 0.5µl T4 DNA ligase (400 units/µl, NEB) and ligation buffer supplied by the manufacturer. The reaction was performed at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit" and the manufacturer's protocol.

Recombinant plasmid was transformed into 100µl of competent *E. coli* DH5 or HB101 by incubating the ligase reaction solution and bacteria for 40 minutes on ice then at 37°C for 3 minutes. This was followed by the addition of 800µl LB broth and incubation at 37°C for 20 minutes. The cells were centrifuged at maximum speed in an Eppendorf microfuge, resuspended in approximately 200µl of the supernatant and plated onto LB ampicillin (100mg/ml) agar.

Screening for recombinant clones was performed by growing 5 randomly selected colonies overnight at 37°C in either 2.0ml (pGEX-KG clones) or 5.0ml (pET clones) LB broth + 100µg/ml ampicillin. Cells were pelleted and plasmid DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions. Approximately 1µg of each individual miniprep was digested with the appropriate restriction enzymes and the digest loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1kb DNA Ladder, GIBCO). Positive clones were selected on the basis of the size of insert.

ORFs were cloned into PGEX-His, by doubly-digesting the PCR product and ligating into similarly digested vector. After cloning, recombinant plasmids were transformed into the *E.coli* host W3110. Individual clones were grown overnight at 37°C in LB broth with 50µg/ml ampicillin.

Certain ORFs may be cloned into the pGEX-HIS vector using *EcoRI-PstI* cloning sites, or *EcoRI-SalI*, or *SalI-PstI*. After cloning, the recombinant plasmids may be introduced in the *E.coli* host W3110.

Expression

Each ORF cloned into the expression vector may then be transformed into the strain suitable for expression of the recombinant protein product. 1 µl of each construct was used to transform 30 µl of *E.coli* BL21 (pGEX vector), *E.coli* TOP 10 (pTRC vector) or *E.coli* BL21-DE3 (pET vector), as described above. In the case of the pGEX-His vector, the same *E.coli* strain (W3110) was used for initial cloning and expression. Single recombinant colonies were inoculated into 2ml LB+Amp (100 µg/ml), incubated at 37°C overnight, then diluted 1:30 in 20 ml of LB+Amp (100 µg/ml) in 100 ml flasks, making sure that the OD₆₀₀ ranged between 0.1 and 0.15. The flasks were incubated at 30°C into gyratory water bath shakers until OD indicated exponential growth suitable for induction of expression (0.4-0.8 OD for pET and pTRC vectors; 0.8-1 OD for pGEX and pGEX-His vectors). For the pET, pTRC and pGEX-His vectors, the protein expression was induced by addition of 1mM IPTG, whereas in the case of pGEX system the final concentration of IPTG was 0.2 mM. After 3 hours incubation at 30°C, the final concentration of the sample was checked by OD. In order to check expression, 1ml of each sample was removed, centrifuged in a microfuge, the pellet

resuspended in PBS, and analysed by 12% SDS-PAGE with Coomassie Blue staining. The whole sample was centrifuged at 6000g and the pellet resuspended in PBS for further use.

GST-fusion proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on LB+Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600 ml of fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.8-1. Protein expression was induced with 0.2mM IPTG followed by three hours incubation. The culture was centrifuged at 8000 rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml cold PBS. The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia) (previously washed with PBS) and incubated at room temperature for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold PBS for 10 minutes, resuspended in 1ml cold PBS, and loaded on a disposable column. The resin was washed twice with 2ml cold PBS until the flow-through reached OD₂₈₀ of 0.02-0.06. The GST-fusion protein was eluted by addition of 700µl cold Glutathione elution buffer 10mM reduced glutathione, 50mM Tris-HCl) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel using either Biorad SDS-PAGE Molecular weight standard broad range (M1) (200, 116.25, 97.4, 66.2, 45, 31, 21.5, 14.4, 6.5 kDa) or Amersham Rainbow Marker (M^r) (220, 66, 46, 30, 21.5, 14.3 kDa) as standards. As the MW of GST is 26kDa, this value must be added to the MW of each GST-fusion protein.

For other ORFs, for each clone to be purified as a GST-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp. (100µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Recombinant protein expression was induced by addition of IPTG (final concentration 0.2mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml cold PBS. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia), previously equilibrated with PBS, and incubated at room temperature with gentle agitation for 30 min. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batchwise) with 10ml cold PBS for 10 min, resuspended in 1ml cold PBS, and loaded onto a disposable column. The resin continued to be washed with cold PBS, until the OD_{280nm} of the flow-through reached 0.02-0.01. The GST-fusion protein was eluted by addition of 700µl cold glutathione elution buffer (10mM reduced glutathione, 50mM Tris-HCl pH 8.0) and fractions collected, until the OD_{280nm} of the eluate indicated all the recombinant protein was obtained. 20µl aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. The molecular mass of the purified proteins was determined using either the Bio-Rad broad range molecular weight standard (M1) (200, 116, 97.4, 66.2, 45.0, 31.0, 21.5, 14.4, 6.5 kDa) or the Amersham Rainbow Marker (M2) (220, 66.2, 46.0, 30.0, 21.5, 14.3 kDa). The molecular weights of GST-fusion proteins are a combination of the 26 kDa GST protein and its fusion partner. Protein concentrations were estimated using the Bradford assay.

His-fusion soluble proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on a LB + Amp agar plate. The bacteria were inoculated into 20ml of LB+Amp liquid culture and incubated overnight in a water bath shaker. Bacteria were diluted 1:30 into 600ml fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000 rpm at 4°C, the supernatant was discarded and the bacterial pellet was resuspended in 7.5ml cold 10mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 10 mM imidazole, pH 8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with 10mM imidazole buffer) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold 10mM imidazole buffer for 10 minutes,

resuspended in 1ml cold 10mM imidazole buffer and loaded on a disposable column. The resin was washed at 4°C with 2ml cold 10mM imidazole buffer until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The resin was washed with 2ml cold 20mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 20 mM imidazole, pH 8) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl cold 250mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 250 mM imidazole, pH 8) and fractions collected until the O.D₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

His-fusion insoluble proteins large-scale purification.

A single colony was grown overnight at 37 °C on a LB + Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600ml fresh medium and let to grow at the optimal temperature (37°C) to O.D₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml buffer B (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed twice and centrifuged again. The supernatant was stored at -20°C, while the pellets were resuspended in 2 ml guanidine buffer (6M guanidine hydrochloride, 100mM phosphate buffer, 10 mM Tris-HCl, pH 7.5) and treated in a homogenizer for 10 cycles. The product was centrifuged at 13000 rpm for 40 minutes. The supernatant was mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with buffer B) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700 g for 5 minutes at 4°C. The resin was washed twice with 10 ml buffer B for 10 minutes, resuspended in 1ml buffer B, and loaded on a disposable column. The resin was washed at room temperature with 2ml buffer B until the flow-through reached the OD₂₈₀ of 0.02-0.06. The resin was washed with 2ml buffer C (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl elution buffer (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

Purification of His-fusion proteins.

For each clone to be purified as a His-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp (100 µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100 µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Expression of recombinant protein was induced by addition of IPTG (final concentration 1.0mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml of either (i) cold buffer A (300mM NaCl, 50mM phosphate buffer, 10mM imidazole, pH 8.0) for soluble proteins or (ii) buffer B (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8) for insoluble proteins. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. For insoluble proteins, pellets were resuspended in 2.0 ml buffer C (6M guanidine hydrochloride, 100mM phosphate buffer, 10mM Tris-HCl, pH 7.5) and treated with a Dounce homogenizer for 10 cycles. The homogenate was centrifuged at 13 000xg for 40 min and the supernatant retained.

Supernatants for both soluble and insoluble preparations were mixed with 150µl Ni²⁺-resin (previously equilibrated with either buffer A or buffer B, as appropriate) and incubated at room temperature with gentle agitation for 30 min. The resin was Chelating Sepharose Fast Flow (Pharmacia), prepared according to manufacturers protocol. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batch-wise) with 10ml buffer A or B for 10 min, resuspended in 1.0 ml buffer A or B and loaded onto a disposable column. The resin continued to be washed with either (i) buffer A at 4°C or (ii) buffer B at room temperature, until the OD_{280nm} of the flow-through reached 0.02-0.01. The resin was further washed with either (i) cold buffer C (300mM NaCl, 50mM phosphate buffer, 20mM imidazole, pH 8.0) or (ii) buffer D (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the the OD_{280nm} of the flow-through reached 0.02-0.01. The His-fusion protein was eluted by addition of 700µl of either (i) cold elution buffer A (300mM NaCl, 50mM phosphate buffer, 250mM imidazole, pH 8.0) or (ii) elution buffer B (8 M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions

collected until the $O.D_{280nm}$ indicated all the recombinant protein was obtained. 20 μ l aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. Protein concentrations were estimated using the Bradford assay.

His-fusion proteins renaturation

In the cases where denaturation was required to solubilize proteins, a renaturation step was employed prior to immunization. Glycerol was added to the denatured fractions obtained above to give a final concentration of 10%(v/v). The proteins were diluted to 200 μ g/ml using dialysis buffer I (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, 2.0M urea, pH 8.8) and dialysed against the same buffer for 12-14 hours at 4°C. Further dialysis was performed with buffer II (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Alternatively, 10% glycerol was added to the denatured proteins. The proteins were then diluted to 20 μ g/ml using dialysis buffer I (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, 2M urea, pH 8.8) and dialysed against the same buffer at 4°C for 12-14 hours. The protein was further dialysed against dialysis buffer II (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Protein concentration was evaluated using the formula:

$$\text{Protein (mg/ml)} = (1.55 \times OD_{280}) - (0.76 \times OD_{260})$$

Purification of proteins

To analyse the solubility, pellets obtained from 3.0ml cultures were resuspended in 500 μ l buffer M1 (PBS pH 7.2). 25 μ l of lysozyme (10mg/ml) was added and the bacteria incubated for 15 min at 4°C. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and the pellet resuspended in buffer M2 [8M urea, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] and incubated for 3 to 4 hours at 4°C. After centrifugation, the supernatant was collected and the pellet resuspended in buffer M3 [6M guanidinium-HCl, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] overnight at 4°C. The

supernatants from all steps were analysed by SDS-PAGE. Some proteins were found to be soluble in PBS, others need urea or guanidium-HCl for solubilization.

For preparative scale purifications, 500ml cultures were induced and fusion proteins solubilized in either buffer M1, M2 or M3 using the procedure described above. Crude extracts were loaded onto a Ni-NTA superflow column (Quiagen) equilibrated with buffer M1, M2 or M3 depending on the solubilization buffer employed. Unbound material was eluted by washing the column with the same buffer. The recombinant fusion protein was eluted with the corresponding buffer containing 500mM imidazole then dialysed against the same buffer in the absence of imidazole.

Mice immunisations

20µg of each purified protein are used to immunise mice intraperitoneally. In the case of some ORFs, Balb-C mice were immunised with Al(OH)₃ as adjuvant on days 1, 21 and 42, and immune response was monitored in samples taken on day 56. For other ORFs, CD1 mice could be immunised using the same protocol. For ORFs 25 and 40, CD1 mice were immunised using Freund's adjuvant, and the same immunisation protocol was used, except that the immune response was measured on day 42, rather than 56. Similarly, for still other ORFs, CD1 mice were immunised with Freund's adjuvant, but the immune response was measured on day 49. Alternatively, 20µg of each purified protein was mixed with Freund's adjuvant and used to immunise CD1 mice intraperitoneally. For many of the proteins, the immunization was performed on days 1, 21 and 35, and immune response was monitored in samples taken on days 34 and 49. For some proteins, the third immunization was performed on day 28, rather than 35, and the immune response was measured on days 20 and 42, rather than 34 and 49.

ELISA assay (sera analysis)

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 7ml of Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10000 rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated

for 2 hours at room temperature and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200 µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200 µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 90 minutes at 37°C. Wells were washed three times with PBT. 100 µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100 µl of substrate buffer for HRP (25 ml of citrate buffer pH5, 10 mg of O-phenildiamine and 10 µl of H₂O) were added to each well and the plates were left at room temperature for 20 minutes. 100 µl H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA was considered positive when OD₄₉₀ was 2.5 times the respective pre-immune sera.

Alternatively, The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10 000rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated for 1 hour at 37°C and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 100µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100µl of substrate buffer for HRP (25ml of citrate buffer pH5, 10mg of O-

phenildiamine and 10 μ l of H₂O₂) were added to each well and the plates were left at room temperature for 20 minutes. 100 μ l of 12.5% H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA titers were calculated arbitrarily as the dilution of sera which gave an OD₄₉₀ value of 0.4 above the level of preimmune sera. The ELISA was considered positive when the dilution of sera with OD₄₉₀ of 0.4 was higher than 1:400.

FACScan bacteria Binding Assay procedure.

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 4 tubes containing 8ml each Mueller-Hinton Broth (Difco) containing 0.25% glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.35-0.5. The culture was centrifuged for 10 minutes at 4000rpm. The supernatant was discarded and the pellet was resuspended in blocking buffer (1% BSA in PBS, 0.4% NaN₃) and centrifuged for 5 minutes at 4000rpm. Cells were resuspended in blocking buffer to reach OD₆₂₀ of 0.07. 100 μ l bacterial cells were added to each well of a Costar 96 well plate. 100 μ l of diluted (1:100, 1:200, 1:400) sera (in blocking buffer) were added to each well and plates incubated for 2 hours at 4°C. Cells were centrifuged for 5 minutes at 4000rpm, the supernatant aspirated and cells washed by addition of 200 μ l/well of blocking buffer in each well. 100 μ l of R-Phicoerytrin conjugated F(ab)₂ goat anti-mouse, diluted 1:100, was added to each well and plates incubated for 1 hour at 4°C. Cells were spun down by centrifugation at 4000rpm for 5 minutes and washed by addition of 200 μ l/well of blocking buffer. The supernatant was aspirated and cells resuspended in 200 μ l/well of PBS, 0.25% formaldehyde. Samples were transferred to FACScan tubes and read. The condition for FACScan (Laser Power 15mW) setting were: FL2 on; FSC-H threshold:92; FSC PMT Voltage: E 01; SSC PMT: 474; Amp. Gains 6.1; FL-2 PMT: 586; compensation values: 0.

OMV preparations

Bacteria were grown overnight on 5 GC plates, harvested with a loop and resuspended in 10 ml 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30 minutes and the bacteria disrupted by sonication for 10' on ice (50% duty cycle, 50% output). Unbroken cells were removed by centrifugation at 5000g for 10 minutes and the total cell envelope

fraction recovered by centrifugation at 50000g at 4°C for 75 minutes. To extract cytoplasmic membrane proteins from the crude outer membranes, the whole fraction was resuspended in 2% sarkosyl (Sigma) and incubated at room temperature for 20 minutes. The suspension was centrifuged at 10000g for 10 minutes to remove aggregates, and the supernatant further ultracentrifuged at 50000g for 75 minutes to pellet the outer membranes. The outer membranes were resuspended in 10mM Tris-HCl, pH8 and the protein concentration measured by the Bio-Rad Protein assay, using BSA as a standard.

Whole Extracts preparation

Bacteria were grown overnight on a GC plate, harvested with a loop and resuspended in 1ml of 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30' minutes.

Western blotting

Purified proteins (500ng/lane), outer membrane vesicles (5µg) and total cell extracts (25µg) derived from MenB strain 2996 were loaded onto a 12% SDS-polyacrylamide gel and transferred to a nitrocellulose membrane. The transfer was performed for 2 hours at 150mA at 4°C, using transfer buffer (0.3 % Tris base, 1.44 % glycine, 20% (v/v) methanol). The membrane was saturated by overnight incubation at 4°C in saturation buffer (10% skimmed milk, 0.1% Triton X100 in PBS). The membrane was washed twice with washing buffer (3% skimmed milk, 0.1% Triton X100 in PBS) and incubated for 2 hours at 37°C with mice sera diluted 1:200 in washing buffer. The membrane was washed twice and incubated for 90 minutes with a 1:2000 dilution of horseradish peroxidase labelled anti-mouse Ig. The membrane was washed twice with 0.1% Triton X100 in PBS and developed with the Opti-4CN Substrate Kit (Bio-Rad). The reaction was stopped by adding water.

Bactericidal assay

MC58 and 2996 strains were grown overnight at 37°C on chocolate agar plates. 5-7 colonies were collected and used to inoculate 7ml Mueller-Hinton broth. The suspension was incubated at 37°C on a nutator and let to grow until OD₆₂₀ was in between 0.5-0.8. The culture was aliquoted into sterile 1.5ml Eppendorf tubes and centrifuged for 20 minutes at maximum speed in a microfuge. The pellet was washed once in Gey's buffer (Gibco) and resuspended in the same buffer to an OD₆₂₀ of 0.5, diluted 1:20000 in Gey's buffer and stored at 25°C.

50µl of Gey's buffer/1% BSA was added to each well of a 96-well tissue culture plate. 25µl of diluted (1:100) mice sera (dilution buffer: Gey's buffer/0.2% BSA) were added to each well and the plate incubated at 4°C. 25µl of the previously described bacterial suspension were added to each well. 25µl of either heat-inactivated (56°C waterbath for 30 minutes) or normal baby rabbit complement were added to each well. Immediately after the addition of the baby rabbit complement, 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 0). The 96-well plate was incubated for 1 hour at 37°C with rotation and then 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 1). After overnight incubation the colonies corresponding to time 0 and time 1h were counted.

Gene Variability

The *ORF4* and *919* genes were amplified by PCR on chromosomal DNA extracted from various *Neisseria* strains (see list of strains). The following oligonucleotides used as PCR primers were designed in the upstream and downstream regions of the genes:

orf 4.1	(forward)	CGAATCCGGACGGCAGGACTC
orf 4.3	(reverse)	GGCAGGGAATGGCGGATTAAAG
919.1	(forward)	AAAATGCCTCTCCACGGCTG or CTGCGCCCTGTGTTAAAATCCCCT
919.6	(reverse)	CAAATAAGAAAGGAATTTTG or GGTATCGCAAACTTCGCCTTAATGCG

The PCR cycling conditions were:

1 cycle	2 min. at 94°
30 cycles	30 sec. at 94°
	30 sec. at ~ 54° or ~ 60° (in according to T _m of the primers)
	40 sec. at 72°
1 cycle	7 min. at 72°

The PCR products were purified from 1 % agarose gel and sequenced using the following primers:

orf 4.1 (forward)	CGAATCCGGACGGCAGGACTC
orf 4.2 (forward)	CGACCGCGCCTTTGGGACTG
orf 4.3 (reverse)	GGCAGGGAATGGCGGATTAAAG
orf 4.4 (reverse)	TCTTTGAGTTTGATCCAACC

- 919.1 (forward) AAAATGCCTCTCCACGGCTG or
CTGCGCCCTGTGTTAAAATCCCCCT
- 919.2 (forward) ATCCTTCCGCTCGGCTGCG
- 919.3 (forward) AAAACAGCGGCACAATCGAC
- 919.4 (forward) ATAAGGGCTACCTCAAATC
- 919.5 (forward) GCGCGTGGATTATTTTGGG
- 919.6 (reverse) CAAATAAGAAAGGAATTTTG or
GGTATCGCAAACTTCGCCTTAATGCG
- 919.7 (reverse) CCCAAGGTAATGTAGTGCCG
- 919.8 (reverse) TAAAAAAAGTTCGACAGGG
- 919.9 (reverse) CCGTCCGCCTGTCGTCGCCC
- 919.10 (reverse) TCGTTCCGGCGGGGTCGGGG

All documents cited herein are incorporated by reference in their entireties.

The following Examples are presented to illustrate, not limit, the invention

EXAMPLE 1

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 1: Oligonucleotides used for PCR for Examples 2-10

ORF	Primer	Sequence	Restriction sites
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT <SEQ ID 3021>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA <SEQ ID 3022>	XhoI
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA <SEQ ID 3023>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC <SEQ ID 3024>	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT <SEQ ID 3025>	BamHI-NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC <SEQ ID 3026>	XhoI
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC <SEQ ID 3027>	BamHI-NdeI
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG <SEQ ID 3028>	XhoI
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT <SEQ ID 3029>	BamHI-NdeI

128	Reverse	CCCGCTCGAG-ATAATAATATCCGCGCCC <SEQ ID 3030>	XhoI
	Forward	CGCGGATCCCATATG-ACTGACAACGCACT <SEQ ID 3031>	BamHI-NdeI
206	Reverse	CCCGCTCGAG-GACCGCGTTGTCGAAA <SEQ ID 3032>	XhoI
	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA <SEQ ID 3033>	BamHI-NdeI
287	Reverse	CCCGCTCGAG-TTCTGTAAAAAAGTATGTGC <SEQ ID 3034>	XhoI
	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG <SEQ ID 3035>	EcoRI-NheI
406	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTGCC <SEQ ID 3036>	XhoI
	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG <SEQ ID 3037>	BamHI-NdeI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG <SEQ ID 3038>	XhoI

Localization of the ORFs

The following DNA and amino acid sequences are identified by titles of the following form: [g, m, or a] [#].[seq or pep], where "g" means a sequence from *N. gonorrhoeae*, "m" means a sequence from *N. meningitidis B*, and "a" means a sequence from *N. meningitidis A*; "#" means the number of the sequence; "seq" means a DNA sequence, and "pep" means an amino acid sequence. For example, "g001.seq" refers to an *N. gonorrhoeae* DNA sequence, number 1. The presence of the suffix "-1" to these sequences indicates an additional sequence found for the same ORF, thus, data for an ORF having both an unsuffixed and a suffixed sequence designation applies to both such designated sequences. Further, open reading frames are identified as ORF #, where "#" means the number of the ORF, corresponding to the number of the sequence which encodes the ORF, and the ORF designations may be suffixed with ".ng" or ".a", indicating that the ORF corresponds to a *N. gonorrhoeae* sequence or a *N. meningitidis A* sequence, respectively. The word "partial" before a sequence indicates that the sequence may be a partial or a complete ORF. Computer analysis was performed for the comparisons that follow between "g", "m", and "a" peptide sequences; and therein the "pep" suffix is implied where not expressly stated. Further, in the event of a conflict between the text immediately preceding and describing which sequences are being compared, and the

279 gnm4.seq

m279.seq

m279.pep

g279.seq

g279.pcp

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

m279.pep ITRICGCLISTVFRASASLSAAGFIRLOWEGTDTGSGRARLAPASLAAMARPTAAALPA
:
g279 MTRICGCLISTVLVSASLSAAGFIRLOWEGTDTGSGRARLAPASLAAMVRPTAAALPA


```

              70          80          90          100          110          120
m279.pep      ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA
               ||||||| | : ||||| :: ||||||| ||||||| ||||||| |||||||
g279           ITTCPGELKLTASTTSPCADSAQICLTCSSSKPKMAAIAPTPCGTADCISSARRRTSLTA
               70          80          90          100          110          120

              130          140          150
m279.pep      SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX
               ||| ||| ||||| : |||
g279           SAKSNSAATSAVYSPRLCPATAAGVLPPTSKX
               130          140          150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3043>:

a279.seq

1	ATGACNCNGA	TTTGC GGCTG	CTTGATTTC A	ACGGTTTNN A	GGGCTTCGGC
51	GAGTTTGT CG	GCGGCGGGTT	TCATGAGGCT	GCAATGGGAA	GGTACNGACA
101	CN GG CAGCGG	CAGGGCGCGT	TTGGCGCCGG	CTTCTTTGGC	GGCAAGCATA
151	GCGCGCTAG A	CGGCGGCGGC	ATTGCGCTGC A	ATCACGACTT	GTCCGGGCGCA
201	GTTGAAGTTG	ACGGCTTCAA	CCACTTCATC	CTGTGCGGAT	TCGGCGCAAA
251	TTTGTTTTAC	CTGTTCATCT	TCCAAGCCGA	GAATCGCCGC	CATTGCGCCC
301	ACGCCTTGCG	GTACGGCGGA	CTGCATCAGT	TCGGCGCGCA	NGCGCACGAG
351	TTTGACCGCG	TCGGCAAAAT	CCAATGCGCC	GGCGGCAACN	AGTGCGGTGT
401	ATTGCGCCGAN	GCTGTGTCCG	GCAACGGCGG	CAGGCGTTTT	GCCGCCCGCT
451	TCCGAATAG				

This corresponds to the amino acid sequence <SEQ ID 3044; ORF 279.a>:

```
a279.pcp.
1 MTXICGCLIS TVXRASASLS AAGFMRLQWE GTDTGSGRAR LAPASLAASI
51 ARSTAAALPA IITCPGELKL TASTTSSCAD SAQICFTCSS SKPRIAAIAP
101 TPCGTADCIS SARXRTSLTA SAKSNAPAAAT SAVYSPXLCP ATAAGVLPPA
151 SE*
```

m279/a279 ORFs 279 and 279.a showed a 88.2% identity in 152 aa overlap

```

      10          20          30          40          50          60
m279.pep    ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRRARLAPASLAAMARPTAAALPA
              :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a279         MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRRARLAPASLAASIARSTAAALPA
              10          20          30          40          50          60

      70          80          90          100         110         120
m279.pep    ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA
              || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a279         ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARXRTLTA
              70          80          90          100         110         120

      130         140         150
m279.pep    SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX
              || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a279         SAKSNAPAATSAVYSPXLCFATAAGVLPPASEX
              130         140         150

```

519 and 519-1 gnm7.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 3045>:

```
m519.seq (partial)
1 ..TCCGTATCG GCGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
51 AATCAACAGT ACTGTTGTG CCGCTTTGGA CGAGGCGGCC GGGgCTTgGG
101 GTGTGAAGGT TTTGCGTTAT GAGATTAAG ACTTGGTCCG GCCGCAAGAA
151 ATCCTTCGCT CAATGCAGCG GCAAATACT AGCTAACCGC AAAAACGGCA
201 CCGTATCGCC GAATCCGAAG GTCGTAAAT CGAACAAATC AACCTTGCCC
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```

251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCGGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTGCGCGAC ATCGGCAGCC
551 TGATTTCTGC CCGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3046; ORF 519>:

```

m519.pep (partial)
  1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
 51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLASGQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLLISAGMK IIDSSKTAK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3047>:

```

g519.seq
  1 atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggcttcaa
 51 atcctttgtc gtcattcccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatctt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc cttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgcttc atacggttcg
301 agcaactaca ttatggcaat taccagctt gccaaacga cgtgcttc
351 cgttatcggt cgatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgccgg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttcgca cgaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
651 ggtcaatgcg tccaatgccg agaaaatcgc cgcgcatcaac cgcgcaaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgccgccct tcaaacccaa agcggggcgg atgcgggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaagg ttgccgaaat cgggaaccct
901 aattttcggc ggcatgaaaa attttcgccg gaagcaaaaa cggccaaata
951 a

```

This corresponds to the amino acid sequence <SEQ ID 3048; ORF 519.ng>:

```

g519.pep
  1 MEFFIILLAA VAVFGFKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAEN
251 RQIAAALQTQ SGADAVNLKI AGQYVTAFAK LAKEDNTRIK PAKVAEIGNP
301 NFRHEKFSF EAKTAK*

```

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

m519/g519

```

                                10      20      30
m519.pep                      SVIGRMELDKTFEERDEINSTVVAALDEAA
                                |||
g519                          YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
                                90      100     110     120     130     140
                                40      50      60      70      80      90
m519.pep                      GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE

```

```
a519.seq
1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51 ATCCTTTGTT GTCATCCCAC AGCAGGAAGT CCACGTTGTC GAAAGCGCTG
101 GGCCTTTCCA TCGCGCCCTG ACCGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTTCGCT AAGAAATATC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTT
351 CGTTATCGGG CGTATCGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCGGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCGCG CGCAAGAAAT
501 CCTTCGCTCA ATCGAGGCGC AAATTACTGC TGAACCGCAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGTT CGTAAATATCG AACAAATCAA CCTTGCCAGT
601 GGTGAGCGCG AAGCCGAATC CCAACAATCC GAAGCGGAGC CTTAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATG CCGCGGCCCT TCAAACCCAA GCGGTCGCGG ATGCGGTCAA
801 TCTGAAGATT CGGGAACAAT ACGTCGCGCG GTTCAACAAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCGGCCAATG TTCCGACATG CGGCACCGTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAACCG CCAAATAA
```

```
a519.pep
  1  MEFFFIILLAA VVVFGEKFSV VIPQOEHVHV ERLGRFHRAL TAGLNILIPF
 51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLAISYGS
101  SNYIMATITQL AQTTLRISVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151  VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201  GOREAEIQQS EGEAAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251  RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLM PANVADIGSL
301  ISAGMKIIS SKTAK*
```

```

                                     10      20      30
m519.pep                          SVIGRMELDKTFFEERDEINSTVVAALDEAA
                                     |||||
a519      YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFFEERDEINSTVVSALDEAA
              90      100      110      120      130      140

              40      50      60      70      80      90
m519.pep    GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
              |||||
a519      GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
              150      160      170      180      190      200

              100      110      120      130      140      150

```

```

m519.pep      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTGGADAV
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a519          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTGGADAV
                210      220      230      240      250      260

                160      170      180      190      200
m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
a519          NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                270      280      290      300      310

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3051>:

```

m519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
101 GGC GTTTCCA TCGCGCCCTG ACGGcCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC TGTGTTGCG GCTTGGACG AGGCGGCCGG GGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3052; ORF 519-1>:

```

m519-1.
1  MEFFIILLVA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51 IDR VAYRHS LKEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPK LASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3053>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51 ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGC GTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGGCCCT TCAAACCCAA GGCGGGGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG

```

851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 3054; ORF 519-1.ng>:

g519-1.pep
1 MEFFIILLAA VAVFGFKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

m519-1/g519-1 ORFs 519-1 and 519-1.ng showed a 99.0% identity in 315 aa overlap

g519-1.pep	10	20	30	40	50	60
	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	70	80	90	100	110	120
	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	130	140	150	160	170	180
	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE					
	130	140	150	160	170	180
g519-1.pep	190	200	210	220	230	240
	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	250	260	270	280	290	300
	LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
g519-1.pep	310					
	ISAGMKIIDS SKTAKX					
m519-1	ISAGMKIIDS SKTAKX					
	310					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3055>:

a519-1.seq
1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCCTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAA

```

401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGC AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATG CCGCCGCCCT TCAAACCAA GCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3056; ORF 519-1.a>:

a519-1.pep.

```

1  MEFFIILLAA VVVFQKSFV VIPOQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLSYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 ORFs 519-1 and 519-1.a showed a 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
a519-1.pep	MEFFIILLAAVVVFQKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSI					
m519-1	MEFFIILLVAVAVVFQKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSI					
	10	20	30	40	50	60
a519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLSYGSNNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLSYGSNNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
a519-1.pep	RMELDKTFEERDEINSTVVSALDEAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
a519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
a519-1.pep	LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
a519-1.pep	ISAGMKIIDSSKTAKX					
m519-1	ISAGMKIIDSSKTAKX					
	310					
	310					

576 and 576-1 gnm22.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3057>:

```
m576.seq.. (partial)
1   ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
51  GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
151 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301 CTGCAATACA AAATCACCAG ACAGGGCGAA GGCAAACAGC CGACCAAGA
351 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
451 GTGATTCCGG GTTGGACCGA AGCGTACAG CTTCTGAAAG AAGGCGGCCG
501 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551 GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651 CATCAAAAAA GTAAATTAA
```

This corresponds to the amino acid sequence <SEQ ID 3058; ORF 576>:

```
m576.pep.. (partial)
1   ..MQQASYAMGV DIGRSLKOMK EQGAEIDLKV FTEAMQAVYD GKEIKMTTEEQ
51  AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFVDKLV
201 KIGAPENAPA KQPAQVDIKK VN*
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3059>:

```
g576.seq.. (partial)
1   ..atggcgctgg acatcgagcg ctccttgaaa caaatgaagg aacaggcgcg
51  ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttctgacagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccc
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcggtt ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcgcccgcgc caccttccct ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcgg cgaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactgggtc aaatcgggcg acccgaaaac
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa
```

This corresponds to the amino acid sequence <SEQ ID 3060; ORF 576.ng>:

```
g576.pep.. (partial)
1   ..MGVDIGRSLK QMKEQGAIED LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51  FLQEQQAKAV EKHKADAKAN KEKGAEFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKNV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 ORFs 576 and 576.ng showed a 97.2% identity in 215 aa overlap

```

              10      20      30      40      50      60
m576.pep      MQQASYAMGV DIGRSLKOMKEQGAIEDLKV FTEAMQAVYD GKEIKMTTEEQAQEVMMKFLQ
              |||

```

```

g576          MGVDIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQ
                10      20      30      40      50

                70      80      90      100     110     120
m576.pep      EQQAKAVEKHKADAKANKEKGEAFLKENAAKDGVKTTASGLQYKITKQEGEGKQPTKDDIV
                |||||:|||||
g576          EQQAKAVEKHKADAKANKEKGEAFLKENAAEDGVKTTASGLQYKITKQEGEGKQPTKDDIV
                60      70      80      90      100     110

                130     140     150     160     170     180
m576.pep      TVEYEGRLIDGTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE
                |||||:|||||
g576          TVEYEGRLIDGTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE
                120     130     140     150     160     170

                190     200     210     220
m576.pep      QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN
                |||:|||||
g576          QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN
                180     190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3061>:

```

a576.seq
1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCG CCGCTTTGGC
51  ACTTTCGCC TCGGCGAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCG TTCTTCGCG CAGGGCGACA CCTCTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC  CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3062; ORF 576.a>:

```

a576.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

m576/a576 ORFs 576 and 576.a showed a 99.5% identity in 222 aa overlap

```

                10      20      30
m576.pep      MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                |||||
a576          CGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                30      40      50      60      70      80

                40      50      60      70      80      90
m576.pep      FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
                |||||
a576          FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
                90      100     110     120     130     140

```


	100	110	120	130	140	150
m576.pep	KDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ					
a576	KDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ					
	150	160	170	180	190	200
	160	170	180	190	200	210
m576.pep	VIPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA					
a576	VILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA					
	210	220	230	240	250	260
	220					
m576.pep	KQPAQVDIKKVN					
a576	KQPAQVDIKKVN					
	270					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3063>:

m576-1.seq

1	ATGAACACCA	TTTTCAAAAT	CAGCGCACTG	ACCCTTTCCG	CCGCTTTGGC
51	ACTTTCGCC	TGCGGCAAAA	AAGAAGCCGC	CCCCGCATCT	GCATCCGAAC
101	CTGCCGCCGC	TTCTTCGCCG	CAGGGCGACA	CCTCTTCGAT	CGGCAGCACG
151	ATGCAGCAGG	CAAGCTATGC	GATGGGCGTG	GACATCGGAC	GCTCCCTGAA
201	GCAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGAAG
251	CCATGCAGGC	AGTGTATGAC	GGCAAAGAAA	TCAAAATGAC	CGAAGAGCAG
301	GCTCAGGAAG	TCATGATGAA	ATTCTTCAG	GAACAACAGG	CTAAAGCCGT
351	AGAAAAACAC	AAGGCGGACG	CGAAGGCCAA	TAAAGAAAAA	GGCGAAGCCT
401	TTCTGAAAGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCGGGC
451	CTGCAATACA	AAATCACCAA	ACAGGGCGAA	GGCAAACAGC	CGACCAAGA
501	CGACATCGTT	ACCGTGAAT	ACGAAGGCCG	CCTGATTGAC	GGTACGGTAT
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCCCGG	TCACCTTCCC	TTTGAGCCAA
601	GTGATTCCGG	GTTGGACCGA	AGGCGTACAG	CTTCTGAAAG	AAGGCGGCGA
651	AGCCACGTTT	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCGG
701	GCGACAAAAT	CGGTCGGAAC	GCCACTTTGG	TATTTGATGT	GAAACTGGTC
751	AAAATCGGCG	CACCCGAAAA	CGCGCCCGCC	AAGCAGCCGG	CTCAAGTCGA
801	CATCAAAAAA	GTAAATTAA			

This corresponds to the amino acid sequence <SEQ ID 3064; ORF 576-1>:

m576-1.pep

1	MNTIFKISAL	TLAALALSA	CGKKEAAPAS	ASEPAAASSA	QGDTSIGST
51	MQQASYAMGV	DIGRSLQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ
101	AQEVMMKFLQ	EQQAKAVEKH	KADAKANKEK	GEAFLKENAA	KDGVKTTASG
151	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID	GTVFDSSKAN	GGPVTFFLSQ
201	VIPGWTEGVQ	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN	ATLVFDVKLV
251	KIGAPENAPA	KQPAQVDIKK	VN*		

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3065>:

g576-1.seq

1	ATGAACACCA	TTTTCAAAAT	CAGCGCACTG	ACCCTTTCCG	CCGCTTTGGC
51	ACTTTCGCC	TGCGGCAAAA	AAGAAGCCGC	CCCCGCATCT	GCATCCGAAC
101	CTGCCGCCGC	TTCTGCCCGC	CAGGGCGACA	CCTCTTCAAT	CGGCAGCACG
151	ATGCAGCAGG	CAAGCTATGC	AATGGGCGTG	GACATCGGAC	GCTCCCTGAA
201	ACAAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGATG
251	CCATGCAGGC	AGTGTATGAC	GGCAAAGAAA	TCAAAATGAC	CGAAGAGCAG
301	GCCCAGGAAG	TGATGATGAA	ATTCTGCAG	GAGCAGCAGG	CTAAAGCCGT
351	AGAAAAACAC	AAGGCGGATG	CGAAGGCCAA	CAAAGAAAAA	GGCGAAGCCT
401	TCCTGAAGGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCGGGT
451	CTGCAGTACA	AAATCACCAA	ACAGGGTGAA	GGCAAACAGC	CGACAAAAGA
501	CGACATCGTT	ACCGTGAAT	ACGAAGGCCG	CCTGATTGAC	GGTACCGTAT
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCCCGG	CCACCTTCCC	TTTGAGCCAA
601	GTGATTCCGG	GTTGGACCGA	AGGCGTACGG	CTTCTGAAAG	AAGGCGGCGA
651	AGCCACGTTT	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCGG

701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3066; ORF 576-1.ng>:

g576-1.pep

1 MNTIFKISAL TISAALALSA CGKKEAPAS ASEPAASAA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLO EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LQYKITQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
 201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPDQVDIKK VN*

g576-1/m576-1 ORFs 576-1 and 576-1.ng showed a 97.8% identity in 272 aa overlap

g576-1.pep	10	20	30	40	50	60
	MNTIFKISALTISAALALSACGKKEAPASASEPAASAAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTISAALALSACGKKEAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
g576-1.pep	70	80	90	100	110	120
	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLOEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLOEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	130	140	150	160	170	180
	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKOPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKOPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	190	200	210	220	230	240
	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
g576-1.pep	250	260	270			
	ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3067>:

a576-1.seq

1 ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
 51 ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCAGCATCT GCATCCGAAC
 101 CTGCCGCCGC TTCTTCCGCG CAGGCGGACA CCTCTTCGAT CGGCAGCAGC
 151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
 201 GCAAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTTACCGAAG
 251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
 301 GCTCAGGAAG TCATGATGAA ATTCTTCAG GAACAACAGG CTAAAGCCGT
 351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
 401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
 451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAGA
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
 551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTGAGCCAA
 601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCCA
 651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG

701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3068; ORF 576-1.a>:

a576-1.pep

1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPAQVDIKK VN*

a576-1/m576-1 ORFs: 576-1 and 576-1.a showed a 99.6% identity in 272 aa overlap

a576-1.pep	10	20	30	40	50	60
	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
a576-1.pep	70	80	90	100	110	120
	DIGRSLKQMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	130	140	150	160	170	180
	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	190	200	210	220	230	240
	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	250	260	270			
	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

919 gnm43.seq

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3069>:

m919.seq

1 ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TACGGCATCG CCGCCGCCAT
 51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
 101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
 151 GGAACGACGG TCGGCGCGCG CGGGGCCGTC TATACCGTTG TACCGCACCT
 201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
 251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
 301 TCGGCCCAAG CCTTTCAAAC CCGCGTCCAT TCCTTTCAGG CAAAACAGTT
 351 TTTTGAACGC TATTTACGCG CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
 401 CCGGTACGGT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGACAGG

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451 CGGACGGCAC AAGCCCGCTT CCGGATTTAC GGTATTCCCG ACGATTTTAT
501 CTCGCTCCCC CTGCCTGCGG GTTTCGCGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCcG ATTCCCcATC ACCGCGCGCA CAACAGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTTACGCC
751 GAAGACCTTG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCyTA CGTTTCCATC GGACGCTATA TGGCGGATAA GGGCTACCTC
901 AAACCTCGGAC AAACCTCCAT GCAGGGCATT AAGTCTTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGGAAG AGCAATGACG GCCCTGTCCG CGCACTGGGC
1051 ACGCCGCTGA TGGGGGAATA TGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGTGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGCAGGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTC CTACCCAACG
1301 GTATGAAGCC CGAATACCGc CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3070; ORF 919>:

m919.pep

```

1 MKKYLFRAL YGIAAAILAA COSKSIQTFP QPDTSVINGP DRPVGIPDPA
51 GTTVGGGGAV YTVVPHLSLP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFOAQOFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGGDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSRFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGSRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KSYMQRNPQR LAEVLGQNPS YIFFRELAYS SNGDPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3071>:

g919.seq

```

1 ATGAAAAAAC ACCTGCTCCG CTCGCCCTG TACGGcatCG CCGCCgccAT
51 CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 TTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAAGC CTGCAATCCT
251 TCCGCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGC cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtacggt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCGGATTTAC GGTATTCCCG ACGATTTTAT
501 CTCGCTCCCC CTGCCTGCGG GTTTCGCGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACCGCCG ACCTCTCCCG ATTCCCcATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCgcgcTT GACGGCAAag cccCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTTCATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAACCCcg tccggcaaat acatCCGCAT cggaTaccgc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctata TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGcatc aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGGAAG GGCATGAGG GCCCGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GCGCAGGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 3072; ORF 919.ng>:

```

g919.pep
  1 MKKHLLRSAL YGIAAAAILAA CQSRSIQTFF QPDTSVINGP DRPAGIPDPA
 51 GTTVAGGGAV YTVVPHLSMP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGPVAGLG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

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ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*:

m919/g919

m919.pep	10	20	30	40	50	60
	MKKYLFRAALYGIAAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
g919	MKKHLLRSALYGIAAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	10	20	30	40	50	60
m919.pep	70	80	90	100	110	120
	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFOAKQFFER					
g919	YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFOAKRFFER					
	70	80	90	100	110	120
m919.pep	130	140	150	160	170	180
	YFTPWQVAGNAGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIIPDDFISVPLPAGLRSGKA					
g919	YFTPWQVAGNAGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
m919.pep	190	200	210	220	230	240
	LVRIRQTGKNSGTIDNTGGTHTADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL					
g919	LVRIRQTGKNSGTIDNAGGTHADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL					
	190	200	210	220	230	240
m919.pep	250	260	270	280	290	300
	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
g919	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
	250	260	270	280	290	300
m919.pep	310	320	330	340	350	360
	KLGQTSMQGIKSYMQRNPQR LAEVLGQNPSYIIFRELAYSNDGPVAGLGTPLMGEYAGA					
g919	KLGQTSMQGIKAYMRQNPQR LAEVLGQNPSYIIFRELAYSNDGPVAGLGTPLMGEYAGA					
	310	320	330	340	350	360
m919.pep	370	380	390	400	410	420
	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420

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                430      440
m919.pep      QKTTGYVWQLLPNGMKPEYRPX
                |||||
g919          QKTTGYVWQLLPNGMKPEYRPX
                430      440

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3073>:

```

a919.seq
1   ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGGCGGCGG .CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGGCCCAAG CCTTTCAAAC CCCCGTCCAT TCCGTTCAAG CAAAACAGTT
351 TTTTGAACGC TATTTACGCG CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACGCGCG ACCTCTCCCA ATTCCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGTT ACCCGCAAAG
1151 CCCTCAACCG CCGTATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 CCGGTGCGCG TGGATTATT TTTGGGATAC GCGGACGAAG CCGCGCAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3074; ORF 919.a>:

```

a919.pep
1   MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51  GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFR LGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMQQNPR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

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m919/a919 ORFs 919 and 919.a showed a 98.6% identity in 441 aa overlap

```

                10      20      30      40      50      60
m919.pep      MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
                |||||
a919          MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
                10      20      30      40      50      60

                70      80      90      100     110     120
m919.pep      YTVVPHLSLPHWAAQDFAKSLQSFR LGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
                |||||
a919          YTVVPHLSLPHWAAQDFAKSLQSFR LGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
                70      80      90      100     110     120

```

m919.pep	130	140	150	160	170	180
	YFTPWQVAGNGSLAGTVTGYE	PVLKGD	DRRTAQARFPIYGIPDDFISV	PLPAGLRSGKA		
a919	YFTPWQVAGNGSLAGTVTGYE	PVLKGD	DRRTAQARFPIYGIPDDFISV	PLPAGLRSGKA		
m919.pep	190	200	210	220	230	240
	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
a919	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
m919.pep	250	260	270	280	290	300
	DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
a919	DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
m919.pep	310	320	330	340	350	360
	KLQGTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFREL	AGSSNDGPV	GALGTPLMGEYAGA			
a919	KLQGTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFREL	AGSSNDGPV	GALGTPLMGEYAGA			
m919.pep	370	380	390	400	410	420
	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
a919	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
m919.pep	430	440				
	QKTTGYVWQLLPNGMKPEYRPX					
a919	QKTTGYVWQLLPNGMKPEYRPX					

121 and 121-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3075>:

m121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCAGCG CTTTACCCCG TACCCCGGCA GGTACGCCG CCAATTGCTG
151 GATTTGCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCGGCTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxCAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACGCCACCC TAAAAGCAGG GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGC GA CGCGTCTCA CACGACGCG
851 CAGATGCCCC TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA

```

This corresponds to the amino acid sequence <SEQ ID 3076; ORF 121>:

```

1 METQLYIGIM SGTSMGDGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL Axxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx
151 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLRSF TAQTVCDAVS HAAADAROMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYY*

```

g121.seq

1	ATGGAACAC	AGCTTTACAT	CGGCATTATG	TCGGGAACCA	GTATGGACGG
51	GGCGGATGCC	GTGCTGGTAC	GGATGGACGG	CGGCAATGG	CTGGGCGCGG
101	AAGGGCAGC	CTTTACCCCC	TACCTGACG	GGTTGCGCCG	CAAAATTGCTG
151	GATTTGCAGC	ACACAGGCAC	AGACGAATG	CACCGCAGCA	GGATGTTGTC
201	GCAAGAACTC	AGCGCGCTGT	ACCGCGAAAC	CGCGCGCGAA	TGCTGTGTCGA
251	GTCAAAACCT	CGCTCCGTGC	GACATTACCG	CCCTCGGCTG	CCACGGGCAA
301	ACCGTCCGAC	ACGCGCGCGA	ACACGGTtac	AGCATACAGC	TTGCCGATTT
351	GCCGCTGCTG	CGGGAAGTCa	cgcgacatttT	TACCGTCgcg	gaccttcCGCA
401	GCCGCGACCT	TGCTGCCGCG	GgagaaAGGTg	GCGCGCTGCT	gacccGCCTTT
451	CACGAAGCCC	TGTTCCGCGA	TGACAGGGAA	ACACGCGTGG	TACTGAACAT
501	CGGCGGGATT	GCCAACATCA	GCGTACTCCC	CCCCGGCGCA	CCCGCCTTCG
551	GCTTCGACAC	AGGGCCGGGC	AATATGCTGA	TGGAcgcgtg	gacgcagggca
601	cacTGGcagc	TGCTTTACGA	CAAAAacggt	gcAAAGcgcg	cacAAGGCAA
651	catatTGCcg	CAACTGCTCG	cgaggctTGT	CGCCaccCG	TATTTCTCAC
701	AACCCcacc	aaAAAGCAGC	GGgcGCGaac	TgtttgcccT	AAattggctc
751	gaaacctAcc	ttgacgycgg	cgaaaaccga	tacgacgtat	tgcggacgct
801	ttcccgatcc	accgcgcaaa	cgtTttggga	cgccgtctca	CACGCAGCGG
851	CAGATGCCCC	TCAATGTAC	ATTTGCGCGC	GCGGCATCCG	CAATCTGTTT
901	TTAATGGCGG	ATTTGGCAGA	ATGTTTCCGC	ACACCGTTTT	CTCGTCACAG
951	CACGCGCGAA	CTGAACCTCG	ATCCTCAATG	GGTGGAGGCG	gccgCATTTg
1001	cgtggttggC	GGCGTGTGG	ATTAACGCA	TCCCGGTAG	TCCGCACAAA
1051	GCGACCGCG	CATCCAAACC	GTGTATTCTG	GCGCGGGAT	ATTATTATTG
1101	A				

g121.pap

1	METQLYIGIM	SGTSMGDGADA	VLVRMDGGKW	LGAEGHAFTP	YPDRLRRKLL
51	DIQDTGTDEL	HRSRMLSQEL	SRLYAQTAAE	LLCSQNLAPE	DITAGLCHGQ
101	TVRHAPHEGY	SIQLADLPLL	AELTRIFTVP	DFRSRDLAAG	GQAGPLVPAF
151	HEALFRDDRE	TRVVNLIGGI	ANISVLPPGA	PAFGDTGPGP	NMLMDAWTQA
201	HWQLPYDKNG	AKAAQGNILP	QLLGRLLAHP	YFSQPHPKST	GRELFALNWL
251	ETYLDGGENR	YDVLRITLSRF	TAQTVWDAYS	HAAADARQMY	ICGGGTRNPV
301	LMADLAECFG	TRVSLHSTAE	LNLDPOWVEA	AAFAWLAAACW	INRIPGSPHK
351	ATGASKPCIL	GAGVSY*			

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDGADAVLIRMDGKKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGDGADAVLVRMDGKKWLGAEGHAFTPYPDRLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPFL					


```

g121      HRSRMLSQELSRLYAQTAELLCSQNLAPCDITALGCHGQTVRHAPEHGYSTQLADLPLL
           70      80      90      100      110      120
           130     140     150     160     170     180
m121.pep  AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
           | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      AELTRIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRVVLNIGGIANISVLPPGA
           130     140     150     160     170     180
           190     200     210     220     230     240
m121.pep  XXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFSQPHPKST
           190     200     210     220     230     240
           250     260     270     280     290     300
m121.pep  GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDASHAAADARQMYICDGGIRNPV
           | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDASHAAADARQMYICGGGIRNPV
           250     260     270     280     290     300
           310     320     330     340     350     360
m121.pep  LMADLAECFGTRVSLHSTADLNLDPOWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
           | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      LMADLAECFGTRVSLHSTAE LNLDPOWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
           310     320     330     340     350     360

m121.pep  XAGYYYYX
           | : : : :
g121      GAGYYYYX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3079>:

```

a121.seq
1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCAGCG CTTTACCCCG TACCCCGGCA GGTACGCGG CAAATGTGCTG
151 GATTTGCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCGGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCGCGACCT TCGCGCCGGC GGACAAGGCG CGCCGCTCGT CCGCGCTTT
451 CACGAAGCCC TGTTCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCGGACGCA CCGCCTTCG
551 GCTTCGACAC AGGACCGGCG AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACCACCCC TAAAAGCAGG GGGCGGAAC TGTTCGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGATTG ACCGCGCAA CCGTTTTCGA CGCCGTCTCA CACGACGCG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACGCGCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCC
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCG CATCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3080; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEHGAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAEL LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWMOA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV

```

301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AFAWMAACW VNRIPGSPHK
 351 ATGASKPCIL GAGYYY*

m121/a121 ORFs 121 and 121.a showed a 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMDGADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
a121	METQLYIGIMSGTSMDGADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAELCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
a121	HRSRMLSQELSRLYAQTAELCSQNLAPSDITALGCHGQTVRHAPEHSYSVQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121.pep	XX					
a121	AERTQIFTVGDFRSRDLAAGGQAPLVPAPFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
a121	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICDGGIRNFV					
a121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFVDAVSHAAADARQMYICGGGIRNFV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
a121	LMADLAECFGTRVSLHSTAE LNLDPQWVEA AFAWMAACWVNRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYY					
a121	GAGYYYY					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3081>:

m121-1.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CCAATTGCTG
151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTGTG
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CGCGGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGGCGCGGC GGACAAGGCG CGCCACTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCGCGCA CAACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGCCTTCG
551 GCTTCGACAC AGGCGCGGCG AATATGCTGA TGGACGCGTG GACGCAGGCA
601 CACTGGCAGC TTCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCGG TATTTGCGAC
701 AACCCACCC TAAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGCAGCGG

```

```

851 CAGATGCCCC TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTG
1001 CGTGGTTGGC GGCCTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3082; ORF 121-1>:

```

m121-1.pep
  1 METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRQQL
  51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
 101 TVRHAPEHGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPAF
 151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWTQA
 201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
 251 ETYLDGGENR YDVLRLTSRF TAQTVCDAYS HAAADARQMY ICGGGIRNPV
 301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
 351 ATGASKPCIL XAGYYY*

```

m121-1/g121 ORFs 121-1 and 121.ng showed a 95.6% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTYPGRLLRQQLDLQDTGADEL					
g121	METQLYIGIMSGTSMGADAVLVRMDGGKWLGAEGHAFTYPDRLLRKLDDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAAELLCSONLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
g121	HRSRILSQELSRLYAQTAAELLCSONLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTRIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDNRETRAVLNIGGIANISVLPPDA					
g121	AELTRIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
g121	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRLTSRFTAQTVCDAYS HAAADARQMYICGGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRLTSRFTAQTVWDAYS HAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m121-1.pep	LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
g121	LMADLAECFGTRVSLHSTAE LNLDPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
	XAGYYYX					
m121-1.pep						
	GAGYYYX					
g121						

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3083>:

```

a121-1.seq
  1 ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG

```

```

51  GCGGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CAAATTGCTG
151 GATTTGCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTGAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGGCGCGGC GGACAAGGCG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCCGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCCGAC
701 AACCCACCC TAAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGATTC ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGACGGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3084; ORF 121-1.a>:

a121-1.pep

```

1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPESY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121-1/a121-1 ORFs 121-1 and 121-1.a showed a 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMGADAVLIRMDGGKW LGAEGHAFTPYPGRLLRRQLDLQDTGADEL					
a121-1	METQLYIGIMSGTSMGADAVLIRMDGGKW LGAEGHAFTPYPGRLLRRKLLDLQDTGADEL					
	10	20	30	40	50	60
m121-1.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEGYSIQLADLPLL					
a121-1	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPESYSVQLADLPLL					
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEGYSIQLADLPLL					
a121-1	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPESYSVQLADLPLL					
	70	80	90	100	110	120
m121-1.pep	AERTRIFTVGDFRSRDLAAGGQAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA					
a121-1	AERTQIFTVGDFRSRDLAAGGQAPLVPFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
m121-1.pep	AERTRIFTVGDFRSRDLAAGGQAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA					
a121-1	AERTQIFTVGDFRSRDLAAGGQAPLVPFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
m121-1.pep	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
a121-1	PAFGFDTPGPNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
m121-1.pep	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
a121-1	PAFGFDTPGPNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVASHAAADARQMYICGGGIRNPV					
a121-1	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFVASHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVASHAAADARQMYICGGGIRNPV					
a121-1	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFVASHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

	310	320	330	340	350	360
m121-1.pep	LMADLAECFGRVSLHSTADLNLDPOQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
a121	LMADLAECFGRVSLHSTAE LNLDPOQWVEAAAFWMAACWVNRI PGSPHKATGASKPCIL					
	310	320	330	340	350	360

m121-1.pep	XAGYYYY
a121	GAGYYYY

128 and 128-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3085>:

m128.seq (partial)

```

1 ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51 AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCGGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTGC AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTGT
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CGCACAAAA AACCAAATC AACCAC
1 TACGCCAGCG AAAAATGCG CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51 wGTCAAAAAA TAYTTCCCYG TCGGCAAwGT ATTAACCGGA CTGTTCGCCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCGTC
151 TGGCACAAG ACGTGCCTA TtkTGAATTG CAACAAAACG GCGAaMCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CCGCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTAKa ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAAAT TTCGTTTGGG AATACAATGT CTTGGCACA mTGTCAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAAA ACTTCCAAsG CGGCATGTT yTsGTCCGGC AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAACTGGCA ACAGGTTTTA GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCCGCCCG AATACAACCG CTTGCGCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCGGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAAATCC TTCAAAGCCT TCCGCGGCCG CGAACCAGAC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 3086; ORF 128>:

m128.pep (partial)

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51 NTVEPLTGIT ERVGRIWGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQTKL NH
//
1 YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGFTEKTVPV
51 WHKDVRYXEL QONGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFSDGTL
101 QLPTAYLVCN FAPPVGGREA RLSHDEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFQXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQVQL DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT
301 GKRFWQEILA VGXSRSGAES FKAFRGREPS IDALLRHS GF DNAV*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3087>:

```

g128.seq
1  atgattgaca acgCactgct ccacttgggc gaagaaccCC GTTTTaatca
51  aatccaaacc gaagACatca AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCT CCGCACAAAA AACCAAGCTC GATCACGACC
401 TCGCGGATTT CGTATTGAGC GCGCGGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGCGATT CCCGAAGACG CGCTCGCCAT GTTTGCGCGC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCAA CATCGACCGC ACCTCGAAA ACGCATTGAA
801 AACCGccaaa CTGCTCGGCT TAAAAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAAAATGCG GGACACGCCC GAACAGGTTT TAACTTCCT GCACGACCTC
901 GCCGCGCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCCG GAACACCTCG GTCTCGCCGA CCCGCAGCCG TGGGACTTGA
1001 GTACGCGCG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTTCTGGCAG GCCTGTTTCG
1101 CCAAATCAAA AAACCTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCC
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAA CCGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGActaca AAGGCCGCGC CCGCTTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAGAAG CGCGTTAAG CCACGACGAA ATCCTCACCC TCTTCCACGA
1401 AacCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGGCAT CAacggcgta GAATGGGACG CGGTGGAAT GCCCAGCCAG
1501 TTTATGGAAA ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCCCG
1551 CCACGAAGAA AccgGCGAGC CCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TcgcCGCCAA AAACCTCCAG CGCGGTATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TCGATATGAT GATTTACAGT GAAAGCGACG AATGCCGTCT
1701 GAAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAAGAA GTcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 GCcggcGGCT ATTCGCGAGG CTATTACAGC TACGCATGGG CCGAAGTCCt
1851 cAGCACCGAT GCCTACGCCG CTTTGAAGA AAGcGCGac gtcGCCGCA
1901 CAGGCAAACG CTTCTGGCAA GAAAtccttg ccgtcggcgg ctcCCGCAGC
1951 gcgGCGGAAT CCTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTGCTGCGC CAaagcggtT TCGACAACGC gGcttgA

```

This corresponds to the amino acid sequence <SEQ ID 3088; ORF 128.ng>:

```

g128.pep
1  MIDNALLHLG EEPFNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTGWA
51  NTVERLTGIT ERVGRWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLLQLPTAY LVCNFAPFVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLKNW QQVLDVRKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAAFEESDD VAATGKRWFQ EILAVGGSRS

```

651 AAESFKAERG REPSIDALLR QSGFDNAA*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng)
from *N. gonorrhoeae*:

m128/g128

```

      10      20      30      40      50      60
g128.pep  MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m128      MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIAKAQHTGWANTVEPLTGIT
          10      20      30      40      50      60

      70      80      90     100     110     120
g128.pep  ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m128      ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90     100     110     120

      130     140     150     160     170     180
g128.pep  TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALQTEGAQLSAKFSQNVLDATDAFGIY
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m128      TLSPAQKTKLNH
          130
          //

                                340     350     360
g128.pep  YAGEKLREAKYAFSETEVKKYFPVGKVLG
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m128      YASEKLREAKYAFSETXVKKYFPVGXVLNG
                                10      20      30

      370     380     390     400     410     420
g128.pep  LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWMNDYK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m128      LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWMNDYK
          40      50      60      70      80      90

      430     440     450     460     470     480
g128.pep  GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVDELGV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m128      GRRRFSGDTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVDELGV
          100     110     120     130     140     150

      490     500     510     520     530     540
g128.pep  SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAANKNFORGMF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m128      SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKKLAANKNFQXGMF
          160     170     180     190     200     210

      550     560     570     580     590     600
g128.pep  LVRQMEFALFDMMIYSESDCRLKNWQQVLDVSRKEVAVIQPPEYNRFANSFGHIFAGGY
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m128      XVRQXEFALFDMMIYSEDEGRKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIFAGGY
          220     230     240     250     260     270

      610     620     630     640     650     660
g128.pep  SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAERGREGS
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m128      SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRGAESFKAERGREGS
          280     290     300     310     320     330
```

```

          670      679
g128.pep  IDALLRQSGFDNAAAX
          |||||:|||||:
m128      IDALLRHSGFDNAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3089>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTACG CGACACGCCC GAACTGCGCG
251 CCGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCAAGATC
401 TCGCGGATTT CGTCCTCAGC GCGCGGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 CGCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGCG GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCGCGCGCGG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GTACGCGCG CGAAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTTCG
1101 CCAAAATCAA AACTCTACG GCATCGGATT TACCGAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCTAC CTCTCTGCA ACTTACCCCC GCCCGTTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCAGTCAG
1501 TTTATGGAAA ATTTCTGTTG GGAATACAAT GTCTTGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATCTCAA CGCGGAATGT TCCTCGTCCG CCAATGGAG
1651 TCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCGCTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CTTTGAAGA AAGCGACGAT GTCGCGGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGGA CGCGAACC GAATAGACGC
2001 ACTCTTGCGC CACAGCGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3090; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51  NTVPELTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDAAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME

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551 FALFDMMIYS EDDEGRKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
 601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
 651 AAESFKAFRG REPSIDALLR HSGFDNAA*

m128/a128 ORFs 128 and 128.a showed a 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIAQHTGTWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIAQHTGTWANTVEPLTGIT					
	10	20	30	40	50	60
m128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNCVADTFELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIWGVVSHLNSVTDTFELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
m128.pep	130					
	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLLENALQTAKLIGFKNYAELSLATKMDTPEQVLNFLHDL					
	250	260	270	280	290	300
m128.pep						140
						YASEKLREAKYAFSETXVKKYFPVGX
a128						ARRAKPYAEKDIAEVKAFARESLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGK
	310	320	330	340	350	360
m128.pep	160	170	180	190	200	210
	VLNGLFAQKKLYGIGFTEKTPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFPVVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFO					
a128	ELGVSGINGVEWDVAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAANKFO					
	490	500	510	520	530	540
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGRKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGRKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF					
	550	560	570	580	590	600

m128-1.seq

This corresponds to the amino acid sequence <SEO ID 3092: ORF 128-1>:

m128-1.pwp.

1 MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTWA
51 NTVEPLTGIT ERVGRINGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI

```

101  GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151  ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201  AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251  KFDNTANIDR TLANALQTAK LLGFKNYAEL SLATKMATDP EQVLNLFHDL
301  ARRAKPYAEK DLAEVKAFAR ESINLADLQP WDLGYASEKL REAKYAFSET
351  EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401  IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLQLPTAY LVCNFAPPVG
451  GREARLSHDE ILILFHETGH GLHLLTQVD ELGVSGINGV EWDARELPSQ
501  FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551  FALFDMMIYS EDDEGRLLKNW QQVLDLVRK VAVIQPPEYN RFALSFGHIF
601  AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651  AAESFKAFRG REPSIDALLR HSGFDNAV*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3093>:

g128-1.seq (partial)

```

1  ATGATTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51  AATCAAAACC GAAGACATCA AATCCGCGCT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCGGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTGCA ACCTTTTCCC CCGCACAAAA AACCAAGCTC GATCAGCACC
401 TGCGCGATTT CGTATTGAGC GGCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCGCG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGATTGAA
801 AACC GCCAAA CTGCTCGGCT TAAAAATTA CGCCGAATTG TCCTGGCAA
851 CCAAATGGC GGACACGCCC GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCCGCGCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCCG GAACACCTCG GTCTCGCCGA CCCGCAGCCG TGGGACTTGA
1001 GCTACGCCCG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTTCTGGCAG GCCTGTTCCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCAAAACC
1201 ATCGCGCGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACCGGCGCG
1251 CGCGTGGATG AACGACTACA AAGGCCGCGC CCGCTTTGCC GACGGCACGC
1301 TGCAACTGCC CACCGCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCCGC
1351 GGCAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACC TCTTCCACGA
1401 AACCGGCCAC GGAATGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGCCGGCAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 3094; ORF 128-1.ng>:

g128-1.pep (partial)

```

1  MIDNALLHLG EEPFRNQIKT EDIKPAVQTA IAEARGQIAA VKAQHTGTWA
51  NTVERLTGIT ERVGRIVGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKTYGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMATDP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPOP WDLGYASEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTQLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV K

```

m128-1/g128-1 ORFs 128-1 and 128-1.ng showed a 94.5% identity in 491 aa overlap

10 20 30 40 50 60

100

g128-1.pep	MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGTWANTVERLTGIT
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT
	10 20 30 40 50 60
g128-1.pep	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
m128-1	ERVGRIWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
	70 80 90 100 110 120
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
g128-1.pep	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAQSESKGTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
	190 200 210 220 230 240
g128-1.pep	TRASELSNDGKFDNTANIDRTLLENALKTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
	250 260 270 280 290 300
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADPQPWDL SYAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTFHETGHLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHLHLLTQVD
	430 440 450 460 470 480
g128-1.pep	ELGVSGINGVK
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3095>:

a128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTGGGCG GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTGC AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTC
201 GGGCGTGTTG TCGCACCTCA ACTCCGTCAC CGACACGCCC GAACTGCGCG
251 CCGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAACTC AACCACGATC
401 TGC GCGATT CGTCTCAGC GGCGCGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCG CCAAATCTC

```

```

501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCCTG TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCCGA CAACCGCAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAAC TA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCCCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCCG
1101 CCAATCAAAA AAATCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCGC CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCTTAC CTGCTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAT ATTTCTGTTG GGAATACAAT GTCTTGGCGC AAATGTCCG
1551 CCACGAAGAA ACCGCGGTTT CCTGCGCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATCTCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TCGCCCTCT TGTATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCGCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCGC CCTTTGAAGA AAGCGACGAT GTCGCGCCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3096; ORF 128-1.a>:

a128-1.pep

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWAA
51 NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GDIELYNRF KTIKNSPEFD TLSHAQTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTA LLGFKNYAEL SLATKMDATP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLPQ WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKQVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDVAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAANKFQ RGMFLVRQME
551 FALFDMMIYS EDEGRLLKNW QOVLDVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAFAEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*

```

m128-1/a128-1 ORFs 128-1 and 128-1.a showed a 97.8% identity in 677 aa overlap

```

          10      20      30      40      50      60
a128-1.pep MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
|||||
m128-1 MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90     100     110     120
a128-1.pep ERVGRWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
|||||:|||||:|||||
m128-1 ERVGRWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90     100     110     120

        130      140      150      160      170      180

```

a128-1.pep	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
a128-1.pep	190 200 210 220 230 240
	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLRREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLRREQIYRAYV
	190 200 210 220 230 240
a128-1.pep	250 260 270 280 290 300
	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
	250 260 270 280 290 300
a128-1.pep	310 320 330 340 350 360
	ARRAKPYAEKDLAEVKAFARESLGLADLQPWDLG YAGEKLR EAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLQPWDLG YASEKLR EAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
a128-1.pep	370 380 390 400 410 420
	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
a128-1.pep	430 440 450 460 470 480
	NDYKGRRRFSDGTLQLPTAYLVCNFTFPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAFPVGGREARLSHDEILILFHETGHGLHLLTQVD
	430 440 450 460 470 480
a128-1.pep	490 500 510 520 530 540
	ELGVSGINGVEWDAVELPSQFMENFWWEYNVLAQMSAHEETGVPLPKE LFDKMLAAKNFQ
m128-1	ELGVSGINGVEWDAVELPSQFMENFWWEYNVLAQMSAHEETGVPLPKE LFDKMLAAKNFQ
	490 500 510 520 530 540
a128-1.pep	550 560 570 580 590 600
	RGMFLVRQMEFALFDMMIYSEDDEGR LKNWQQV LDSVRKEVAVVRPPE YNRFANSFGHIF
m128-1	RGMFLVRQMEFALFDMMIYSEDDEGR LKNWQQV LDSVRKKVAVIQPPE YNRFALSFGHIF
	550 560 570 580 590 600
a128-1.pep	610 620 630 640 650 660
	AGGYSAGYYSYAWAEVLSADAYA AFEESDDVAATGKRFWQEILAVGGS RSAAESFKA FRG
m128-1	AGGYSAGYYSYAWAEVLSADAYA AFEESDDVAATGKRFWQEILAVGGS RSAAESFKA FRG
	610 620 630 640 650 660
a128-1.pep	670 679
	REPSIDALLRHSGFDNAAX
m128-1	REPSIDALLRHSGFDNAVX
	670

```

1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAATCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GGCAGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAT AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCCGCGACA TGGCGGCGGC AAGCCGsAAA ATCCCGGAcA GCCGcYTCAA
351 GGCCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGTACTCAC
401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 3098; ORF 206>:

m206.pep..

```

1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT
101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3099>:

g206.seq

```

1  atgttttccc cgcacaaaac ctttttcctc tgtctcggcg cactgctcct
51  cgcctcatgc ggcacgacct cgggcaaaca cggccaacgg aaacccaaac
101 agacagtccg gcaaattcaa gccgtccgca tcagccacat cggcgcgaca
151 caaggctcgc aggaactcat gctccacagc ctcggactca tcggcacgcc
201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcggca
251 tgattcaatt ggttacaaa aacgccctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atccccgaca gccgctcaa
351 ggccggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgaat tcatccatgc ccccggcagc
451 ggcaaaacca tcaaaaccga aaaactctcc acaccgtttt acgccaaaaa
501 ctaccttgga gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 3100; ORF 206.ng>:

g206.pep

```

1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPRT
101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
g206	MFSPDKTLFLCLGALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS					
	10	20	30	40	50	60
m206.pep	LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT ARDMAAASRK IPDSRXKAGD					
g206	LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPRT ARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLS TPFYAKNYLG AHTFFTE					
g206	IVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLS TPFYAKNYLG AHTFFTE					
	130	140	150	160	170	

130 140 150 160 170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3101>:

```
a206.seq
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCCGACA GCCGCCTTAA
351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAACCA TCAAACCGA AAAACTCTCC ACACCGTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 3102; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 ORFs 206 and 206.a showed a 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRKIPDSRXKAGD					
a206	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRKIPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLS TPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLS TPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

287

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3103>:

```
m287.seq
1  ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTTC CCCTTTCAGC
51  CTGCGGGGGC GCGGGTGGCG GATCGCCCGA TGTCAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTCTCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCCG AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCGG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCCGCA GCGGGGCAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCCGGTT
551 CTTTACATCC CATCCCCGCG TCAAACCCTG CACCTGCGAA TGGCGGTAGC
```



```

601 AATTTTGAA GGGTTGATT GGCTAATGGC GTTTGTATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGGA TGAAGAAGTA CAGCTAAAT CAGAATTTGA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCGGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCCGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGCAAG
1201 TTGCGCGCAA AAGTCGATTT CCGCAGCAAA TCTGTGGACG GCATTATCGA
1251 CAGCGCGGAT GATTGTCATA TGGGTACGCA AAAATTCAA GCCGCCATCG
1301 ATGGAAACGG CTTTAAGGGG ACTTGGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCCG ACAGATGCGG AAAAGGGCGG ATTCGGCGTG TTGCGCGCA
1451 AAAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 3104; ORF 287>:

m287.pep

```

1 MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAK
51 EDAPQAGSQ QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMAANA
151 DGMQDDPSA GGQAGNTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFRVRLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRS
301 ARSRRSLPAE MPLIPVNOAD TLIVDGEAVS LTGHSGNIFA PEGNYRYLTY
351 GAEKLPFGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMGTKQKFK AALDNGGFKG TWTENGSGDV
451 SGKFGYPAGE EVAGKYSYRP TDAEKGFGV FAGKKEQD*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3105>:

g287.seq

```

1 atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51 ctgtgggggc ggcgggtggc gatcgcccga tgtcaagtcg gcggacacgc
101 cgtcaaaacc ggcgcggccc gttgttgctg aaaatgccgg ggaaggggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgcgcgaagc
201 cgatacgag gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 ttccggcaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaaa atgccgcgca
351 atccgcaaat caaacaggga acaaccaacc cgcgggttct tcagattccg
401 ccccgcgctc aaacctgcc cctgcgaatg gcggtagcga ttttggaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaatataac
501 ttgacccac tgtaaaggcg attcttgtaa ttgtgataat ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaagcgat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaacc acctactcgt tctgcacggt cgaggaggtc gttccgggcc
751 gagattccgc tgattcccgt caatcaggcc gatacgctga ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcgatcg
901 tatgcctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttggttg
951 cacggccgtg tacaacggcg aagtgtgca tttccatag gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccg caaaagtcga ttccggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatggaag cggctttaag gggacttgga
1151 cggaatgg cggggggat gtttccgga ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattcggc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 3106; ORF 287.ng>:

g287.pep

```

1 MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV

```

```

51 LPKEKKDEEA AGGAPQADTQ DATAGEGSQD MAAVSAENTG NGGAATTDNP
101 KNEDAGAQND MPQNAESAN QTGNNQFAGS SDSAPASNPA PANGGSDFGFR
151 TNVGNVSVVID GPSQNTLTH CKGDSCNGDN LLDEEAPSKS EFEKLSDEEK
201 IKRYKKDEQR ENFVGLVADR VKKDGTNKYI IFYTDKPPTR SARSRRSLPA
251 EIPLIPVNQA DTLIVDGEAV SLTGHSNIF APEGNYRYLT YGAEKLPFGS
301 YALRVQGEPA KGEMLVGTAV YNGEVLHFHM ENGRFPYPSGG RFAAKVDFGS
351 KSVDDGIIDSG DDLHMGTKF KAAIDGNGFK GTWTENGGGD VSGRFYGPAG
401 EEVAGKYSYR PTDAEKGFGF VFAGKKDRD*

```

m287/g287 ORFs 287 and 287.ng showed a 70.1% identity in 499 aa overlap

```

m287.pep      10      20      30      40      49
               MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSE-----KETEA
g287          10      20      30      40      50      60
               MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPEKKKDEEA

m287.pep      50      60      70      80      90      100      109
               KEDAPQAGSQGQAGPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT
g287          70      80      90      100      110
               AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDAGAQNMPQNAA--

m287.pep      110      120      130      140      150      160      169
               DSSTPNHTPDNMLAGNMENQATDAGESSQPANQPDMANAADGMQDDPSAGGQNAGNTA
g287          -----

m287.pep      170      180      190      200      210      220      229
               AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNTLTHCKGDS
g287          120      130      140      150      160      170
               -ESANQTGNNQFAGSSDSAPASNPAPANGGSDFGRTNVGNVSVVIDGPSQNTLTHCKGDS

m287.pep      230      240      250      260      270      280      289
               CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP
g287          180      190      200      210      220      230
               CNGDNLLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVKKDGTNKYIIFYTD

m287.pep      290      300      310      320      330      340      349
               KPTSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLT
g287          240      250      260      270      280      290
               KPPT-----RSARSRRSLPAEIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLT

m287.pep      350      360      370      380      390      400      409
               YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGS
g287          300      310      320      330      340      350
               YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFPAKVDVFGS

m287.pep      410      420      430      440      450      460      469
               KSVDDGIIDSGDDLHMGTKFKAADGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYR
g287          360      370      380      390      400      410
               KSVDDGIIDSGDDLHMGTKFKAADGNGFKGTWTENGGGDVSGRFYGPAGEEVAGKYSYR

m287.pep      470      480      489
               PTDAEKGFGFVFAGKKEQDX

```

g287

|||||:|
PTDAEKGFGVAGKKDRDX
420 430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3107>:

a287.seq

```

1 ATGTTTAAAC GCAGTGTGAT TGCAATGGCT TGTATTGTTG CCCTTTCAGC
51 CTGTGGGGGC GGCGGTGGCG GATCGCCGA TGTAAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTACTG AAGATGTCGG GGAAGAGGTG
151 CTGCCGAAAG AAAAGAAAGA TGAGGAGGCG GTGAGTGGTG CGCCGCAAGC
201 CGATACGCAG GACGCAACCG CCGGAAAAGG CGGTCAAGAT ATGGCGGCAG
251 TTTCGGCAGA AAATACAGGC AATGGCGGTG CGGCAACAAC GGATAATCCC
301 GAAAATAAAG ACGAGGGACC GCAAAATGAT ATGCCGCAA ATGCCGCCGA
351 TACAGATAGT TCGACACCGA ATCACACCCC TGCACCGAAT ATGCCAACCA
401 GAGATATGGG AAACCAAGCA CCGGATGCCG GGAATCGGC ACAACCGGCA
451 AACCAACCGG ATATGGCAA TGCGGCGGAC GGAATGCAGG GGGACGATCC
501 GTCGGCAGG GAAAATGCCG GCAATACGGC AGATCAAGCT GCAAATCAAG
551 CTGAAACAA TCAAGTCGGC GGCTCTCAA ATCTGCCTC TTCAACCAAT
601 CCTAACGCCA CGAATGGCGG CAGCGATTTT GGAAGGATAA ATGTAGCTAA
651 TGGCATCAAG CTGACAGCG GTTCGAAAA TGTAACGTTG ACACATTGTA
701 AAGACAAAGT ATGCGATAGA GATTCTTAG ATGAAGAAGC ACCACCAAAA
751 TCAGAATTG AAAAATTAAG TGATGAAGAA AAAATTAATA AATATAAAAA
801 AGACGAGCAA CGAGAGAATT TTGTCGGTTT GGTGCTGAC AGGGTAGAAA
851 AGAATGGAAC TAACAAATAT GTCATCATT ATAAAGACAA GTCCGCTTCA
901 TCTTCATCTG CCGGATTCAG GCGTCTGCA CGGTCGAGGC GGTGCGTTCC
951 GGCCGAGATG CCGCTGATTC CCGTCAATCA GCGGATACG CTGATTGTCG
1001 ATGGGGAAGC GGTACGCTG ACGGGGCATT CCGGCAATAT CTTCGCGCCC
1051 GAAGGGAATT ACCGGTATCT GACTTACGGG GCGGAAAAAT TGTCCGCGCG
1101 ATCGTATGCC CTCAGTGTGC AAGGCGAACC GGCAAAAGGC GAAATGCTTG
1151 CGGGCACGGC CGTGACAAAC GGCGAAGTGC TGCATTTCCTA TATGAAAAAC
1201 GGCGTCCGT CCGCTCCCG AGGCAGGTTT CCGGCAAAAG TCGATTTCGG
1251 GACCAAATCT GTGGACGGCA TTATCGACAG CGGCGATGAT TTGCATATGG
1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGGCTT TAAGGGGACT
1351 TGGACGAAA ATGGCGGCGG GGATGTTTCC GGAAGGTTT ACGCCCGGC
1401 CGGCGAAGAA GTGGCGGGA AATACAGCTA TCGCCCGACA GATGCGGAAA
1451 AGGGCGGATT CCGCGTGTTC GCCGCAAAA AAGAGCAGGA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 3108; ORF 287.a>:

a287.pep

```

1 MFKRSVIAMA CIVALSACGG GGGSPDVKS ADTLSKPAAP VVTEDVGEEV
51 LPKEKKDEEA VSGAPQADTQ DATAGKGGQD MAAVSAENTG NGGAATTDNP
101 ENKDEGPOND MPQNAADTDS STPNHTPAPN MPTRDMGNOA PDAGESAQPA
151 NOPDMANAD GMQDDPSAG ENAGNTADQA ANQAEENQVG GSQNPASSTN
201 PNATNGGSDF GRINVANGIK LDSGSENVTL THCKDKVCDR DFLDEEAPPK
251 SEFEKLSDEE KINKYKKDEQ RENFVGLVAD RVEKNGTNKY VIIYKDKSAS
301 SSSARFRRSA RSRRSLPAEM PLIPVNQADT LIVDGEAVSL TGHSGNIFAP
351 EGNRYRLTYG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMFEN
401 GRPSPSGGRF AAKVDFGSKS VDGIIIDSGD LHMGTQKFKA VIDGNGFKGT
451 WTENGGGDVS GRFYGPAGEE VAGKYSYRPT DAEKGGFGVF AGKKEQD*

```

m287/a287 ORFs 287 and 287.a showed a 77.2% identity in 501 aa overlap

```

10 20 30 40 49
m287.pep MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETE
|||||:|
a287 MFKRSVIAMACIVALSACGGGGGGSPDVKSADTLSKPAAPVVTEDVGEEVLPKEKKDEEA
10 20 30 40 50 60

50 60 70 80 90 100 109
m287.pep KEDAPQAGSQGQAPSAGSQAQSDMAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT
||||:| |:::||||| |||||:|:|:|:|
a287 VSGAPQADTQ--DATAGKGGQDMAVSAENTGNGGAATTDNPNKDEGPONDMPQNAADT
70 80 90 100 110

```

	110	120	130	140	150	160	169
m287.pep	DSSTPNHTPDNMLAGNMENQATDAGESSQPANQPDMANAADGMQGDPSAGGQNAGNTA						
a287	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGDPSAG-ENAGNTA						
	120	130	140	150	160	170	
	170	180	190	200	210	220	229
m287.pep	AQQANQAGNNQAAGSSDPIPASNPAPANGGSNFGVRDLANGVLIDGPSQNTLTHCKGDS						
a287	DQAANQAENNOVGGSQNPASSTNPNATNGGSDFGRINVANGIKLDSGSENVTLTHCKDKV						
	180	190	200	210	220	230	
	230	240	250	260	270	280	289
m287.pep	CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP						
a287	CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFGVLVADRVEKNGTNKYVIYKD						
	240	250	260	270	280	290	
	290	300	310	320	330	340	
m287.pep	KP--TSFARFRRSARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRY						
a287	KSASSSARFRRSARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRY						
	300	310	320	330	340	350	
	350	360	370	380	390	400	
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF						
a287	LTYGAEKLSSGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF						
	360	370	380	390	400	410	
	410	420	430	440	450	460	
m287.pep	GSKSVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS						
a287	GSKSVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGRFGYPAGEEVAGKYS						
	420	430	440	450	460	470	
	470	480	489				
m287.pep	YRPTDAEKGFGVFAGKKEQDX						
a287	YRPTDAEKGFGVFAGKKEQDX						
	480	490					

406

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3109>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGCGGGA GGTAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCTGTGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACT GGAATATTTC GCAGTAGACA

```

```

701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAG CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGGCAG AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3110; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRIYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGSSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDPS DIRPYGNHTG NSAPSVREADN
301 SHEGYGYSDE VVRQHRQGP *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3111>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTGCA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTGCGGGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCGCGG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTCTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGGCAG AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3112; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRIYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGSSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDPS DIQPYGNHTG NSAPSVREADN
301 SHEGYGYSDE AVRQHRQGP *

```

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACG	TLTGIPSHGGGKRFVEQEL	VAASARA	AVK	DMDLQALHGR	
m406	MQARLLIPILFSVFILSACG	TLTGIPSHGGGKRFVEQEL	VAASARA	AVK	DMDLQALHGR	

	10	20	30	40	50	60
	70	80	90	100	110	120
g406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDITYPRYETTAETTSGGLTG					
m406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDITYPRYETTAETTSGGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406.pep	LTTSLSTLNAPALSRTQSDGSGSRSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
m406	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSCKGPKTEGLMVDPSDIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAAYKENYALWMGPYKVSCKGPKTEGLMVDPSDIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406.pep	SHEGYGYSDEAVRQHRQGQPX					
m406	SHEGYGYSDEVVRQHRQGQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3113>:

```

a406.seq
1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGGCAG GACATAGACA
951 AGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3114; ORF 406.a>:

```

a406.pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT
101 DITYPRYETT AETTSGGLTG LTTSLSTLNA PALSRQSDG SGSSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA

```

251 AYKENYALWM GPYKVSKEGK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
 301 SHEGYGYSDE AVRRHRQGQP *

m406/a406 ORFs 406 and 406.a showed a 98.8% identity in 320 aa overlap

	10	20	30	40	50	60
m406.pep	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAARKMDLQALHGR					
a406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAARKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
a406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m406.pep	LTTSLSLTNAPALSRTQSDGSGSKSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTTSLSLTNAPALSRTQSDGSGSKSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m406.pep	FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m406.pep	IKPKTNAFEAAYKENYALWMPYKVSKEGK PTEGLMVDFS DIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAYKENYALWMPYKVSKEGK PTEGLMVDFS DIQPYGNHMGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
m406.pep	SHEGYGYSDEVVRQHRQGQPX					
a406	SHEGYGYSDEAVRRHRQGQPX					
	310	320				

EXAMPLE 2

Expression of ORF 919

The primer described in Table 1 for ORF 919 was used to locate and clone ORF 919. The predicted gene 919 was cloned in pET vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 919-His fusion protein purification. Mice were immunized with the purified 919-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; PP, purified protein, TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm

that 919 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 are provided in Figure 10. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 3

Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 11. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 4

Expression of ORF 576 and 576-1

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera

were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).. These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 12. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 5

Expression of ORF 519 and 519-1

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 13. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 6

Expression of ORF 121 and 121-1

The primer described in Table 1 for ORF 121 was used to locate and clone ORF 121. The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 121 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 121 are provided in Figure 14. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 121 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 7

Expression of ORF 128 and 128-1

The primer described in Table 1 for ORF 128 was used to locate and clone ORF 128. The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 128 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 128 are provided in Figure 15. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J.*

Immunol 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 128 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 8

Expression of ORF 206

The primer described in Table 1 for ORF 206 was used to locate and clone ORF 206. The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 206 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 16. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 206 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 9

Expression of ORF 287

The primer described in Table 1 for ORF 287 was used to locate and clone ORF 287. The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A). These experiments confirm that 287 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 287 are provided in Figure 17. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 287 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 10

Expression of ORF 406

The primer described in Table 1 for ORF 406 was used to locate and clone ORF 406. The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 406 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 406 are provided in Figure 18. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 406 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 11

Table 2 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 225 among different strains.

Table 2

225 gene variability: List of used <i>Neisseria</i> strains		
Identification Strains number		Source / reference
Group B		
zo01_225	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo02_225	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zo03_225	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo04_225	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zo05_225	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zo06_225	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zo07_225	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zo08_225	528	R. Moxon / Seiler <i>et al.</i> , 1996
zo09_225	NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zo10_225	BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zo11_225	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zo12_225	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zo13_225	NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zo14_225	NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zo15_225	SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zo16_225	NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zo17_225	NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zo18_225	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zo19_225	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zo20_225	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zo21_225	MC58	R. Moxon
zo96_225	2996	Our collection
Group A		
zo22_225	205900	R. Moxon
zo23_225	F6124	R. Moxon
z2491	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998
Group C		
zo24_225	90/18311	R. Moxon
zo25_225	93/4286	R. Moxon

Others

zo26_225 A22 (group W) R. Moxon / Maiden *et al.*, 1998
 zo27_225 E26 (group X) R. Moxon / Maiden *et al.*, 1998
 zo28_225 860800 (group Y) R. Moxon / Maiden *et al.*, 1998
 zo29_225 E32 (group Z) R. Moxon / Maiden *et al.*, 1998

Gonococcus

zo32_225 Ng F62 R. Moxon / Maiden *et al.*, 1998
 zo33_225 Ng SN4 R. Moxon

fa1090 FA1090 R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

>FA1090 <SEQ ID 3115>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLLGIAIYRYGGTSVSTGFDCS
 GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
 RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN*

Z2491 <SEQ ID 3116>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRVPARRAGNA
 DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAIYRYGGTSISTGFDCSGF
 MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN*

Z001_225 <SEQ ID 3117>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAIYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDSRFLN*

Z002_225 <SEQ ID 3118>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDSRFLN*

Z003_225 <SEQ ID 3119>

MDSFFKPAVWAVLWLMFAVRLADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDSRFLN*

Z004_225 <SEQ ID 3120>

MSDFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z005_225 <SEQ ID 3121>

MSDFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z006_225 <SEQ ID 3122>

MSDFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z007_225 <SEQ ID 3123>

MSDFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z008_225 <SEQ ID 3124>

MSDFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z009_225 <SEQ ID 3125>

MSDFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z010_225 <SEQ ID 3126>

MSDFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z011_225 <SEQ ID 3127>

MSDFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
IAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN*

Z012_225 <SEQ ID 3128>

MSDFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z013_225 <SEQ ID 3129>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFQHIKFRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z014_225 <SEQ ID 3130>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z015_225 <SEQ ID 3131>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIKFRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN*

Z016_225 <SEQ ID 3132>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z017_225 <SEQ ID 3133>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z018_225 <SEQ ID 3134>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z019_225 <SEQ ID 3135>

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DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z020_225 <SEQ ID 3136>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA
DELIGNAMGLNEQPVLVFNRAFPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIKFRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
IAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN*

Z021_225 <SEQ ID 3137>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG
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DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z022_225 <SEQ ID 3138>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR

SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSRFLN*

Z023_225 <SEQ ID 3139>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
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DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSRFLN*

Z024_225 <SEQ ID 3140>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
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DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSRFLN*

Z025_225 <SEQ ID 3141>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
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DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSRFLN*

Z026_225 <SEQ ID 3142>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSRFLN*

Z027_225 <SEQ ID 3143>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSRFLN*

Z028_225 <SEQ ID 3144>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSRFLN*

Z029_225 <SEQ ID 3145>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSRFLN*

Z032_225 <SEQ ID 3146>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Z033_225 <SEQ ID 3147>

MDSFFKPAVWAVLWLMFAVRSALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Z096_225 <SEQ ID 3148>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDPSRFLN*

Figure 19 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 225, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 12

Table 3 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 235 among different strains.

Table 3

235 gene variability: List of used <i>Neisseria</i> strains		
Identification Strains number		Reference
Group B		
gnmzq01	NG6/88	Seiler <i>et al.</i> , 1996
gnmzq02	BZ198	Seiler <i>et al.</i> , 1996
gnmzq03	NG3/88	Seiler <i>et al.</i> , 1996
gnmzq04	1000	Seiler <i>et al.</i> , 1996
gnmzq05	1000	Seiler <i>et al.</i> , 1996
gnmzq07	BZ169	Seiler <i>et al.</i> , 1996
gnmzq08	528	Seiler <i>et al.</i> , 1996
gnmzq09	NGP165	Seiler <i>et al.</i> , 1996
gnmzq10	BZ133	Seiler <i>et al.</i> , 1996
gnmzq11	NGE31	Seiler <i>et al.</i> , 1996
gnmzq13	NGE28	Seiler <i>et al.</i> , 1996
gnmzq14	NGH38	Seiler <i>et al.</i> , 1996
gnmzq15	SWZ107	Seiler <i>et al.</i> , 1996
gnmzq16	NGH15	Seiler <i>et al.</i> , 1996
gnmzq17	NGH36	Seiler <i>et al.</i> , 1996
gnmzq18	BZ232	Seiler <i>et al.</i> , 1996
gnmzq19	BZ83	Seiler <i>et al.</i> , 1996
gnmzq21	MC58	Virji <i>et al.</i> , 1992
Group A		
gnmzq22	205900	Our collection

gnmzq23 F6124 Our collection
 z2491 Z2491 Maiden *et al.*, 1998

Group C

gnmzq24 90/18311 Our collection
 gnmzq25 93/4286 Our collection

Others

gnmzq26 A22 (group W) Maiden *et al.*, 1998
 gnmzq27 E26 (group X) Maiden *et al.*, 1998
 gnmzq28 860800 (group Y) Maiden *et al.*, 1998
 gnmzq29 E32 (group Z) Maiden *et al.*, 1998
 gnmzq31 *N. lactamica* Our collection

Gonococcus

gnmzq32 Ng F62 Maiden *et al.*, 1998
 gnmzq33 Ng SN4 Our collection

fa1090 FA1090 Dempsey *et al.* 1991

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3149>

MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ01 <SEQ ID 3150>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANNL
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ02 <SEQ ID 3151>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ03 <SEQ ID 3152>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST

AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ04 <SEQ ID 3153>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ05 <SEQ ID 3154>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ07 <SEQ ID 3155>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ08 <SEQ ID 3156>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ09 <SEQ ID 3157>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ10 <SEQ ID 3158>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ11 <SEQ ID 3159>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ13 <SEQ ID 3160>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ14 <SEQ ID 3161>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ15 <SEQ ID 3162>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ16 <SEQ ID 3163>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ17 <SEQ ID 3164>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ18 <SEQ ID 3165>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ19 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ21 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ22 <SEQ ID 3167>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ23 <SEQ ID 3168>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ24 <SEQ ID 3169>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ25 <SEQ ID 3170>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ26 <SEQ ID 3171>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ27 <SEQ ID 3172>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ28 <SEQ ID 3173>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDsvTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ29 <SEQ ID 3174>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDsvTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ31 <SEQ ID 3175>

MKPLILGLAAVLALSACQVQKAPDFDYTAFKESKPASILVVPPLNESPDVNGTWGMLAST
 AEPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITITEYGTS
 YQILDsvTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAAYDLLSPYSHNGILKGPRFVEEQPK*

GNMZQ32 <SEQ ID 3176>

MKPLILGLAAVLALSACQVRKAPDLDTYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDsvTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ33 <SEQ ID 3177>

MKPLILGLAAVLALSACQVRKAPDLDTYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDsvTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

Z2491 <SEQ ID 3178>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDsvTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

Figure 20 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 235, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 13

Table 4 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 287 among different strains.

Table 4

287 gene variability: List of used *Neisseria* strains

Identification Strains number	Reference
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Group B

287_2	BZ198	Seiler <i>et al.</i> , 1996
287_9	NGP165	Seiler <i>et al.</i> , 1996
287_14	NGH38	Seiler <i>et al.</i> , 1996
287_21	MC58	Virji <i>et al.</i> , 1992

Group A

z2491	Z2491	Maiden <i>et al.</i> , 1998
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Gonococcus

fa1090	FA1090	Dempsey <i>et al.</i> 1991
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References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

287_14 <SEQ ID 3179>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQDDPSAGGENAGNTAAQGTNQAENNQ
 TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGPSQNTLTHCKGDCSGNNFLDEEV
 QLKSEFEKLSADAKISNYKKDGKNDGKNDKFVGLVADSVQMKGINQYIIIFYKPKPTSFA
 FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLP
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPSRGRFAAKVDFGSKSVDGII
 DSGDGLHMTQKFKAAIDGNGFKGTWTENGGDVSCKFYGPAGEEVAGKYSYRPTDAEKG
 GFGVFAGKKEQD*

287_2 <SEQ ID 3180>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQDDPSAGGENAGNTAAQGTNQAENNQ
 TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGPSQNTLTHCKGDCSGNNFLDEEV
 QLKSEFEKLSADAKISNYKKDGKNDGKNDKFVGLVADSVQMKGINQYIIIFYKPKPTSFA
 FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLP
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPSRGRFAAKVDFGSKSVDGII
 DSGDGLHMTQKFKAAIDGNGFKGTWTENGGDVSCKFYGPAGEEVAGKYSYRPTDAEKG
 GFGVFAGKKEQD*

287_21. <SEQ ID 3181>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNMPQNAAGTDSSTPNHTPDP
 NMLAGNMENQATDAGESSQPANQPDMAANTADGMQDDPSAGGQAGNTAAQGANQAGNNQ
 AAGSSDPIPASNPAPANGGSNFRVLDLNGVLIDGPSQNTLTHCKGDCSGNNFLDEEV
 QLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIIFYKPKPTSFAFRRS

ARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVDGIIIDSGD
DLHMGTOQKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGFGV
FAGKKEQD*

287_9 <SEQ ID 3182>

MFKRSLVIAMACIVALSACGGGGGGSPDVKSADTLSPKPAAPVVTEDVGEEVLPKEKKDEEA
VSGAPQADTQDATAGKGGQDMAAVSAENTGNNGAATTNPNKDEGPQNDMPQNAADTDS
STPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADMGGDDPSAGENAGNTADQA
ANQAEENNQVGGSQNPASSTNPNATNGGSDFGGRINVANGIKLDSGSENVTLTHCKDKVCDR
DFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVITYKDKSAS
SSSARFRRSARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYG
AEKLSGGSYALSQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKS
VDGIIIDSGDDLHMGTOQKFKAVIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPT
DAEKGFGVFAGKKEQD*

FA1090 <SEQ ID 3183>

MFKRSLVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEVLPKEKKDEEA
AGGAPQADTQDATAGEGSDMAAVSAENTGNNGAATTNPNKEDAGAQNMPQNAAESAN
QTGNNQAPAGSSDSAPASNPAPANGGSDFGRTNVGNSVVIDGPSQNTLTHCKGDSNGDN
LLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVEKNGTNKYVITYKDKPPT
SARSRRLPAEIPPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGS
YALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFAAKVDFGSKSVDGIIIDSG
DDLHMGTOQKFKAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPTDAEKGFGV
VFAGKKDRD*

Z2491 <SEQ ID 3184>

MFKRSLVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVSEKETEAKEDAPQAGSQG
QGAPSAQGSQDMAAVSEENTGNNGAVTADNPKNEDEVAQNMPQNAAGTDSSTPNHTPDP
NMLAGNMENQATDAGESSQPANQPDMANAADMGGDDPSAGGQAGNTAAQGANQAGNNQ
AAGSSDFIPASNAPANGGNSFRVLDLAVGLIDGPSQNTLTHCKGDSGSGNNFLDEEV
QLKSEFEKLSADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFARFRRS
ARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVDGIIIDSGD
DLHMGTOQKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGFGV
FAGKKEQD*

Figure 21 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 287, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 14

Table 5 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 519 among different strains.

Table 5

519 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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number**Group B**

zv01_519	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv02_519	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zv03_519ass	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv04_519	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zv05_519	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zv06_519ass	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zv07_519	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zv11_519	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zv12_519	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zv18_519	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zv19_519	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zv20_519ass	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zv21_519ass	MC58	R. Moxon
zv96_519	2996	Our collection

Group A

zv22_519ass	205900	R. Moxon
z2491_519	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Others

zv26_519	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zv27_519	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zv28_519	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zv29_519ass	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998

Gonococcus

zv32_519	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
fa1090_519	FA1090	R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090_519 <SEQ ID 3185>
MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRVIG
RMELDKTFFERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA AEAIRQIAAALQTQGGADAVNLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

Z2491_519 <SEQ ID 3186>

MEFFIILLAAVVVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV01_519 <SEQ ID 3187>

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV02_519 <SEQ ID 3188>

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV03_519 <SEQ ID 3189>

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV04_519 <SEQ ID 3190>

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV05_519 <SEQ ID 3191>

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV06_519ASS <SEQ ID 3192>

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERK
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV07_519 <SEQ ID 3193>

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV11_519 <SEQ ID 3194>

MEFFIILLAAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV12_519 <SEQ ID 3195>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV18_519 <SEQ ID 3196>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV19_519 <SEQ ID 3197>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV20_519ASS <SEQ ID 3198>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSM
ISAGMKIIDSSKTAK*

ZV21_519ASS <SEQ ID 3199>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV22_519ASS <SEQ ID 3200>

MEFFIILLAAVVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV26_519 <SEQ ID 3201>

MEFFIILLAAVVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV27_519 <SEQ ID 3202>

MEFFI ILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSTAK*

ZV28_519 <SEQ ID 3203>

MEFFI ILLAAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSTAK*

ZV29_519ASS <SEQ ID 3204>

MEFFI ILLAAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREPEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSTAK*

ZV32_519 <SEQ ID 3205>

MEFFI ILLAAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSTAK*

ZV96_519 <SEQ ID 3206>

MEFFI ILLAAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSTAK*

Figure 22 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 519, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 15

Table 6 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 919 among different strains.

Table 6

919 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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number**Group B**

zm01	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm02	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zm03	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm04	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zm05	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zm06	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zm07	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zm08n	528	R. Moxon / Seiler <i>et al.</i> , 1996
zm09	NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zm10	BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zm11asbc	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zm12	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zm13	NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zm14	NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zm15	SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zm16	NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zm17	NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zm18	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zm19	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zm20	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zm21	MC58	R. Moxon
zm96	2996	Our collection

Group A

zm22	205900	R. Moxon
zm23asbc	F6124	R. Moxon
z2491	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Group C

zm24	90/18311	R. Moxon
zm25	93/4286	R. Moxon

Others

zm26	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zm27bc	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zm28	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zm29asbc	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998
zm31asbc	<i>N. lactamica</i>	R. Moxon

Gonococcus

zm32asbc	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
zm33asbc	Ng SN4	R. Moxon

fa1090	FA1090	R. Moxon
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References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden et al., Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3207>

MKKHLLRSALYGIAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
 YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
 YFTPWQVAGNGSLAGTVTGYEPEVLKGDGRRTARARFIYGI PDDFISVPLPAGLRSGKN
 LVRI RQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPI LGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSGNEGVPVAGLGTPLMGEYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

Z2491 <SEQ ID 3208>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
 YFTPWQVAGNGSLAGTVTGYEPEVLKGDGRRTAQARFIYGI PDDFISVPLPAGLRSGKA
 LVRI RQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPI LGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMQNPORLAEVLGQNPSYIFFRELTSNDGVPVAGLGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM01 <SEQ ID 3209>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTVTGYEPEVLKGDGRRTAQARFIYGI PDDFISVPLPAGLRSGKA
 LVRI RQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPI LGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGVPVAGLGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM02 <SEQ ID 3210>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTVTGYEPEVLKGDGRRTAQARFIYGI PDDFISVPLPAGLRSGKA
 LVRI RQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPI LGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGVPVAGLGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM03 <SEQ ID 3211>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTVTGYEPEVLKGDGRRTAQARFIYGI PDDFISVPLPAGLRSGKA
 LVRI RQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPI LGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGVPVAGLGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM04 <SEQ ID 3212>

MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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YFTPWQVAGNGSLAGTVTGYEPLKGGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMOGIKAYMQNPORLAEVLGQNPYSIIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM05 <SEQ ID 3213>

MKKYLFRALYGIAAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPLKGGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMOGIKAYMRQNPORLAEVLGQNPYSIIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM06 <SEQ ID 3214>

MKKYLFRALYGIAAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPLKGGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMOGIKSYMQRNPORLAEVLGQNPYSIIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM07 <SEQ ID 3215>

MKKYLFRALYGIAAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPLKGGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMOGIKSYMQRNPORLAEVLGQNPYSIIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM08N <SEQ ID 3216>

MKKYLFRALYGIAAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEPLKGGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMOGIKAYMRQNPORLAEVLGQNPYSIIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM09 <SEQ ID 3217>

MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPLKGGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMOGIKSYMQRNPORLAEVLGQNPYSIIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM10 <SEQ ID 3218>

MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPLKGGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL

KLGQTSMQGKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM11ASBC <SEQ ID 3219>
MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPI LGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQTSMQGKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM12 <SEQ ID 3220>
MKKYLFRALYGIAGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPI LGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQTSMQGKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM13 <SEQ ID 3221>
MKKYLFRALYGIAGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPI LGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQTSMQGKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM14 <SEQ ID 3222>
MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPI LGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQTSMQGKSYMRQNPQRLAEVLGQNPSYIFFRELTGSRNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM15 <SEQ ID 3223>
MKKYLFRALYGIAGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDLAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPI LGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQTSMQGKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM16 <SEQ ID 3224>
MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPGRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGGHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPI LGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQTSMQGKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM17 <SEQ ID 3225>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM18 <SEQ ID 3226>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM19 <SEQ ID 3227>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM20 <SEQ ID 3228>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM21 <SEQ ID 3229>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM22 <SEQ ID 3230>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMQONPORLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM23ASBC <SEQ ID 3231>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL

KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK
MKEPGYVWQLLPNGMKPEYRP*

ZM24 <SEQ ID 3232>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM25 <SEQ ID 3233>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM26 <SEQ ID 3234>

MKKYLFRAALYGISAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM27BC <SEQ ID 3235>

MKKYLFRAALYGISAAAILAACQSKSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK
MKEPGYVWQLLPNGMKPEYRP*

ZM28 <SEQ ID 3236>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM29ASBC <SEQ ID 3237>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATTHPITRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM31ASBC <SEQ ID 3238>

MKKHLFRAALYGIAAAILAACQSKSIQTFFPQPDTSIIKGPDRPAGIPDPAGTTVGGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
 LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSGNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM32ASBC <SEQ ID 3239>

MKKHLLRSALYGIAAAILAACQSRSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIPTDDFISVPLPAGLRGGKA
 LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSGGNDGPVGALGTPLMGGYAGA
 IDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM33ASBC <SEQ ID 3240>

MKKHLLRSALYGIAAAILAACQSRSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIPTDDFISVPLPAGLRGGKN
 LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSGNEGPVGALGTPLMGEYAGA
 IDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM96 <SEQ ID 3241>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFOAKQFFER
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
 LVRIRQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

Figure 23 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 919, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 16

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 7: Oligonucleotides used for PCR to amplify complete or partial ORFs

ORF	primer	Sequence	Restriction sites
001	Forward	CGCGGATCCCATATG-TGGATGGTGCTGGTCAT	BamHI-
	Reverse	CCCGCTCGAG-TGCCGTCTTGTCCAC	NdeI
003	Forward	CGCGGATCCCATATG-GTCGTATTCGTGGC	XhoI
	Reverse	CCCGCTCGAG-AAAATCATGAACACGCGC	BamHI-
005	Forward	CGCGGATCCCATATG-GACAATATTGACATGT	NdeI
	Reverse	CCCGCTCGAG-CATCACATCCGCCCG	XhoI
006	Forward	CGCGGATCCCATATG-CTGCTGGTGCTGG	BamHI-
	Reverse	CCCGCTCGAG-AGTTCCGGCTTTGATGT	NdeI
007	Forward	CGCGGATCCCATATG-GCCGACAACAGCATCAT	XhoI
	Reverse	CCCGCTCGAG-AAGGCGTTCATGATATAAG	BamHI-
008	Forward	CGCGGATCCCATATG-AACAACAGACATTTTG	NdeI
	Reverse	CCCGCTCGAG-CCTGTCCGGTAAAAGAC	XhoI
009	Forward	CGCGGATCCCATATG-CCCCGCGCTGCT	BamHI-
	Reverse	CCCGCTCGAG-TGGCTTTTGCCACGTTTT	NdeI
011	Forward	CGCGGATCCCATATG-AAGACACACCGCAAG	XhoI
	Reverse	CCCGCTCGAG-GGCGGTCAGTACGGT	BamHI-
012	Forward	CGCGGATCCCATATG-CTCGCCCGTTGCC	NdeI
	Reverse	CCCGCTCGAG-AGCGGGGAAGAGGCAC	XhoI
013	Forward	CGCGGATCCCATATG-CCTTTGACCATGCT	BamHI-
	Reverse	CCCGCTCGAG-CTGATTCGGCAAAAAAATCT	NdeI
018	Forward	CGCGGATCCCATATG-CAGCAGAGGCAGTT	XhoI
	Reverse	CCCGCTCGAG-GACGAGGCGAACGCC	BamHI-
019	Forward	AAAGAATTC-CTGCCAGCCGGCAAGACCCCGGC	NdeI
	Reverse	AAACTGCAG-TCAGCGGGCGGGGACAATGCCCAT	XhoI
023	Forward	AAAGAATTC-AAAGAATATTCGGCATGGCAGGC	Eco RI
	Reverse	AAACTGCAG-TTACCCCCAAATCACTTTAACTGA	Pst I
025	Forward	AAAGAATTC-TGCGCCACCCAACAGCCTGCTCC	Eco RI
	Reverse	AAACTGCAG-TCAGAACGCGATATAGCTGTTCGG	Pst I
031	Forward	CGCGGATCCCATATG-GTCTCCCTTCGCTT	BamHI-
	Reverse	CCCGCTCGAG-ATGTAAGACGGGGACAAC	NdeI
032	Forward	CGCGGATCCCATATG-CGGCGAAACGTGC	XhoI
			BamHI-

	Reverse	CCCGCTCGAG-CTGGTTTTTTGATATTTGTG	NdeI
033	Forward	CGCGGATCCCATATG-GCGGCGGCAGACA	XhoI
	Reverse	CCCGCTCGAG-ATTTGCCGCATCCCGAT	BamHI-
034	Forward	CGCGGATCCCATATG-GCCGAAAACAGCTACGG	NdeI
	Reverse	CCCGCTCGAG-TTTGACGATTTGGTTCAATT	XhoI
036	Forward	CGCGGATCCCATATG-CTGAAGCCGTGCG	BamHI-
	Reverse	CCCGCTCGAG-CCGGACTGCGTATCGG	NdeI
038	Forward	CGCGGATCCCATATG-ACCGATTTCCGCCA	XhoI
	Reverse	CCCGCTCGAG-TTCTACGCCGTA CTGCC	BamHI-
039	Forward	CGCGGATCCCATATG-CCGTCCGAACCGC	NdeI
	Reverse	CCCGCTCGAG-TAGGATGACGAGGTAGG	XhoI
041	Forward	CGCGGATCCCATATG-TTCGTGCGCGAACCGC	BamHI-
	Reverse	CCCGCTCGAG-GCCCAAAA ACTCTTTCAA	NdeI
042	Forward	CGCGGATCCCATATG-ACGATGATTTGCTTGC	XhoI
	Reverse	CCCGCTCGAG-TTTCAGCCTGCATTTGAC	BamHI-
043	Forward	AAAAAAGGTACC-ATGGTTGTTCAAATCAAATATC	NdeI
	Reverse	AAACTGCAG-TTATTGCGCTTCACCTCCGCCG	XhoI
043a	Forward	AAAAAAGGTACC-GCAAAGTGCATGGCGGCTTGGACGGTGC	Kpn I
	Reverse	AAAAAACTGCAG-	Pst I
		TTAATCCTGCAACACGAATTCGCCCGTCCG	Kpn I
044	Forward	CGCGGATCCCATATG-CCGTCCGACTAGAG	Pst I
	Reverse	CCCGCTCGAG-ATGCGCTACGGTAGCCA	BamHI-
046	Forward	AAAGAATTC-ATGTCGGCAATGCTCCCGACAAG	NdeI
	Reverse	AAACTGCAG-TCACTCGGCGACCCACACCGTGAA	XhoI
047	Forward	CGCGGATCCCATATG-GTCATCATA CAGGCG	Eco RI
	Reverse	CCCGCTCGAG-TCCGAAAAAGCCCATTTTG	Pst I
048	Forward	AAAGAATTC-ATGCTCAACAAAGGCGAAGAATTGCC	BamHI-
	Reverse	AAACTGCAG-TCAAGATTCGACGGGGATGATGCC	NdeI
049	Forward	AAAGAATTC-ATGCGGGCGCAGGCGTTTGATCAGCC	XhoI
	Reverse	AAACTGCAG-AAGGCGTATCTGAAAAAATGGCAG	Eco RI
050	Forward	CGCGGATCCCATATG-GGCGCGGGCTGG	Pst I
	Reverse	CCCGCTCGAG-AATCGGGCCATCTTCGA	BamHI-
052	Forward	AAAAAAGAATTC-ATGGCTTTGGTGGCGGAGGAAAC	NdeI
	Reverse	AAAAAAGTGCAG-TCAGGCGGCGT TTTTCACCTTCCT	XhoI
052a	Forward	AAAAAAGAATTC-GTGGCGGAGGAAACGGAAATATCCGC	Eco RI
			Sal I
			Eco RI

	Reverse	AAAAAACTGCAG-TTAGCTGTTTTTGGAAACGCCGTCCAACCC	Pst I
073	Forward	CGCGGATCCCATATG-TGTATGCCATATAAGAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACCGGATTGTCCGAC	XhoI
075	Forward	CGCGGATCCCATATG-CCGTCTTACTTCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCACCAATGCCGATTATTT	XhoI
077a	Forward	AAAAAAGAATTC-GGCGGCATTTTCATCGACACCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGAACATCTGCACAAACGCAAT	Pst I
080	Forward	AAAGAATTC-GCGTCCGGGCTGGTTTGGTTTACAATTC	Eco RI
	Reverse	AAACTGCAG-CTATTCTTCGGATTCTTTTTTCGGG	Pst I
081	Forward	AAAGAATTC-ATGAAACCACTGGACCTAAATTCATCTG	Eco RI
	Reverse	AAACTGCAG-TCACTTATCCTCCAATGCCTC	Pst I
082	Forward	AAAGAATTC-ATGTGGTTGTTGAAGTTGCCTGC	Eco RI
	Reverse	AAACTGCAG-TTACGCGGATTCGGCAGTTGG	Pst I
084	Forward	AAAGAATTC-TATCACCAGAATATGAATACGGCTACCG	Eco RI
	Reverse	AAACTGCAG-TTATACTTGGGCGCAACATGA	Pst I
085	Forward	CGCGGATCCCATATG-GGTAAAGGGCAGGACT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAAGCCTTAAACGCTTCG	XhoI
086	Forward	AAAAAAGGTACC-TATTTGGCATCAAAAGAAGGCGG	Kpn I
	Reverse	AAACTGCAG-TTACTCCACCCGATAACCGCG	Pst I
087	Forward	AAAGAATTC-ATGGGCGGTAAAACCTTTATGC	Eco RI
	Reverse	AAACTGCAG-TTACGCCGCACACGCAATCGC	Pst I
087a	Forward	AAAAAAGAATTC-AAGCTATTAGGCGTGCCGATTGTGATTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCTGCAAGATGCCAGCTTGCC	Pst I
088	Forward	AAAAAAGAATTC-ATGTTTTTATGGCTCGCACATTTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAGCGGATTTTGAGGGTACTCAAACC	Pst I
089	Forward	CGCGGATCCCATATG-CCGCCAAAATCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCGCATACCAAAGCCA	XhoI
090	Forward	CGCGGATCCCATATG-CGCATAGTCGAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAAAACGGCGGTACG	XhoI
091	Forward	AAAGAATTC-ATGGAAATACCCGTACCGCCGAGTCC	Eco RI
	Reverse	AAACTGCAG-TCAGCGCAGGGGGTAGCCCAAGCC	Pst I
092	Forward	AAAGAATTC-ATGTTTTTTATTTCAATCCG	Eco RI
	Reverse	AAACTGCAG-TCAAATCTGTTTCGACAATGC	Pst I
093	Forward	AAAGAATTC-ATGCAGAATTTTGGCAAAGTGGC	Eco RI
	Reverse	AAACTGCAG-CTATGGCTCGTCATACCGGGC	Pst I
094	Forward	AAAGAATTC-ATGCCGTCACGGAAGCGCATCAACTC	Eco RI
	Reverse	AAACTGCAG-TTATCCCGGCCATACCGCCGAACA	Pst I
095	Forward	AAAGAATTC-ATGTCTTTTCATTTGAACATGGACGG	Eco RI
	Reverse	AAACTGCAG-TCAACGCCGCAGGCACTAACGCCC	Pst I
096	Forward	AAAGAATTC-ATGGCTCGTCATACCGGGCAGGG	Eco RI

	Reverse	AAACTGCAG-TCAAAGGAAAAGGCCGTCTGAAAAGCG	Pst I
097	Forward	AAAGAATTC-ATGGACACTTCAAAACAAACACTGTTG	Eco RI
	Reverse	AAACTGCAG-TCAGCCCAAATACCAGAATTCAG	Pst I
098	Forward	AAAGAATTC-GATGAACGCAGCCCAGCATGGATACG	Eco RI
	Reverse	AAACTGCAG-TTACGACATTCTGATTTGGCA	Pst I
102	Forward	AAAAAAGAATTC-GGCCTGATGATTTTGGAAGTCAACAC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
105	Forward	CGCGGATCCCATATG-TCCGCAAACGAATACG	BamHI-
	Reverse	CCCGCTCGAG-GTGTCTGCCAGTTTCAG	NdeI
107	Forward	AAAAAAGAATTC- CTGATGATTTTGGAAAGTCAACACCCATTATCC	XhoI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Eco RI
107b	Forward	AAAAAAGAATTC- GATACCCAAGCCCCCGCCGGCACAACTACTG	Pst I
	Reverse	AAAAAACTGCAG- TTACGCGTCGCCTTTAAAGTATTTGAGCAGGCTGGAGAC	Eco RI
108	Forward	AAAGAATTC-ATGTTGCCGGGCTTCAACCG	Pst I
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Eco RI
108a	Forward	AAAAAAGAATTC-GGTAACACATTTCGGCAGCTTAGACGGTGG	Pst I
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Eco RI
109	Forward	AAAGAATTC-ATGTATTATCGCCGGGTATGGG	Pst I
	Reverse	AAACTGCAG-CTAGCCCAAAGATTTGAAGTGTC	Eco RI
111	Forward	CGCGGATCCCATATG-TGTTTCGGAACAAACCGC	Pst I
	Reverse	CCCGCTCGAG-GCGGAGCAGTTTTTCAAA	BamHI-
114	Forward	CGCGGATCCCATATG-GCTTCCATCACTTCGC	NdeI
	Reverse	CCCGCTCGAG-CATCCGCGAAATCGTC	XhoI
117	Forward	AAAAAAGGTACC-ATGGTCGAAGAACTGGAAGTCTG	Kpn I
	Reverse	AAACTGCAG-TTAAAGCCGGGTAACGCTCAATAC	Pst I
118	Forward	AAAGTCGACATGTGTGAGTTCAAGGATATTATAAG	Sal I
	Reverse	AAAGCATGC-CTATTTTTTGTGTAATAATCAAATC	Sph I
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT	BamHI-
	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC	NdeI
122	Forward	CGCGGATCCCATATG-GTCATGATTAAATCCGCA	XhoI
	Reverse	CCCGCTCGAG-AATCTTGGTAGATTGGATTT	BamHI-
125	Forward	AAAGAATTC-ATGTCGGGCAATGCCTCCTCTCC	NdeI
	Reverse	AAACTGCAG-TCACGCCGTTTCAAGACG	XhoI
125a	Forward	AAAAAAGAATTC-ACGGCAGGCAGCACCGCCGCACAGGTTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTATTTTGCCACGTCGGTTTCTCCGGTGAACAACGC	Pst I
126	Forward	CGCGGATCCCATATG-CCGTCTGAAACCC	BamHI-

	Reverse	CCCGCTCGAG-ATATTCCGCCGAATGCC	NdeI
127	Forward	AAAGAATTC-ATGGAAATATGGAATATGTTGGACACTTG	XhoI
	Reverse	AAACTGCAG-TTAAAGTGTTTCGGAGCCGGC	Eco RI
127a	Forward	AAAAAAGAATTC-AAGGAACTGATTATGTGTCTGTCGGG	Pst I
	Reverse	AAACTGCAG-TTAAAGTGTTTCGGAGCCGGC	Eco RI
128	Forward	CGCGGATCCCATATG-ACTGACAACGCACT	Pst I
	Reverse	CCCGCTCGAG-GACCGCGTTGTGCGAAA	BamHI-
130	Forward	CGCGGATCCCATATG-AAACAACCTCCGCGA	NdeI
	Reverse	CCCGCTCGAG-GAATTTTGCACCGGATTG	XhoI
132	Forward	AAAGAATTC-ATGGAACCTTCAAAACCTTAATTTG	XhoI
	Reverse	AAAAAACTGCAG-TCACCATGTCTGGCATTGAAAAAC	Eco RI
134	Forward	CGCGGATCCCATATG-TCCCAAGAAATCCTC	Pst I
	Reverse	CCCGCTCGAG-CAGTTTGACCGAATGTTC	BamHI-
135	Forward	CGCGGATCCCATATG-AAATACAAAAGAATCGTATT	NdeI
	Reverse	CCCGCTCGAG-AAATTCGGTCAGAAGCAGG	XhoI
137	Forward	AAAAAAGGTACC-ATGATTACCCATCCCCAATTCGATCC	Kpn I
	Reverse	AAAAAACTGCAG-TCAGTGCTGTTTTTTCATGCCGAA	Pst I
137a	Forward	AAAAAAGAATTC-GGCCGCAAACACGGCATCGGCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TTAAGCGGGATGACGCGGCAGCATACC	Pst I
138	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Xba I
141	Forward	AAAGAATTC-ATGAGCTTCAAAACCGATGCCGAAATCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAACAAGCCGTGAATCACGCC	Pst I
142	Forward	CGCGGATCCCATATG-CGTGCCGATTTCATG	BamHI-
	Reverse	CCCGCTCGAG-AAACTGCTGCACATGGG	NdeI
143	Forward	AAAAAAGAATTC-ATGCTCAGTTTCGGCTTTCTCGGCGTTCAGAC	XhoI
	Reverse	AAAAAACTGCAG-TCAAACCCCGCCGTGTGTTTCTTTAAT	Eco RI
144	Forward	AAAAAAGAATTC-GGTCTGATCGACGGGCGTGCCGTAAC	Pst I
	Reverse	AAAAAATCTAGA-TCGGCATCGGCCGGCATATGTCCG	Eco RI
146	Forward	AAAAAAGAATTC-CGCCAAGTCGTATTGACCACGACAAAGTC	Xba I
	Reverse	AAAAAACTGCAG-TTAGGCATCGGCAAATAGGAAACTGGG	Eco RI
147	Forward	AAAAAAGAATTC-ACTGAGCAATCGGTGGATTTGGAAAC	Pst I
	Reverse	AAAAAATCTAGA-TTAGGTAAAGCTGCGGCCCATTTGCGG	Eco RI
148	Forward	AAAAAAGAATTC-ATGGCGTTAAAAACATCAAACCTGGAACACGC	Xba I
	Reverse	AAAAAATCTAGA-TCAGCCCTTCATACAGCCTTCGTTTTG	Eco RI
149	Forward	CGCGGATCCCATATG-CTGCTTGACAACAAAGT	Xba I
			BamHI-

	Reverse	CCCGCTCGAG-AACTTCACGTTACGCC	NdeI
150	Forward	CGCGGATCCCATATG-CAGAACACAAATCCG	XhoI
	Reverse	CCCGCTCGAG-ATAAACATCACGCTGATAGC	BamHI-
151	Forward	AAAAAAGAATTC- ATGAAACAAATCCGCAACATCGCCATCATCGC	NdeI
	Reverse	AAAAAACTGCAG-TCAATCCAGCTTTTAAAGTGGCGGCG	XhoI
152	Forward	AAAAAAGAATTC- ATGAAAAACAAAACCAAAGTCTGGGACCTCCC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGGACAGGAGCAGGATGGCGGC	Pst I
153	Forward	AAAAAAGAATTC-ATGGCGTTTGCTTACGGTATGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTCATGTTTTCCGTTTCATT	Pst I
153a	Forward	AAAAAAGAATTC-CGGACTTCGGTATCGGTTCCCCAGCATTG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGCCGACGAAATACTCAGACTTTTCGG	Pst I
154	Forward	CGCGGATCCCATATG-ACTGACAACAGCCC	BamHI-
	Reverse	CCCGCTCGAG-TCGGCTTCCTTTTCGGG	NdeI
155	Forward	AAAAAAGAATTC-ATGAAAATCGGTATCCCACGCGAGTC	XhoI
	Reverse	AAAAAACTGCAG-TTACCCTTTCTTAAACATATTCAGCAT	Eco RI
156	Forward	AAAAAAGAATTC-GCACAGCAAAACGGTTTTGAAGC	Pst I
	Reverse	AAAAAACTGCAG-TCAAGCAGCCGCGACAAACAGCCC	Eco RI
157	Forward	CGCGGATCCCATATG-AGGAACGAGGAAAAAC	Pst I
	Reverse	CCCGCTCGAG-AAAACACAATATCCCCGC	BamHI-
158	Forward	AAAAAAGAATTC-GCGGAGCAGTTGGCGATGGCAAATTCTGC	NdeI
	Reverse	AAAAAATCTAGA-TTATCCACAGAGATTGTTTCCAGTTC	XhoI
160	Forward	CGCGGATCCCATATG-GACATTCTGGACAAAC	Eco RI
	Reverse	CCCGCTCGAG-TTTTTGCCCGCCTTCTTT	Xba I
163	Forward	AAAAAAGGTACC-ACCGTGCCGGATCAGGTGCAGATGTG	Kpn I
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
163a	Forward	AAAAAAGAATTC-CGGCTGGTGACGATAATGAGCCAGAC	Eco RI
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
164	Forward	CGCGGATCCCATATG-AACCGGACTTATGCC	BamHI-
	Reverse	CCCGCTCGAG-TTTGTTTCCGTCAAACCTGC	NdeI
165	Forward	CGCGGATCCGCTAGC-GCTGAAGCGACAGACG	XhoI
	Reverse	CCCGCTCGAG-AATATCCAATACTTTCGCG	BamHI-
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA	NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAAGTATGTGC	XhoI
209	Forward	CGCGGATCCCATATG-CTGCGGCATTTAGGA	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-TACCCCTGAAGGCAAC	XhoI
211	Forward	AAAAAAGAATTC-ATGTTGCGGGTTGCTGCTGC	Eco RI
	Reverse	AAAAAACTGCAG-CTATCCTGCGGATTGGCATTGAAA	Pst I
212	Forward	CGCGGATCCCATATG-GACAATCTCGTATGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGGGTTAGATCCTTCC	XhoI
215	Forward	CGCGGATCCCATATG-GCATGGTTGGGTCTGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATATCTTTTGTATCATAAATC	XhoI
216	Forward	CGCGGATCCCATATG-GCAATGGCAGAAAACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TACAATCCGTGCCGCC	XhoI
217	Forward	CGCGGATCCCATATG-GCGGATGACGGTGTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACCCCGAATATCGAATCC	XhoI
218	Forward	CGCGGATCCCATATG-GTCGCGGTCTGATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TAACTCATAGAATCCTGC	XhoI
219	Forward	CGCGGATCCGCTAGC-ACGGCAAGGTTAAG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTAAACCATCTCCTCAAAAC	XhoI
223	Forward	CGCGGATCCCATATG-GAATTCAGGCACCAAGTA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCTTCCCGCGTGTC	XhoI
225	Forward	CGCGGATCCCATATG-GACGAGTTGACCAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTTCAGAAAGCGGGAC	XhoI
226	Forward	AAAGAATTC-CTTGCGATTATCGTGCGCACGCG	Eco RI
	Reverse	AAACTGCAG-TCAAAATCCCAAACGGGGAT	Pst I
228	Forward	CGCGGATCCCATATG-TCGCAAGAAGCCAAACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI
229	Forward	CGCGGATCCCATATG-CAAGAGGTTTGTCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACACAATATAGCGGATGAAC	XhoI
230	Forward	CGCGGATCCCATATG-CATCCGGGTGCCGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAGTTTGGCGGCTTCGG	XhoI
232	Forward	AAAAAAGAATTC-ATGTACGCTAAAAAAGGCGGTTTGGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGGTTTTTTCCTGATTGCCGCCGC	Pst I
232a	Forward	AAAAAAGAATTC-GCCAAGGCTGCCGATACACAAATTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACATTGTCGTTGCCGCCAGATG	Pst I
233	Forward	CGCGGATCCCATATG-GCGGACAAACCCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGCATTGAGCAG	XhoI
234	Forward	CGCGGATCCCATATG-GCCGTTTCACTGACCG	BamHI-

	Reverse	GCCCAAGCTT-ACGGTTGGATTGCCATG	NdeI
235	Forward	CGCGGATCCCATATG-GCCTGCCAAGTTCAAA	Hind III
	Reverse	CCCGCTCGAG-TTTGGGCTGCTCTTC	BamHI-
236	Forward	CGCGGATCCCATATG-GCGCGTTTCGCCTT	NdeI
	Reverse	CCCGCTCGAG-ATGGGTCGCGCGCCGT	XhoI
238	Forward	CGCGGATCCGCTAGC-AACGGTTTGGATGCCCG	BamHI-
	Reverse	CCCGCTCGAG-TTTGTCTAAGTTCCTGATATG	NdeI
239	Forward	CCGGAATTCTACATATG-CTCCACCATAAAGGTATTG	XhoI
	Reverse	CCCGCTCGAG-TGGTGAAGAGCGGTTTAG	EcoRI-
240	Forward	CGCGGATCCCATATG-GACGTTGGACGATTTC	NdeI
	Reverse	CCCGCTCGAG-AAACGCCATTACCCGATG	XhoI
241	Forward	CCGGAATTCTACATATG-CCAACACGTCCAAC	BamHI-
	Reverse	CCCGCTCGAG-GAATGCGCCTGTAATTAATC	NdeI
242	Forward	CGCGGATCCCATATG-ATCGGCAAACCTTGTTG	XhoI
	Reverse	GCCCAAGCTT-ACCGATACGGTCGCAG	BamHI-
243	Forward	CGCGGATCCCATATG-ACGATTTTTTCGATGCTGC	NdeI
	Reverse	CCCGCTCGAG-CGACTTGGTTACCGCG	XhoI
244	Forward	CGCGGATCCCATATG-CCGTCTGAAGCCC	BamHI-
	Reverse	CCCGCTCGAG-TTTTTTCGGTAGGGGATTT	NdeI
246	Forward	CGCGGATCCCATATG-GACATCGGCAGTGC	XhoI
	Reverse	CCCGCTCGAG-CCCGCGCTGCTGGAG	BamHI-
247	Forward	CGCGGATCCCATATG-GTCGGATCGAGTTAC	NdeI
	Reverse	CCCGCTCGAG-AAGTGTTCTGTTTGCGCA	XhoI
248	Forward	CGCGGATCCCATATG-CGCAAACAGAACACT	BamHI-
	Reverse	CCCGCTCGAG-CTCATCATTATTGCTAACA	NdeI
249	Forward	CGCGGATCCCATATG-AAGAATAATGATTGCTTC	XhoI
	Reverse	CCCGCTCGAG-TTCCCGACCTCCGAC	BamHI-
251	Forward	CGCGGATCCCATATG-CGTGCTGCGGTAGT	NdeI
	Reverse	CCCGCTCGAG-TACGAAAGCCGGTCGTG	XhoI
253	Forward	AAAAAAGAATTC-ATGATTGACAGGAACCGTATGCTGCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I

253a	Forward	AAAAAAGAATTC-AAAATCCTTTTGAAAACAAGCGAAAACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I
254	Forward	AAAAAAGAATTC-ATGTATACAGGCGAACGCTTCAATAC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATTACGTAACCGTACACGCTGAC	Xba I
255	Forward	CGCGGATCCCATATG-GCCGCGTTGCGTTAC	BamHI-
	Reverse	CCCGCTCGAG-ATCCGCAATACCGACCAG	NdeI
			XhoI
256	Forward	CGCGGATCCGCTAGC-TTTTAACACCGCCGGAC	BamHI-
	Reverse	CCCGCTCGAG-ACGCCTGTTTGTGCGG	NheI
			XhoI
257	Forward	CGCGGATCCCATATG-GCGGTTTCTTTCCTG	BamHI-
	Reverse	CCCGCTCGAG-GCGCGTGAATATCGCG	NdeI
			XhoI
258	Forward	AAAAAAGAATTC-GATTATTTCTGGTGGATTGTTGCGTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
258a	Forward	AAAAAAGAATTC-GCGAAGGCGGTGGCGCAAGGCGA	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
259	Forward	CGCGGATCCCATATG-GAAGAGCTGCCTCCG	BamHI-
	Reverse	CCCGCTCGAG-GGCTTTTCCGGCGTTT	NdeI
			XhoI
260	Forward	CGCGGATCCCATATG-GGTGCGGGTATGGT	BamHI-
	Reverse	CCCGCTCGAG-AACAGGGCGACACCCT	NdeI
			XhoI
261	Forward	AAAAAAGAATTC-CAAGATACAGCTCGGGCATTTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCAACAAGCCTTGGTCACT	Pst I
263	Forward	CGCGGATCCCATATG-GCACGTTTAACCGTA	BamHI-
	Reverse	CCCGCTCGAG-GGCGTAAGCCTGCAATT	NdeI
			XhoI
264	Forward	AAAAAAGGTACC-GCCGACGCAGTGGTCAAGGCAGAA	Kpn I
	Reverse	AAACTGCAG-TCAGCCGGCGGTCAATACCGCCCG	Pst I
265	Forward	AAAAAAGAATTC-GCGGAGGTCAAGAGAAGGTGTTTG	Eco RI
	Reverse	AAAAAACTGCAG-TTACGAATACGTCGTCAAATGCG	Pst I
266	Forward	AAAGAATTC-CTCATCTTTGCCAACGCCCCCTTC	Eco RI
	Reverse	AAACTGCAG-CTATTCCCTGTTGCGCGTGTGCCA	Pst I
267	Forward	AAAGAATTC-TTCTTCCGATTGATGTTAATCG	Eco RI
	Reverse	AAACTGCAG-TTAGTAAAAACCTTTCTGCTTGGC	Pst I
269	Forward	AAAGAATTC-TGCAAACCTTGCGCCACGTGCCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
269a	Forward	AAAAAAGAATTC-GACTTTATCCAAAACACGGCTTCGCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
270	Forward	AAAGAATTC-GCCGTCAAGCTCGTTTTGTGCAATG	Eco RI
	Reverse	AAACTGCAG-TTATTCGGCGGTAAATGCCGTCTG	Pst I
271	Forward	CGCGGATCCCATATG-CCTGTGTGCAGCTCGAC	BamHI-
	Reverse	CCCGCTCGAG-TCCCAGCCCCGTGGAG	NdeI
			XhoI

272	Forward	AAAGAATTC-ATGACCGCAAAGGAAGAACTGTTCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAGCAGTTCCAAATCGGGGCT	Pst I
273	Forward	AAAGAATTC-ATGAGTCTTCAGGCGGTATTTATATACCC	Eco RI
	Reverse	AAACTGCAG-TTACGCGTAAGAAAAAACTGC	Pst I
274	Forward	CGCGGATCCCATATG-ACAGATTTGGTTACGGAC	BamHI-
	Reverse	CCCGCTCGAG-TTTGCTTTCAGTATTATTGAA	NdeI
276	Forward	AAAAAAGAATTC- ATGATTTTGCCGTCGTCCATCACGATGATGCG	XhoI
	Reverse	AAAAAACTGCAG-CTACACCACCATCGGCGAATTTATGGC	Eco RI
277	Forward	AAAAAAGAATTC-ATGCCCCGCTTTGAGGACAAGCTCGTAGG	Pst I
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Eco RI
277a	Forward	AAAAAAGAATTC-GGGGCGGCGGCTGGGTTGGACGTAGG	Pst I
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Eco RI
278	Forward	AAAAAAGGTACC-GTCAAAGTTGTATTAATCGGGCCTTTGCC	Pst I
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Kpn I
278a	Forward	AAAAAAGAATTC-AAAACTCTCCTAATTCGTCATAGTCG	Pst I
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Eco RI
279	Forward	CGCGGATCCCATATG-TTGCTGCAATCACGATT	Pst I
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA	BamHI-
280	Forward	AAAAAAGGTACC-GCCCCCTGCCGTTGTAAACCAG	NdeI
	Reverse	AAAAAACTGCAG-TTATTGCTTCATCGCGTTGGTCAAGGC	XhoI
281	Forward	AAAAAAGAATTC-GCACCCGTCGGCGTATTCCTCGTCATGCG	Kpn I
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Pst I
281a	Forward	AAAAAAGAATTC-TCCTACCACATCGAAATTCCTTCCGG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
282	Forward	AAAAAAGAATTC-CTTTACCTTGACCTGACCAACGGGCACAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACCTGCCAGTTGCGGGAATATCGT	Eco RI
283	Forward	CGCGGATCCCATATG-GCCGTCTTTACTTGGAAG	Pst I
	Reverse	CCCGCTCGAG-ACGGCAGTATTTGTTTACG	BamHI-
284	Forward	CGCGGATCCCATATG-TTGCTGCAAAAGAATCG	NdeI
	Reverse	CCCGCTCGAG-CCGACTTTGCAAAAAC TG	XhoI
286	Forward	CGCGGATCCCATATG-GCCGACCTTTCGAAAA	BamHI-
	Reverse	CCCGCTCGAG-GAAGCGCGTTCCCAAG	NdeI
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG	XhoI
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC	EcoRI-
288	Forward	CGCGGATCCCATATG-CACACCGGACAGG	NheI
	Reverse	CCCGCTCGAG-CGTATCAAAGACTTGCGT	XhoI
290	Forward	CGCGGATCCCATATG-GCGGTTTGGGGCGGA	BamHI-

	Reverse	CCCGCTCGAG-TCGGCGCGGCGGGC	NdeI
292	Forward	CGCGGATCCCATATG-TGCGGGCAAACGCCC	XhoI
	Reverse	CCCGCTCGAG-TTGATTTTTCGGGATGATT	BamHI-
294	Forward	AAAAAAGAATTC-GTCTGGTCGATTCGGGTGTCAGAAC	NdeI
	Reverse	AAAAAACTGCAG-TTACCAGCTGATATAAAACATCGCTTT	XhoI
295	Forward	CGCGGATCCCATATG-AACCGGCCGGCCTCC	Eco RI
	Reverse	CCCGCTCGAG-CGATATTTGATTCCGTTGC	Pst I
297	Forward	AAAAAAGAATTC-GCATAATTGCTTCGACAGAGAG	BamHI-
	Reverse	AAAAAACTGCAG-TCAATCCGATTGCGACACGGT	NdeI
298	Forward	AAAAAAGAATTC-CTGATTGCCGTGTGGTTCAGCCAAAACCC	XhoI
	Reverse	AAAAAACTGCAG-TCATGGCTGTGTACTTGATGGTTGCGT	Eco RI
299	Forward	CGCGGATCCGCTAGC-CTACCTGTCGCCTCCG	Pst I
	Reverse	CCCGCTCGAG-TTGCCTGATTGCAGCGG	BamHI-
302	Forward	AAAAAAGAATTC-ATGAGTCAAACCGATACGCAACG	NheI
	Reverse	AAAAAACTGCAG-TTAAGGTGCGGGATAGAATGTGGGCGC	XhoI
305	Forward	AAAAAAGGTACC-GAATTTTACCGATTTCAGCACCGGA	Eco RI
	Reverse	AAAAAACTGCAG-TCATTCCCAACTTATCCAGCCTGACAG	Pst I
305a	Forward	AAAAAAGGTACC-TCCCGTTCGGGCAGTACGATTATGGG	Kpn I
	Reverse	AAAAAACTGCAG-TTACAAACCGACATCATGCAGGGTGAA	Pst I
306	Forward	CGCGGATCCCATATG-TTATGAACAAATTTTCCC	Kpn I
	Reverse	CCCGCTCGAG-CCGCATCGGCAGAC	Pst I
308	Forward	CGCGGATCCCATATG-TTAAATCGGGTATTTTATC	BamHI-
	Reverse	CCCGCTCGAG-ATCCGCCATTCCCTGC	NdeI
311	Forward	AAAAAAGGTACC-ATGTTCAATTTTGGCTGGGTGTTT	XhoI
	Reverse	AAACTGCAG-ATGTTCAATTTTCCCTGCCTTCGGC	Kpn I
312	Forward	AAAAAAGGTACC-ATGAGTATCCCATCCGGCGAAATT	Pst I
	Reverse	AAACTGCAG-TCAGTTTTTCATCGATTGAACCGG	Kpn I
313	Forward	AAAAAAGAATTC-ATGGACGACCCGCGCACCTACGGATC	Pst I
	Reverse	AAAAAACTGCAG-TCAGCGGCTGCCGCCGATTTTGCT	Eco RI
401	Forward	CGCGGATCCCATATG-AAGGCGGCAACACAGC	Pst I
	Reverse	CCCGCTCGAG-CCTTACGTTTTTCAAAGCC	BamHI-
402	Forward	AAAAAAGAATTC-GTGCCTCAGGCATTTTCATTTACCCTTGC	NdeI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	XhoI
402a	Forward	AAAAAAGAATTC-AGGCTGATTGAAAACAAACACGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Xba I
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG	Eco RI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG	Xba I
			BamHI-
			NdeI
			XhoI

501	Forward	CGCGGATCCCATATG-GCAGGCGGAGATGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGTGTGATGTTACCC	XhoI
502	Forward	CGCGGATCCCATATG-GTAGACGCGCTTAAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCTGCATGGCGGCG	XhoI
503	Forward	CGCGGATCCCATATG-TGTTGCGGGAAAGGCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGCGCATTCCTCGCA	XhoI
504	Forward	CGCGGATCCCATATG-AGCGATATTGAAGTGACG	BamHI- NdeI
	Reverse	GCCCAAGCTT-TGATTCAAGTCCTTGCCG	HindIII
505	Forward	CGCGGATCCCATATG-TTTCGTTTACAATTCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGTTTTATAGCGG	XhoI
510	Forward	CGCGGATCCCATATG-CCTTCGCGGACAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCACTGGCAGCG	XhoI
512	Forward	CGCGGATCCCATATG-GGACATGAAGTAACGGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGAATAGCCTTTGACG	XhoI
515	Forward	CGCGGATCCCATATG-GAGGAAATAGCCTTCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAATGCCGCAAAGCATC	XhoI
516	Forward	CGCGGATCCCATATG-TGTACGTTGATGTTGTGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCGGGCGGCATC	XhoI
517	Forward	CGCGGATCCCATATG-GGTAAAGGTGTGGAAATA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGCGCCCAGCCGT	XhoI
518	Forward	AAAGAATTC-GCTTTTTTACTGCTCCGACCGGAAGG	Eco RI
	Reverse	AAACTGCAG-TCAAATTCAGACTCTGCCAC	Pst I
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC	XhoI
520	Forward	CGCGGATCCCATATG-CCTGCGCTTCTTTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATTTACATTTCAGTCGGC	XhoI
521	Forward	CGCGGATCCCATATG-GCCAAAATCTATACCTGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATACGCCCCAGTTCC	XhoI
522	Forward	CGCGGATCCCATATG-ACTGAGCCGAAACAC	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTCTGATTTCAAATCGGCA	HindIII
523	Forward	CGCGGATCCCATATG-GCTCTGCTTTCCGCG	BamHI- NdeI

	Reverse	CCCGCTCGAG-AGGGTGTGTGATAATAAGAAG	XhoI
525	Forward	CGCGGATCCCATATG-GCCGAAATGGTTCAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCCGTGCATATCATAAA	XhoI
527	Forward	AAAGAATTC-TTCCCTCAATGTTGCCGTTTTCG	Eco RI
	Reverse	AAACTGCAG-TTATGCTAAACTCGAAACAAATTC	Pst I
529	Forward	CGCGGATCCGCTAGC-TGCTCCGGCAGCAAAAC	BamHI- NheI
	Reverse	GCCCAAGCTT-ACGCAGTTCGGAATGGAG	HindIII
530	Forward	CGCGGATCCCATATG-AGTGCGAGCGCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGACCGACTGATTCCG	XhoI
531	Forward	AAAAAAGAATTC-TATGCCGCCGCTACCAAATCTACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACAGCGCCGTGCCGACGACAAG	Pst I
532	Forward	AAAAAAGAATTC-ATGAGCGGTCAGTTGGGCAAAGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCGGTATCAAA	Pst I
532a	Forward	AAAAAAGAATTC-TTGGGTGTCGCGTTTGAGCCGGAAGT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCGGTATCAAA	Pst I
535	Forward	AAAGAATTC-ATGCCCTTTCCCGTTTTTCAGAC	Eco RI
	Reverse	AAACTGCAG-TCAGACGACCCCGCCTTCCCC	Pst I
537	Forward	CGCGGATCCCATATG-CATACCCAAAACCAATCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCCTGCAAATAAAGGGTT	XhoI
538	Forward	CGCGGATCCCATATG-GTCGAGCTGGTCAAAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGGCATTTCGGTTTCGTC	XhoI
539	Forward	CGCGGATCCGCTAGC-GAGGATTTCAGGAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TACCAATGTCGGCAAATC	XhoI
542	Forward	AAAGAATTC-ATGCCGTCTGAAACCGTGTC	Eco RI
	Reverse	AAACTGCAG-TTACCGCGAACCGGTCAGGAT	Pst I
543	Forward	AAAAAAGAATTC-GCCTTCGATGGCGACGTTGTAGGTAC	Eco RI
	Reverse	AAAAAATCTAGA-TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
543a	Forward	AAAAAAGAATTC-GGCAAAACTCGTCATGAATTTGC	Eco RI
	Reverse	AAAAAATCTAGA-TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
544	Forward	AAAGAATTC-GCGCCCGCCTTCTCCCTGCCCGACCTGCACGG	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
544a	Forward	AAAAAAGAATTC-GCAAAATGACTATAAAAAACAAAACTTCCAAGTACTTGC	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
547	Forward	AAAGAATTC-ATGTTTCGTAGATAACGGATTTAATAAAAC	Eco RI
	Reverse	AAACTGCAG-TTAACAACAAAAACAAACCGCTT	Pst I
548	Forward	AAAGAATTC-GCCTGCAAACCTCAAGACAACAGTGCGGC	Eco RI

	Reverse	AAACTGCAG-TCAGAGCAGGGTCCTTACATCGGC	Pst I
550	Forward	AAAAAAGTCGAC- ATGATAACGGACAGGTTTCATCTCTTTTCATTTTCC	Sal I
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAATCCCC	Pst I
550a	Forward	AAAAAAGAATTC-GTAAATCACGCCTTTGGAGTCGCAAACGG	Eco RI
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAATCCCC	Pst I
552	Forward	AAAAAAGAATTC-TTGGCGCGTTGGCTGGATAC	Eco RI
	Reverse	AAACTGCAG-TTATTTCTGATGCCTTTTCCCAAC	Pst I
554	Forward	CGCGGATCCCATATG-TCGCCCCGCGCCCAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCCCTGTCAGACAC	XhoI
556	Forward	AAAGAATTC-GCGGGCGGTTTTGTTTGGACATCCCG	Eco RI
	Reverse	AAACTGCAG-TTAACGGTGCGGACGTTTCTGACC	Pst I
557	Forward	CGCGGATCCCATATG-TGCGGTTTCCACCTGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCCGCCTTCAGAAAGG	XhoI
558	Forward	AAAGAATTC-GAGCTTTATATGTTTCAACAGGGGACGGC	Eco RI
	Reverse	AAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
558a	Forward	AAAAAAGAATTC-ATTAGATTCTATCGCCATAAACAGACGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
560	Forward	AAAAAAGAATTC- TCGCCTTTCCGGGACGGGGCGCACAAGATGGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATGCGGTTTCAGACGGCATTTTGGC	Pst I
561	Forward	CCGGAATTCTACATATG-ATACTGCCAGCCCGT	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCAGCTTTCTTCAGATG	XhoI
562	Forward	CGCGGATCCCATATG-GCAAGCCCGTCGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGACCAACTCCAACCTCGT	XhoI
565	Forward	CGCGGATCCCATATG-AAGTCGAGCGCGAAATAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCATTGATCGGCGGC	XhoI
566	Forward	CGCGGATCCCATATG-GTCGGTGGCGAAGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCATGGGCGAAGTCA	XhoI
567	Forward	CCGGAATTCTACATATG-AGTGCGAACATCCTTG	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCCCCGACACCCTCG	XhoI
568	Forward	CGCGGATCCCATATG-CTCAGGGTCAGACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGCGGCGTTCAG	XhoI
569	Forward	AAAAAAGAATTC-CTGATTGCCTTGTGGGAATATGCCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATGCATAGACGCTGATAACGGCAAT	Pst I
570	Forward	CGCGGATCCCATATG-GACACCTTCAAAAAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGGCGTTCATTTCTTT	XhoI

571	Forward	AAAAAAGAATTC- ATGGGTATTGCCGGCGCCGTAATGTTTTGAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATGGCCGACGCGCGGCTACCTGACG	Pst I
572	Forward	CGCGGATCCCATATG-GCGCAAAAAGGCAAAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCAGTGTGCCGATA	XhoI
573	Forward	CGCGGATCCCATATG-CCCTGTTTGTGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGTGTCAATTCGCC	XhoI
574	Forward	CGCGGATCCCATATG-TGGTTTGCCGCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACTTCGATTTTATTCTGGG	XhoI
575	Forward	CGCGGATCCCATATG-GTTTCGGGCGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGAATCTGAACAG	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC	XhoI
577	Forward	CGCGGATCCCATATG-GAAAGGAACGGTGTATTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGCTGTTTGGTAGATTCTG	XhoI
578	Forward	CGCGGATCCCATATG-AGAAGGTTTCGTACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCAACGCCTCCACG	XhoI
579	Forward	CGCGGATCCCATATG-AGATTGGGCGTTTCCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGAATTGATGATGTGTATGT	XhoI
580	Forward	CGCGGATCCCATATG-AGGCAGACTTCGCCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACTTCCCCCGAAGTG	XhoI
581	Forward	CGCGGATCCCATATG-CACTTCGCCCAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCCGTTTGGCTTTGG	XhoI
582	Forward	AAAAAAGAATTC-TTTGGAGAGACCGCGCTGCAATGCGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATGCCGTCCCAGTCGTTGAA	Xba I
583	Forward	AAAAAAGAATTC-ACTGCCGGCAATCGACTGCATAATCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGAGGTCAATATGATGAAATTG	Pst I
584	Forward	AAAAAAGAATTC- GCGGCTGAAGCATTGAATTACAATATTGTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGAACTGAACCGTCCCATTGACGCT	Pst I
585	Forward	AAAAAAGGTACC-TCTTTCTGGCTGGTGCAGAACACCCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTTCGCACTTTTTCTGTTTGGGA	Pst I
586	Forward	CGCGGATCCCATATG-GCAGCCCATCTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTCAGCGAATCAAGTTTC	XhoI
587	Forward	CGCGGATCCCATATG-GACCTGCCCTTGACGA	BamHI-

	Reverse	CCCGCTCGAG-AAATGTATGCTGTACGCC	NdeI
588	Forward	AAAAAAGAATTC-GCCGTCCTGACTTCCTATCAAGAACCAGG	XhoI
	Reverse	AAAAAACTGCAG-TTATTTGTTTTTGGGCAGTTTCACTTC	Eco RI
589	Forward	AAAAAAGAATTC-	Pst I
		ATGCAACAAAAAATCCGTTTCCAAATCGAAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAATCGATTTTACCCGTTTCAGGCG	Pst I
590	Forward	AAAAAAGAATTC-ATGAAAAAACCTTTGATTTCAGTTGCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTGCTGCGGCTCTGAAACCAT	Pst I
591	Forward	AAAAAAGAATTC-CACTACATCGTTGCCAGATTGTGCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAACCGAGCAGCCGGGTAACGTCGTT	Pst I
592a	Forward	AAAAAAGAATTC-CGCGATTACACCGCCAAGCTGAAAATGGG	Eco RI
	Reverse	AAAAAACTGCAG-TTACCAAACGTCGGATTTGATACG	Pst I
593	Forward	CGCGGATCCGCTAGC-CTTGAACCTGAACGGACTC	BamHI-
	Reverse	CCCGCTCGAG-GCGGAAGCGGACGATT	NheI
594a	Forward	AAAAAAGAATTC-GGTAAGTTCGCCGTTTCAGGCCTTTCA	XhoI
	Reverse	AAAAAACTGCAG-TTACGCCGCCGTTTCCTGACACTCGCG	Eco RI
595	Forward	AAAAAAGAATTC-TGCCAGCCGCCGGAGGCGGAGAAAGC	Pst I
	Reverse	AAAAAACTGCAG-TTATTTCAAGCCGAGTATGCCGCG	Eco RI
596	Forward	CGCGGATCCCATATG-TCCCAACAATACGTC	Pst I
	Reverse	CCCGCTCGAG-ACGCGTTACCGGTTTGT	BamHI-
597	Forward	CGCGGATCCCATATG-CTGCTTCATGTCAGC	NdeI
	Reverse	GCCCAAGCTT-ACGTATCCAGCTCGAAG	XhoI
601	Forward	CGCGGATCCCATATG-ATATGTTCCCAACCGGCAAT	HindIII
	Reverse	CCCGCTCGAG-AAAACAATCCTCAGGCAC	BamHI-
602	Forward	CGCGGATCCGCTAGC-TTGCTCCATCAATGC	NdeI
	Reverse	CCCGCTCGAG-ATGCAGCTGCTAAAAGCG	XhoI
603	Forward	AAAAAAGAATTC-CTGTCCTCGCGTAGGCGGGGACGGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAGATGCCGGCAAGTTCGGC	Pst I
604	Forward	CGCGGATCCGCTAGC-CCCGAAGCGCACTT	BamHI-
	Reverse	CCCGCTCGAG-GACGGCATCTGCACGG	NheI
606a	Forward	AAAAAAGAATTC-CGCGAATACCGCGCCGATGCGGGCGC	XhoI
	Reverse	AAAAAACTGCAG-TTAAAGCGATTTGAGGCGGGCGATACG	Eco RI
607	Forward	AAAAAAGAATTC-ATGCTGCTCGACCTCAACCGCTTTTC	Pst I
	Reverse	AAAAAACTGCAG-TCAGACGGCCTTATGCGATCTGAC	Eco RI
608	Forward	AAAAAAGAATTC-ATGTCCGCCCTCCTCCCCATCATCAACCG	Pst I
	Reverse	AAAAAACTGCAG-TTAGTCTATCCAAATGTCGCGTTC	Eco RI
609	Forward	CGCGGATCCCATATG-GTTGTGGATAGACTCG	Pst I
			BamHI-
			NdeI

	Reverse	CCCGCTCGAG-CTGGATTATGATGTCTGTC	XhoI
610	Forward	CGCGGATCCCATATG-ATTGGAGGGCTTATGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCTTCAACATCTTTGCC	XhoI
611	Forward	CGCGGATCCCATATG-CCGTCTCAAAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGACTTTGAACGCGCAA	XhoI
613	Forward	CGCGGATCCCATATG-TCGCGTTCGAGCCG3	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCCTGTAAAATAAGCGGC	XhoI
614	Forward	CGCGGATCCCATATG-TCCGTCGTGAGCGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCATACTGCGGCGTTC	XhoI
616	Forward	AAAAAAGAATTC-ATGTCAAACACAATCAAAATGGTTGTCGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAGTCCGGGCGGCAGGCAGCTCG	Xba I
619a	Forward	AAAAAAGAATTC-GGGCTTCTCGCCGCCTCGCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATTTTTTGTGTTTTAAACGAGATA	Pst I
622	Forward	CGCGGATCCCATATG-GCCGCCCTGCCTAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGTCCAAATGATAAATCTG	XhoI
624	Forward	CGCGGATCCCATATG-TCCCCGCGCTTTTACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGATTCGGGCCTGCGC	XhoI
625	Forward	CGCGGATCCCATATG-TTTGCAACCAGGAAAATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCAAAATTACCGCCTT	XhoI
627a	Forward	AAAAAAGAATTC-AAAGCAGGCGAGGCAGGCGCGCTGGG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGAATGAAACAGGGTACCCGTCATCAAGGC	Pst I
628	Forward	AAAAAAGGTACC-GCCTTACAAACATGGATTTTGC GTTC	Kpn I
	Reverse	AAAAAACTGCAG-CTACGCACCTGAAGCGCTGGCAAA	Pst I
629a	Forward	AAAAAAGAATTC-GCCACCTTTATCGCGTATGAAAACGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACAACACCGCCGTCGGTTCAAACC	Pst I
630a	Forward	AAAAAAGAATTC-GCGGCTTTGGGTATTTCTTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGAGACTTCGCCAATGGAGCCGGG	Pst I
635	Forward	AAAAAAGAATTC- ATGACCCAGCGACGGGTCTGGCAAGCAAAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATCCACTATAATCCTGTGCT	Pst I
638	Forward	AAAAAAGAATTC-ATGATTGGCGAAAAGTTTATCGTAGTTGG	Eco RI
	Reverse	AAAAAACTGCAG-TCACGAACCGATTATGCTGATCGG	Pst I
639	Forward	CGCGGATCCCATATG-ATGCTTTATTTTGTTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCGCGGCTGCCGAC	XhoI
642	Forward	CGCGGATCCCATATG-CGGTATCCGCCGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGATTGCGGGGCATTA	XhoI

643	Forward	CGCGGATCCCATATG-GCTTCGCCGTCGGCAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACCGAAAAACAGACCGC	XhoI
644	Forward	AAAAAAGAATTC- ATGCCGTCTGAAAGGTCGGCGGATTGTTGCCC	Eco RI
	Reverse	AAAAAATCTAGA-CTACCCGCAATATCGGCAGTCCAATAT	Pst I
645	Forward	AAAAAAGAATTC-GTGGAACAGAGCAACACGTTAAATCG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGAGGAAACCGAAGACCAGGCCGC	Pst I
647	Forward	AAAAAAGAATTC-ATGCAAAGGCTCGCCGCAGACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGATTATCAGGGATATCCGGTAGAA	Pst I
648	Forward	AAAAAAGAATTC- ATGAACAGGCGCGACGCGCGGATCGAACG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGCTGTGTGCTGATTGAATGCGAC	Pst I
649	Forward	AAAAAAGAATTC-GGTACGTCAGAACCCGCCACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGCGGAAACTGCCGCCGTC	Pst I
650	Forward	AAAAAAGAATTC-ATGTCCAAACTCAAACCATCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGGCATGGCGGTCTGTTTT	Pst I
652	Forward	AAAAAAGGTACC- GCTGCCGAAGACTCAGGCCTGCCGCTTTACCG	Kpn I
	Reverse	AAAAAACTGCAG-TTATTTGCCAGTTGGTAGAATGCGGC	Pst I
653	Forward	AAAAAAGAATTC-GCGGCTTTGCCGGTAATTTTCATCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTATGCCGGTCTGGTTGCCGGCGGCGA	Pst I
656a	Forward	AAAAAAGAATTC-CGGCCGACGTCGTTGCGTCCTAAGTC	Eco RI
	Reverse	AAAAAACTGCAG-CTACGATTTGGCGATTTCACATCGT	Pst I
657	Forward	AAAAAAGAATTC-GCAGAATTTGCCGACCGCCATTTGTGCGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATAGGGACTGATGCAGTTTTTTTGC	Pst I
658	Forward	CGCGGATCCCATATG-GTGTCCGGAATTGTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCAGAATGTTTACCGTT	XhoI
661	Forward	AAAAAAGAATTC- ATGCACATCGGCGGCTATTTTATCGACAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TCACGACGTGTCTGTTCCGCCGTCGGGC	Pst I
663	Forward	CGCGGATCCCATATG-TGTATCGAGATGAAATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTAAAAATCGGGGCTGC	XhoI
664	Forward	CGCGGATCCCATATG-GCGGCTGGCGCGGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAATCGAGTTTTACACCAC	XhoI
665	Forward	AAAAAAGAATTC-ATGAAATGGGACGAAACGCGCTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAAAATTTGCCGACGATTTC	Pst I
666	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Xba I
667	Forward	AAAAAAGAATTC- CCGCATCCGTTTGATTTCATTTCGTATTCGTCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATGACACAATAGGCGCAAGTC	Pst I

669	Forward	AAAAAAGAATTC-ATGCGCCGCATCATTAACACACCAGCC	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTATCCGTTTGATGTCGGC	Pst I
670a	Forward	AAAAAAGAATTC-AAAAACGCTTCGGGCGTTTCGTCTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTAGGAGCTTTTGGAACGCGTCGGACTGGC	Pst I
671	Forward	CGCGGATCCCATATG-ACCAGCAGGGTAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAACTATAAAAAACGCAAG	XhoI
672	Forward	CGCGGATCCCATATG-AGGAAAATCCGCACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGGATAGGCGGTTG	XhoI
673	Forward	AAAAAAGAATTC-ATGGATATTGAAACCTTCCTTGCAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAACCCAGCTCGCGCAGGAA	Pst I
674	Forward	AAAAAAGAATTC-ATGAAAACAGCCCGCCGCGTTCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACGGCGTTTGGGCTCGTCGGG	Pst I
675	Forward	CGCGGATCCCATATG-AACACCATCGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCTTCGTCTTCAAACCTGT	XhoI
677a	Forward	AAAAAAGAATTC-AGACGGCATTCCCGATCAGTCGATTTTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGTATGCGCGAAATCGACCGCCCG	Pst I
680	Forward	CGCGGATCCGCTAGC-ACGAAGGGCAGTTCGG	BamHI- NheI
	Reverse	CCCGCTCGAG-CATCAAAAACCTGCCGC	XhoI
681	Forward	AAAAAAGAATTC-ATGACGACGCCGATGGCAATCAGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCGTCTTCCGCAAAAAACAGC	Pst I
683	Forward	CGCGGATCCCATATG-TGCAGCACACCGGACAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAGTTTTTTTCCGCATACG	XhoI
684	Forward	CGCGGATCCCATATG-TGCGGTACTGTGCAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTCGACCATCTGTTGCG	XhoI
685	Forward	CGCGGATCCCATATG-TGTTTGCTTAATAATAAACATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCA	XhoI
686	Forward	CGCGGATCCCATATG-TGCGGCGGTTTCGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGATTCTGATGAAG	XhoI
687	Forward	CGCGGATCCCATATG-TGCGACAGCAAAGTCCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCGCGGCTTTTTGTT	XhoI
690	Forward	CGCGGATCCCATATG-TGTTCTCCGAGCAAAGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TATTCGCCCCGTGTTTGG	XhoI
691	Forward	CGCGGATCCCATATG-GCCACGGCTTATATCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGGCAGGAAGAAAG	XhoI

694	Forward	CGCGGATCCCATATG-TTGGTTTCCGCATCCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCTGCGTCGGTGCGGT	XhoI
695	Forward	CGCGGATCCCATATG-TTGCCTCAAACCTCGTCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	XhoI
696	Forward	CGCGGATCCCATATG-TTGGGTTGCCGGCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGATTGCCGCAATGATG	XhoI
700a	Forward	AAAAAAGAATTC-GCATCGACAGACGGTGTGTCGTGGAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCTACCGGCACGACTTCCAAACC	Pst I
701	Forward	CGCGGATCCCATATG-AAGACTTGTTTGATACTTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCCGACAACAGCCTC	XhoI
702	Forward	AAAAAAGAATTC-ATGCCGTGTTCCAAAGCCAGTTGGATTTC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACCCCATTCACCCGGAGAACCGA	Pst I
703	Forward	CGCGGATCCGCTAGC-CAAACGCTGGCAACCG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTTGCAGGTTTGATGTTTG	XhoI
704a	Forward	AAAAAAGAATTC-GCTTCTACCGGTACGCTGGCGCG	Eco RI
	Reverse	AAAAAACTGCAG- TTAGTTTTCGCGGATAATATGGCGGGTGCG	Pst I
707	Forward	CGCGGATCCGCTAGC-GAAATTATTAACGATGCAGA	BamHI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGA	XhoI
708	Forward	CGCGGATCCGCTAGC-CCTTTTAAGCCATCCAAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TTGACCGGTGAGGACG	XhoI
710	Forward	CGCGGATCCCATATG-GAAACCCACGAAAAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGGTTTCGGTCAG	XhoI
714	Forward	CGCGGATCCCATATG-AGCTATCAAGACATCTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGTAGGTAAATCGGAT	XhoI
716	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTAGAACCGCATTGTC	XhoI
718	Forward	CGCGGATCCCATATG-GAGCCGATAATGGCAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCGCGGGCATGGTCTTGTC	XhoI
720	Forward	CGCGGATCCCATATG-AGCGGATGGCATAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTTGCATAGCTGTTGACCA	XhoI
723	Forward	CGCGGATCCCATATG-CGACCCAAGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATGCGAATCCGCCGCC	XhoI

725	Forward	CGCGGATCCCATATG-GTGCGCACGGTTAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTATCCTTAAGGGTTA	XhoI
726	Forward	CGCGGATCCCATATG-ACCATCTATTTCAAAAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCGATGTTTAGCGTCC	XhoI
728	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	XhoI
729	Forward	CGCGGATCCCATATG-TGCACCATGATTCCCCA	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTTGTCGGTTTGGGTATC	HindIII
731	Forward	CGCGGATCCGCTAGC-GCCGTGCCGGAGG	BamHI- NheI
	Reverse	CCCGCTCGAG-ACGGGCGCGGCAG	XhoI
732	Forward	CCGGAATTCTACATATG-TCGAAACCTGTTTTTAAGAA	EcoRI- NdeI
	Reverse	CCCGCTCGAG-CTTCTTATCTTTTTTATCTTTC	XhoI
733	Forward	CGCGGATCCCATATG-GCCTGCGGCGGCAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGCTTGCCTCCTTTAC	XhoI
734	Forward	CGCGGATCCCATATG-GCCGATACTTACGGCTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGATTTTGAATCAAAGAG	XhoI
735	Forward	CGCGGATCCCATATG-AAGCAGCAGGCGGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTCCGTAGCCGAGGG	XhoI
737	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	XhoI
739	Forward	CGCGGATCCCATATG-GCAAAAAAACCGAACA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAAGAGTTTGTGCGAGAATT	XhoI
740	Forward	CGCGGATCCCATATG-GCCAATCCGCCCGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAACGCGCCAAAATAGTG	XhoI
741	Forward	CGCGGATCCCATATG-TGCAGCAGCGGAGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTGGCGGCAAGGC	XhoI
743	Forward	CGCGGATCCCATATG-GACGGTGTGTGCCTGTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTACGGATCAAATTGACG	XhoI
745	Forward	CGCGGATCCCATATG-TTTTGGCAACTGACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAATCAGATGCCTTTAGG	XhoI
746	Forward	CGCGGATCCCATATG-TCCGAAAACAAACAAAAC	BamHI-

	Reverse	CCCGCTCGAG-TTCATTCGTTACCTGACC	NdeI
747	Forward	CCGGAATTCTAGCTAGC-CTGACCCCTTGGG	XhoI
	Reverse	GCCCAAGCTT-TTTTGATTTTAATTGACTATAGAAC	EcoRI-
749	Forward	CGCGGATCCCATATG-TGCCAGCCGCCG	NheI
	Reverse	CCCGCTCGAG-TTCAAGCCGAGTATGC	HindIII
750	Forward	CGCGGATCCCATATG-TGTTGCCCCGAACCTG	BamHI-
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCAA	NdeI
758	Forward	CGCGGATCCCATATG-AACAATCTGACCGTGTT	XhoI
	Reverse	CCCGCTCGAG-TGGCTCAATCCTTTCTGC	BamHI-
759	Forward	CGCGGATCCGCTAGC-CGTTTACACACACCAC	NdeI
	Reverse	CCCGCTCGAG-CCAGTTGTAGCCTATTTTG	XhoI
763	Forward	CGCGGATCCCATATG-CTGCCTGAAGCATGGCG	BamHI-
	Reverse	CCCGCTCGAG-TTCCGCAAATACCGTTTCC	NdeI
764	Forward	CGCGGATCCCATATG-TTTTCTCCGCCCTGA	XhoI
	Reverse	CCCGCTCGAG-TCGCTCCCTAAAGCTTTC	BamHI-
765	Forward	CGCGGATCCCATATG-TTAAGATGCCGTCCG	NdeI
	Reverse	CCCGCTCGAG-ACGCCGACGTTTTTTATTAA	XhoI
767	Forward	CGCGGATCCCATATG-CTGACGGAAGGGGAAG	BamHI-
	Reverse	CCCGCTCGAG-TTTCTGTACAGCAGGGG	NdeI
768	Forward	CGCGGATCCCATATG-GCCCCGCAAAAACCCG	XhoI
	Reverse	CCCGCTCGAG-TTTCATCCCTTTTTTGAGC	BamHI-
770	Forward	CGCGGATCCCATATG-TGCGGCAGCGGCGAA	NdeI
	Reverse	CCCGCTCGAG-GCGTTTGTCGAGATTTTC	XhoI
771	Forward	CGCGGATCCCATATG-TCCGTATATCGCACCTTC	BamHI-
	Reverse	CCCGCTCGAG-CGGTTCTTTAGGTTTGAG	NdeI
772	Forward	CGCGGATCCCATATG-TTTGCGGCGTTGGTGG	XhoI
	Reverse	CCCGCTCGAG-CAATGCCGACATCAAACG	BamHI-
774	Forward	CGCGGATCCCATATG-TCCGTTTACCCGTTCC	NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	XhoI
790	Forward	CGCGGATCCCATATG-GCAAGAAGGTCAAAAAC	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-GGCGTTGTTCCGGATTTCG	XhoI
900	Forward	CGCGGATCCCATATG-CCGTCTGAAATGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATGGAAAAGTCTGTTGTC	XhoI
901	Forward	CGCGGATCCCATATG-CCCGATTTTTCGATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAATGGAACAATACCAGG	XhoI
902	Forward.	CCGGAATTCTACATATG-TTGCACTTTCAAAGGATAATC	EcoRI- NdeI
	Reverse	CCCGCTCGAG-AAAAATGTACAATGGCGTAC	XhoI
903	Forward	CCGGAATTCTAGCTAGC-CAGCGTCAGCAGCACAT	EcoRI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGAA	XhoI
904	Forward	AAAAAAGGTACC-ATGATGCAGCACAAATCGTTTC	Kpn I
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
904a	Forward	AAAAAAGAATTC-CGGCTCGGCATTGTGCAGATGTTGCA	Eco RI
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
905	Forward	CGCGGATCCCATATG-AACAAAATATACCGCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCACTGATAACCGACAGAT	XhoI
907	Forward	CGCGGATCCCATATG-GGCGCGCAACGTGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCCACTGCCAGCG	XhoI
908	Forward	AAAGAATTC-GCAGAGTTAGTAGGCGTTAATAAAAATAC	Eco RI
	Reverse	AAACTGCAG-TTAATATGGTTTTGTCGTTTCG	Pst I
909	Forward	CGCGGATCCCATATG-TGCGCGTGGGAAACTTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGGTTTTGAACTTTGGTTTT	XhoI
910	Forward	AAAGAATTC-GCATTGCGCGGCGACTCTGCCGAGCG	Eco RI
	Reverse	AAACTGCAG-TCAGCGATCGAGCTGCTCTTT	Pst I
911	Forward	AAAGAATTC-GCTTTCCGCGTGGCCGGCGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-GTCGACTTATTCGGCGGCTTTTCCGC	Pst I
912	Forward	AAAAAAGAATTC- CAAATCCGTCAAACGCCACTCAAGTATTGAG	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTCCGTCCACGCCTTTCGC	Pst I
913	Forward	CGCGGATCCCATATG-GAAACCCGCCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGTTGTGTTCCAGGTTG	XhoI
915	Forward	CGCGGATCCCATATG-TGCCGGCAGGCGGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAAAATATAGGTATCAGG	XhoI
914	Forward	AAAGAATTC-GACAGAATCGGCGATTTGGAAGCACG	Eco RI
	Reverse	AAACTGCAG-CTATATGCGCGGCAGGACGCTCAACGG	Pst I
916	Forward	CGCGGATCCCATATG-GCAATGATGGCGGCTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI

917	Forward	AAAAAAGAATTC-CCTGCCGAAAAACCGGCACCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCCCCGCCTTCACATCCTG	Pst I
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC	BamHI-
	Reverse	CCCGCTCGAG-CGGGCGGTATTCTGGG	NdeI
			XhoI
920	Forward	CGCGGATCCCATATG-CACCGCGTCTGGGTC	BamHI-
	Reverse	CCCGCTCGAG-ATGGTGCGAATGACCGA	NdeI
			XhoI
921	Forward	AAAAAAGAATTC-TTGACGGAAATCCCCGTGAATCC	Eco RI
	Reverse	AAAAAACTGCAG-TCATTTCAAGGGCTGCATCTTCAT	Pst I
922	Forward	CGCGGATCCGCTAGC-TGTACGGCGATGGAGGC	BamHI-
	Reverse	CCCGCTCGAG-CAATCCCGGGCCGCC	NdeI
			XhoI
923	Forward	CGCGGATCCCATATG-TGTTACGCAATATTGTCCC	BamHI-
	Reverse	CCCGCTCGAG-GGACAAGGCGACGAAG	NdeI
			XhoI
925	Forward	CGCGGATCCCATATG-AAACAAATGCTTTTAGCCG	BamHI-
	Reverse	CCCGCTCGAG-GCCGTTGCATTTGATTTTC	NdeI
			XhoI
926	Forward	CGCGGATCCCATATG-TGCGCGCAATTACCTC	BamHI-
	Reverse	CCCGCTCGAG-TCTCGTGCGCGCCG	NdeI
			XhoI
927	Forward	CGCGGATCCCATATG-TGCAGCCCCGCAGC	BamHI-
	Reverse	CCCGCTCGAG-GTTTTTTGCTGACGTAGT	NdeI
			XhoI
929a	Forward	AAAAAAGAATTC-CGCGGTTTGCTCAAAACAGGGCTGGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAAGAAAGACGGAACTACTGCC	Xba I
931	Forward	AAAAAAGAATTC-GCAACCCATGTTTTGATGGAAAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTGCCCCGACAACAACGCGACG	Pst I
935	Forward	AAAAAAGAATTC-GCGGATGCGCCCGCGATTTTGGATGACAAGGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAAACCGCCAATCCGCCGACAC	Pst I
936	Forward	CGCGGATCCCATATG-GCCGCCGTGCGCGC	BamHI-
	Reverse	CCCGCTCGAG-GCGTTGGACGTAGTTTTG	NdeI
			XhoI
937	Forward	AAAAAAGAATTC-CCGGTTTACATTCAAACCGGCGCAAC	Eco RI
	Reverse	AAAAAACTGCAG-TTAAATGTATGCTGTACGCCAA	Pst I
939a	Forward	AAAAAAGAATTC-GGTTCCGGCAGCTGTGATGAAACC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGCAAACCTTGGATAAAGTTGGC	Pst I
950	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI-
	Reverse	CCCGCTCGAG-TTAGAACCGCATTTGCC	NdeI
			XhoI
953	Forward	CGCGGATCCCATATG-GCCACCTACAAAGTGGAC	BamHI-
	Reverse	CCCGCTCGAG-TTGTTTGGCTGCCTCGAT	NdeI
			XhoI
957	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	BamHI-

	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	NdeI
958	Forward	CGCGGATCCCATATG-GCCGATGCCGTTGCG	XhoI
			BamHI-
	Reverse	GCCCAAGCTT-GGGTCGTTTGTTCGTC	NdeI
959	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	HindIII
			BamHI-
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	NdeI
961	Forward	CGCGGATCCCATATG-GCCACAAGCGACGACG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-CCACTCGTAATTGACGC	NdeI
972	Forward	AAAAAAGAATTC- TTGACTAACAGGGGGGGAGCGAAATTAAAAAC	XhoI
			Eco RI
	Reverse	AAAAAATCTAGA-TTAAAAATAATCATAATCTACATTTTG	Xba I
973	Forward	AAAAAAGAATTC-ATGGACGGCGCACAAACCGAAAAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTTCACGCGGGTCGCCATCAGCGT	Pst I
982	Forward	CGCGGATCCCATATG-GCAGCAAAGACGTAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CATCATGCCGCCCATCC	XhoI
983	Forward	CGCGGATCCCATATG-TTAGCTGTTGCAACAACAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI
987	Forward	CGCGGATCCCATATG-CCCCACTGGAAGAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TAATAAACCTTCTATGGGC	XhoI
988	Forward	CGCGGATCCCATATG-TCTTTAAATTACGGGAAAAAG	BamHI-
			NdeI
	Reverse	GCCCAAGCTT-TGATTTGCCTTTCCGTTTT	HindIII
989	Forward	CCGGAATTCTACATATG-GTCCACGCATCCGGCTA	EcoRI-
			NdeI
	Reverse	CCCGCTCGAG-TTTGAATTTGTAGGTGTATTGC	XhoI
990	Forward	CGCGGATCCGCTAGC-TTCAGAGCTCAGCTT	BamHI-
	2		NheI
	Reverse	CCCGCTCGAG-AAACAGCCATTGAGCGA	XhoI
992	Forward	CGCGGATCCCATATG-GACGCGCCCGCCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CCAAATGCCCAACCATTC	XhoI
993	Forward	CGCGGATCCCATATG-GCAATGCTGATTGAAATCA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAACACATCGCGCCCG	XhoI
996	Forward	CGCGGATCCCATATG-TGCGGCAGAAAATCCGC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCTAAACCCCTGTTTTCTC	XhoI
997	Forward	CCGGAATTCTAGCTAGC-CGGCACGCCGACGTT	EcoRI-
			NheI
	Reverse	CCCGCTCGAG-GACGGCATCGCTCAGG	XhoI

Underlined sequences indicate restriction recognition sites.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1>:

```

g001.seq
1   ATGCTGCCGC AGGGGAAGGC GCGCGGAGG GTGTCGGCGA ACGAGGTGTG
51  CGGCAGGGCT TGGCCCCGA TGGTGTGGT CATCTGCCAG ACGCTGCCGA
101 AACGCGATAC TTAAACGGC TCGGTACGC ATACTTTACC GGTTTGGGCG
151 ATTTTGCCGA GGTGTTGCG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201 GCGGTTTTTC GGTCTGCTT GTAACTCGGC GCGCGGCGT TCGTCTTGTC
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTTCGGT GCTGATGGTG
301 CCGTCTGAAG CGATGTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351 CCGGATTGTC CCGGCTTCAT CCGGCAGGTG GGACAATACG GCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2; ORF 001.ng>:

```

g001.pep
1   MLPQKAARR VSANEVSGRA CARMVLVICQ TLPKRDTLNG SGTHTLPVWA
51  ILPRSLRSKS TIITFSARFF GSVCSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEAMLRKSS GEKHSVHAD C PASSGRWDNT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3>:

```

m001.seq
1   ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTG
51  CGGCAssCTT ss.GCTTGGGA YGGTGTGGT CATCTGCCAA ACGCTGCCGA
101 AACGCGATAC TTAAACGGT TCGGTACGC ATACTGTGCC GGTTTGGGCG
151 ATTTTGCCGA GATCGTTACG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201 GCGGTTTTTC GGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTTCGGT GCTGATGGTG
301 CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351 CCGGATTGTC CCTCCGCAT CCGGCAGGTG GGACAAGACG GCATAG

```

This corresponds to the amino acid sequence <SEQ ID 4; ORF 001>:

```

m001.pep
1   MLPQKAARR MSANEVCGXL XAWXVLVICQ TLPKRDTLNG SGTHTVPVWA
51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEPILRKSS GEKHSVHAD C PSASGRWDKT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 5>:

```

a001.seq
1   ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTG
51  CGGCAAGGCT TGGGCTTGA TGGTGTGGT CATCTGCCAA ACGCTGCCGA
101 AACGCGATAC TTAAACGGT TCGGTACGC ATACTGTGCC GGTTTGGGCG
151 ATTTTGCCGA GGTGTTACG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201 GCGGTTTTTC GGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTTCGGT GCTGATGGTG
301 CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351 CCGGATTGTC CCTTGTGCAT CCGGCAGGTG GGACAAAACG GCATAG

```

This corresponds to the amino acid sequence <SEQ ID 6; ORF 001.a>:

```

a001.pep
1   MLPQKAARR MSANEVCGKA WAWMVLVICQ TLPKRDTLNG SGTHTVPVWA
51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEPILRKSS GEKHSVHAD C PCASGRWDKT A*

```

m001/a001 96.2% identity over a 131 aa overlap

```

          10      20      30      40      50      60
m001.pep  MLPQKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRSKS
          |||||
a001.pep  MLPQKAARRMSANEVCGKAWAWMVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRSKS

```

	10	20	30	40	50	60
	70	80	90	100	110	120
m001.pep	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
a001.pep	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
	70	80	90	100	110	120
	130					
m001.pep	PSASGRWDKTAX					
a001.pep	PCASGRWDKTAX					
	130					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 001 shows 89.3% identity over a 131 aa overlap with a predicted ORF (ORF 001.ng) from *N. gonorrhoeae*:

m001/g001

	10	20	30	40	50	60
m001.pep	MLPQGKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRSKS					
g001	MLPQGKAARRVVSANEVSGRACARMVLVICQTLPKRDTLNGSGTHTLPVWAILPRSLRSKS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m001.pep	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
g001	TIITFSARFFGSVCNSAARRSSCPSPKIGAVPFIGSVLMVPSEAMLRKSSGEKHSVHADC					
	70	80	90	100	110	120
	130					
m001.pep	PSASGRWDKTAX					
g001	PASSGRWDNTAX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 7>:

g003.seq

```

1  ATGGTCGTAT TCGTGGCTGA AGGCGTATTC GGTTCGCGCTG TTTTGGGTCA
51  CTTGGTATTG CTCTTCGGTC AGGGTGCGTT TGAGTTCGGC GTCACCTCGGT
101 TTTTATACG TTGCCCGGTC GAAGCCTTTG CCTTGCCTGT CGGCTTTGGT
151 TTTGCCCGGC AGCGGTTCTG CCGCTTTGCG GATGTCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAGG TAGTCCTGAT GGTATTCCTC GCGGTCGTAG
251 AAGTTTTTCA GCGGTTTCGT TTCAACAACG AGGGGCAGTT GGTATTTTGT
301 CTGCTCGCGT TTGAGGGCGG CGGCGATGAC GGCTTTTTCG GCGGGGTCGG
351 TGAGTACAC GCCGCTGCGG TATTGCGTGC CGGTGTCGTT ACCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAA TAATATTGCA GGATGTCGTC
451 CAGgCTGagT TTGTCGGCAT CGTaggtcac tTTGACGGTC TCGGCATGAC
501 CCGTATGGCG GTaggacact tctTCgtanc TcGGGtTTTC CGTGttGCCG
551 TTGGCgttac cGGATACCGC gtcaACCACG CCGTcgatgc gttggaAATa
601 ggCTTCCAag ccccaaaagc agccgccggc gaagtaaagtg gtgcccgtgt
651 tcatgattGC TGa

```

This corresponds to the amino acid sequence <SEQ ID 8; ORF 003.ng>:

g003.pep

```

1  MVVFVAEGVF GRAVLGHLVL LFGQGAFFFG VTRFFIRCRV EAFALRCGFG
51  FARQRFVGFA DVDVAVAVGV FNQVLMVFL GVVEVFQRFV FNNEGQLVFL
101 LLAFEGGGDD GFFGGVGVVH AAAVLRAGVV TLFVEAGRIN DAEIILQDVV

```

151 QAEFVGIVGH FDGLGMTRMA VGHEFFVRVER VAVGVTGYRV NHAVDALIEIG
201 FQAPKAAAGE VNGARVHDC

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 9>:

m003.seq
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCGCGCTG TTTTGGGTAA
51 CTGgTATTG CTCTTCGGTC AGGGTGCgTT TGAGTTCGGC GTCACTCGGT
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTTGCGGGG CGGTCTTGGT
151 TTTGCCCCGC AGCGGTTCGT CAGCKTTGCG GATGTCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTg
301 CTGCTCGCGT TTGAGGGCGk CGGCGATGAC GGCTTTTTCG kCGGGGTCGG
351 TGTAgtACAC GCCGCTGCGG TATTGCGTAC CGGTGTCGTT GCCCTGTTTg
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
451 TAGGCTGAGT TTGTCCGCAT CGTAGGTCAC TTTGACGGTT TCGGCGTGgC
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCGC
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGGAATA
601 GGCTTCCAAG CCCAGAAGC AGCg.CCGGC GAGGTAAATG GTGCGCGTGT
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 10; ORF 003>:

m003.pep Length: 221
1 MVVFVAEGIF GRAVLGNLXL LFGQGAfEFG VTRFFIRCRV EAFALRGGLG
51 FARQRFVSXA DVDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL
101 LLAFEGXGDD GFFXGVGVVH AAVLRTGVV ALFVEAGRIN DAEIILQDVV
151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF RAVGVVAGYR VNHAVDALIEI
201 GFQAPEAAXG EVNGARVHDF *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 11>:

a003.seq
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCGCGCTG TTTTGGGTAA
51 CTTGGTATTG CTCTTCGGTC AGGGTGCgTT TGAGTTCGGC GTCACTCGGT
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTTGCGGTG CGGTCTTGGT
151 TTTGCCCGGC AGCGGTTCGT CCGCTTTGCG GATATCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTg
301 CTGCTCGCGT TTGAGGGCGG CGGCGATGAC GGCTTTTTCG GCGGGGTCGG
351 TGTAgtACAC GCCGCTGCGG TATTGCGTAC CGGTGTCGTT GCCCTGTTTg
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
451 TAGGCTGAGT TTGTCCGCAT CGTAGGTCAC TTTGACGGTT TCGGCGTGgC
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCGC
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGGAATA
601 GGCTTCCAAG CCCAGAAGC AGCCGCCGGC GAGGTAGATG GTGCGCGTGT
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 12; ORF 003.a>:

a003.pep
1 MVVFVAEGIF GRAVLGNLVL LFGQGAfEFG VTRFFIRCRV EAFALRCGLG
51 FARQRFVGFA DIDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL
101 LLAFEGGGDD GFFGGVGVVH AAVLRTGVV ALFVEAGRIN DAEIILQDVV
151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF RAVGVVAGYR VNHAVDALIEI
201 GFQAPEAAG EVDGARVHDF *

m003/a003 95.9% identity over a 220 aa overlap

	10	20	30	40	50	60
m003.pep	MVVFVAEGIFGRAVLGNLXLFFGQGAfEFGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
a003	MVVFVAEGIFGRAVLGNLVLFFGQGAfEFGVTRFFIRCRVEAFALRCGLGFARQRFVGFA					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNEGQLVFLLLAFEGXGDDGFFXGVGVVH					
a003	DIDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNEGQLVFLLLAFEGGGDDGFFGGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
a003	AAAVLRTGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDALFQAPAAAXGEVNGARVHDFX					
a003	RVAVGVAGYRVNHAVDALFQAPAAAGEVDGARVHDFX					
	190	200	210	220		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 003 shows 88.6% identity over a 219 aa overlap with a predicted ORF (ORF 003.ng) from *N. gonorrhoeae*:

m003/g003

	10	20	30	40	50	60
m003.pep	MVVFVAEGVIFGRAVLGNLXLLFGQGAFFGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
g003	MVVFVAEGVIFGRAVLGHLVLLFGQGAFFGVTRFFIRCRVEAFALRCGFGFARQRFVGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNEGQLVFLLLAFEGXGDDGFFXGVGVVH					
g003	DVDVAVAVGVFNQVVLVFLGVVEVFQRFVFNNEGQLVFLLLAFEGGGDDGFFGGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
g003	AAAVLRAGVTLFVEAGRINDAEIILQDVVQAEFVGIVGHFDGLGMTRMAVGHFFV-RVF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDALFQAPAAAXGEVNGARVHDFX					
g003	RVAVGVAGYRVNHAVDALFQAPKAAAGEVNGARVHDC					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 13>:

g004.seq

```

1  ATGgtagAAC GGCATATCCA GCATTGCGG AACGGTCATC TTCATTGTAT
51  GCGCCCATGC CAACAagtga gccAAAtgtT CGGCGGCAGG GCCTacgatT
101 TCCGCGCCGA TAAagcggcc gGTGgctTTT tcgGCataca ggcgcaTatg
151 gCCTTTGTTT ACCAgcatca cgcggtgcg accttgatTTT TTGAACGATA
201 CTTCCGCgaT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTTGCgga ctggtaaACA CCACGCCAAT
301 GGTgctgcgg cGCAACCGC TGCCGATAtt cgGgtagcgg ccccgcggtta
351 ttgcccggca atcttacctt ggtcggcggc ttcatGCAGC AGGGGCagtt
401 ggttgacgc gtcgcccgcg ataAAGATAT GCGGAATgct ggtCTGCATg
451 gtCAGCGGAT CGGCAACGGG tacgccgcgc gcgtctttgT CGATATTGAT
501 GTTTTCCAAA CCGATATtgT CAACGTTCCG ACGGCgACCT ACGGCTGCCA

```



```

551 ACATATATTC GGCAACAAAT ACGCCTTTTT CGCCATCCTG CTCCCAATGG
601 ACTtctACAT TGCCGTCTGC GTCGAGTTG ACCTCGGTTT TAGCATCCAG
651 ATGCAGTTTC AATtctTCTC CGAACACGGC TTTGCGCTCG TCTGAAACAA
701 CGGGGTCGGA AATGCCGCCG ATGATTCCGC CCAAACGAA AATTTCAACT
751 TTCACACCCA AACGGTGCAA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 14; ORF 004.ng>:

g004.pep

```

1 MVERHIQHLR NGHLMRPC QQVSQMFGR AYDFRADKAA GGFFGIQAHM
51 AFVYQHHAHA TLIFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHAN
101 GAAQAATAADI RVAAPRYCPA ILPWSAASCS RGSWLDASPA IKICGMLVCM
151 VSGSATGTPR ASLSILMFSK PILSTFGRRP TAANIYSATN TPFSPSCSQW
201 TSTLPSASSL TSVLASRCSF NSSPNTAFAS SETTGSEMP MIPPKPKIST
251 FPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 15>:

m004.seq

```

1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51 GTGCCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCAGG GCCTACGATT
101 TCCGCGCCGA TAAAGCGGCC GGTGGCTTTT TCGGCATACA GCGCGATATG
151 GCCTTTGTTC ACCAGCATCA CGCGGCTGCG GCCTTGGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTAGAC CGACAAAGCC GATTGCGGA CTGGTAAACA CCACGCCGAT
301 GGTGCTGCGC CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGGCAATC TTGCCTTGGT CGGCAGCTTC ATGCAGCAGA GGCAGTTGGT
401 TGGACGCATC GCCTGCGATG AAGATATGCG GAATACTGGT CTGCATGGTC
451 AGCGGGTCGG CAACAGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATATT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCATC GAGTTTGACC TCGGTTTTAG CATCCAGATG
651 CAGTTTCAAT TCTTCGCCGA ACACGGCGTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCGGATG ATTCGCCCA AACCGAAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 16; ORF 004>:

m004.pep

```

1 MVERHIQHLR NGHLMCPs QQVROMFGR AYDFRADKAA GGFFGIQAHM
51 AFVHQHHAHA ALVFERFYAD DKFVGLVLRG NLRVFQTDKA DLRTGKHAD
101 GAAPQTAADI RVAALSPAI LPWSAASCSR GSWLDASPA KICGILVCMV
151 SGSATGTPRA SFSILIFSKE ILSTFGRRP AASIYSATN TPFSPSCSQW
201 STLPSASSLT SVLASRCSFN SSPNTAFAS ETTGSEMP MIPPKPKIST
251 TPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 17>:

a004.seq

```

1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51 GTGCCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCCGG ACCTACGATT
101 TCTGCGCCGA TGAAGCGGCC GGTGGCTTTT TCGGCATACA GCGCGATATG
151 GCCTTTGTTT ACCAGCATCA CGCGGCTGCG GCCTTGGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTGCGGA CTGGTGAACA CTACGCCGAT
301 GGTGCTGCGG CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGGCAATC TTGCCTTGGT CGGCGGCTTC ATGCAGCAGG GGCAGTTGGT
401 TGGACGCGTC GCCCGCAATA AAGATATGCG GAATACTGGT CTGCATAGTC
451 AGCGGATCGG CAACGGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATGT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCTACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCATC GAGTTTGACC TCGGTTTTAG CATCCAAATG
651 CAGTTTCAAT TCTTACCGA ACACGGCTTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCGGATG ATGCCACCA AACCGAAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 18; ORF 004.a>:

a004.pep

```

1  MVERHIQHLR NGHLLMCPS QQVRQMFQGR TYDFCADEAA GGFFGIQAHM
51 AFVYQHHAHA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGEHYAD
101 GAAAQTAADI RVAAALSPAI LPWSAASCSR GSWLDASPAI KICGILVCIV
151 SGSATGTPRA SFSILMFSPK ILSTFGRRT AASIYSATNT PFSPPSCSWT
201 STLPSASSLA SVLASKCSFN SSNTAFASS ETTGSEMPPM MPPKPKISTF
251 TPKRCNA*

```

m004/a004 94.9% identity over a 257 aa overlap

m004.pep	10	20	30	40	50	60
	MVERHIQHLRNGHLLMCPSQQVRQMFQGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA					
a004	MVERHIQHLRNGHLLMCPSQQVRQMFQGRAYDFRADKAAGGFFGIQAHMAFVYQHHAHA					
	10	20	30	40	50	60
m004.pep	70	80	90	100	110	120
	ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAALSPAI					
a004	ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGEHYADGAAAQTAADIRVAAALSPAI					
	70	80	90	100	110	120
m004.pep	130	140	150	160	170	180
	LPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTPRASFSILIFSKPILSTFGRRT					
a004	LPWSAASCSRGSWLDASPAIKICGILVCIVSGSATGTPRASFSILMFSPKILSTFGRRT					
	130	140	150	160	170	180
m004.pep	190	200	210	220	230	240
	AASIYSATNTPFSPPSCSWTSTLPSASSLTVLASRCSFNSSNTAFASSETTGSEMPPM					
a004	AASIYSATNTPFSPPSCSWTSTLPSASSLTVLASRCSFNSSNTAFASSETTGSEMPPM					
	190	200	210	220	230	240
m004.pep	250					
	IPPKPKISTFTPKRCNAX					
a004	MPPKPKISTFTPKRCNAX					
	250					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 004 shows 93.4% identity over a 258 aa overlap with a predicted ORF (ORF 004.ng) from *N. gonorrhoeae*:

m004/g004

m004.pep	10	20	30	40	50	60
	MVERHIQHLRNGHLLMCPSQQVRQMFQGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA					
g004	MVERHIQHLRNGHLLMRPCQQVSMFQGRAYDFRADKAAGGFFGIQAHMAFVYQHHAHA					
	10	20	30	40	50	60
m004.pep	70	80	90	100	110	119
	ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAA-LSPA					
g004	TLIFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHANGAAAQTAADIRVAAPRYCPA					
	70	80	90	100	110	120
m004.pep	120	130	140	150	160	179
	ILPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTPRASFSILIFSKPILSTFGRRT					

g005.seq

1	ATGGGGATGG	ACAATATTGA	TATGTTTCATG	CCTGAACAAG	AGGAAATCCA
51	ATCAATGTGG	AAAGAAATTT	TACTGAATTA	CGGTATTTTC	CTGCTCGAAC
101	TGCTTACCGT	GTTCGGCGCA	ATTGCGCTGA	TTGTGTGGC	TATTCGTACAG
151	AGTAAGAAAC	AGTCGGAAAG	CGGCAGTGTC	GTACTGACAG	TATTTTCGGA
201	AAATTATAAA	AAACAGCGGC	AATCGTTTGA	AACATTCTTT	TTAAGCGGAGG
251	AAGAGACAAA	ACATCAGGAA	AAAAAAGAAA	AGAAAAAGGA	AAAGGCGGAA
301	GCCAAAGCAG	AGAAAAAGCG	TTTGAAGGAG	GGCGGGGAGA	AATCTGCCGA
351	AACGC AAAA	TCCGCGCTTT	TTGTGTTGGA	TTTTGACGGC	GATTTGTATG
401	CACACGCGGT	AGAAATCCTTG	CGTCATGAGA	TTACGGCGGT	GCTTTTGATT
451	GCCAAGCCTG	AAGATGAGGT	TCTGCTCAGA	TTGGAAAGTC	CGGGCGGCGT
501	GGTTCACGGT	TACGGTTTGG	CGGCTTCGCA	GCTTAGGCGT	TTGCGCGAAC
551	GCAATATTCC	GCTGAccgct	gccgTCGATA	AGGTCGCGGC	AAGCGgcggc
601	tatatgatgc	cgtgtgtgGC	GGATAAAATT	GTTTCCGCTc	cgtttgcggt
651	catcggttcg	gtgggtgtgg	tgGcggaagt	gcCGAATATc	CaccgCctGT
701	TGAAAAACA	TGATATTGAT	GTGGATGTGA	TGACGGCGGG	CGAATTTAAG
751	CGCACGGTTA	CTTTTATGGG	TGAAAATACG	GAAAAGGGCA	AACAGAAATT
801	CCGGCAGGAA	CTGGAGGAAA	CGCATCAGTT	GTTC AAGCAG	TTTGTCAGTG
851	AAAACCGCCC	CGGTGTGGAT	ATTGAAAAAA	TAGCCAGCGG	CGAGCATTGG
901	TTCGGCCGGC	AGGCGTTGGC	GTGGAAC TTG	ATTGACGAGA	TTTCGACCAG
951	TGATGATTTG	TTGTTGAAAG	CGTTTGAAAA	CAAACAGGtt	aTCGAAGTGA
1001	AATATCAGGA	GAAGCGAAGC	CTGATCCAGC	GCATTGGTTT	GCAGGCGGAA
1051	GCTTCCGTTG	AAAAGTTGTT	TGCCAAACTT	GTC AACC GG C	GAGCGGATGT
1101	GATGTAG				

```
g005.pap
1  MGMNDNIDMF  PEQEEIQSMW  KEILLNYGIF  LLELLTVFGA  IALIVLAIQV
51  SKKQSESGSV  VLTDFSNEY  KQRQSFTFF  LSEETKHQE  KKEKKKEKAE
101  AKAEEKRLKE  GGEKSAETQ  SRLFVLDFD  DLYAHAVESL  RHEITAVALL
151  AKPEDEVLLR  LSPGGVVHG  YGLAASQLR  LRERNIPLTV  AVDKVAASGG
201  YMMACVADKI  VSAPFAVIG  VGVVAEVPNI  HRLCLKHDID  VDVMTAGEFK
251  RTVTFMGENT  EKGKQKFRQ  LEETHQLFKQ  FVSENRPGLD  IEKIATGEHW
301  FGRQALALNL  IDEISTDDL  LLKAFENKQV  IEVKYQEKRS  LIQRIGLQAE
351  ASVEKLFKL  VNRADVM*
```

```
m005.seq
1  ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51  GTGGAAAGAA ATTTTACTGA ATTACGTTAT TTCCTGCTC GAACTGCTTA
101 CCGTGTTCGG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AWAGCGGCAG TGTCGTACTG ACGGATTTTT CGGAAAATTA
201 TAAAAACAGC CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CACAACATCA GGAAAAAGAG GAAAAGAAAA AGGAAAAGGC GGAAGCCAAA
```

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301 GCAGAGAAAA A.CGTTTGAA GGAGGGTGGG GAGAAATCTG CCGAAACGCA
351 nAAATCACGC CTTTTTGTGT TGGANNNNNN NNNNNNNNNN NNNNNNNNNN
401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNGCGAGCGG CGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGCTTCC GCTCCGTTTG CGATTGTCGG
651 TTCGTGGGT GTGGTGGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGAAAAG GGCAAACAGA AATCCGACA
801 GGAACGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTTGCAGGC GGAAGCTTCT
1051 GTTGAAGAGT TGTTTGCCAA ACTTGTC AAC CGGCGGGCGG ATGTGATGT A
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 22; ORF 005>:

m005.pep

```

1 MDNIDMFMP EEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQSXSGSVVL TDFSENYKKQ RQSFEAFFLS GEEAQHQEKE EKKKEKAEAK
101 AEKXRLKEGG EKSAETXKSR LFVLXXXXXX XXXXXXXXXX XXXXXXXXXX
151 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXASGGYM
201 MACVADKIAS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG
301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIQLQAEAS
351 VEKLFKLVN RRADV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 23>:

a005.seq

```

1 ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51 GTGGAAAGAA ATTTTACTGA ATTACGGTAT TTTCTGCTC GAACTGCTTA
101 CCGTGTTCGG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AACACGTCCG AAAGCGGCAG TGTCGTACTG ACGGATTTT CGGAAAATTA
201 TAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CAAAACATCA GGAAAAAGAG GAAAAGAAAA AGGAAAAGGC GGAAGCCAAA
301 GCAGAGAAAA AGCGTTTGAA GGAGGGTGGG GAGAAATCTT CCGAAACGCA
351 AAAATCCGC CTTTTGTGT TGGATTGGA CGGCGATTG TATGCACACG
401 CCGTAGAATC CTTGCGTCAT GAGATTACGG CGGTGCTTTT GATTGCCAAG
451 CCTGAAGATG AGGTTCTGCT TAGATTGGA AGTCCGGGCG GCGTGTTCA
501 CGGTTACGGT TTGGCGGCTT CGCAGCTTAG GCGTTTGCGC GAACGCAATA
551 TTCCGCTGAC CGTCGCCGTC GATAAGGTGG CGGCGAGCGG TGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGTTTCC GCTCCGTTG CGATTGTCGG
651 TTCGGTGGGT GTTGTAGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGAAAAG GGCAAACAGA AATCCGACA
801 GGAACGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTTGCAGGC GGAAGCTTCT
1051 GTTGAAGAGT TGTTTGCCAA ACTTGTC AAC CGGCGGGCGG ATGTGATGTA
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 24; ORF 005.a>:

a005.pep

```

1 MDNIDMFMP EEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQSESGSVVL TDFSENYKKQ RQSFEAFFLS GEEAKHQEKE EKKKEKAEAK
101 AEKXRLKEGG EKSSSETQKSR LFVLDFDGLD YAHAVESLRH EITAVLLIAK
151 PEDEVLLRLE SPGGVVHGYG LAASQLRLRL ERNIPLTVAV DKVAASGGYM
201 MACVADKIVS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG

```

301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIQLQAEAS
 351 VEKLFKLVN RRADVM*

m005/a005 79.2% identity over a 366 aa overlap

m005.pep	MDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQXSXSGSVL
a005	MDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQSESGSVL
m005.pep	TDFSENYKKQSQSFEEFLSGEEAQHQEKEKKKEKAEAKAEKKRLKEGGEKSAETXKSR
a005	TDFSENYKKQSQSFEEFLSGEEAKHQEKEKKKEKAEAKAEKKRLKEGGEKSSSETQKSR
m005.pep	LFVLXX
a005	LFVLDLFDGLYAHAVESLRHEITAVLLIAKPEDEVLLRLLESPGGVVHGYGLAASQLRRLR
m005.pep	XXXXXXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSVGVVAEVPNIHRLKKHDIDVD
a005	ERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAIVGSVGVVAEVPNIHRLKKHDIDVD
m005.pep	VMTAGEFKRTVTFMGENTEGKQKFRQLEETHQLFKQFVSENRPQLDIEEVATGEHWFG
a005	VMTAGEFKRTVTFMGENTEGKQKFRQLEETHQLFKQFVSENRPQLDIEEVATGEHWFG
m005.pep	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFKLVN
a005	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFKLVN
m005.pep	RRADVMX
a005	RRADVMX

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 005 shows 77.0% identity over a 366 aa overlap with a predicted ORF (ORF 005.ng) from *N. gonorrhoeae*:

m005/g005

m005.pep	MDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQXSXSGSV
g005	MGMDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQSESGSV
m005.pep	VLTDFSENYKKQSQSFEEFLSGEEAQHQEKEKKKEKAEAKAEKKRLKEGGEKSAETXK
g005	VLTDFSENYKKQSQSFETFFLSEETKHQEKKEKKKEKAEAKAEKKRLKEGGEKSAETQK

	120	130	140	150	160	170
m005.pep	SRLFVLXXX					
		:				
g005	SRLFVLDFDGLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPGGVVHGYGLAASQLRR					
	130	140	150	160	170	180
	180	190	200	210	220	230
m005.pep	XXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSVGVVAEVPNIHRLKKHDID					
	:					
g005	LRERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAVIGSVGVVAEVPNIHRLKKHDID					
	190	200	210	220	230	240
	240	250	260	270	280	290
m005.pep	VDVMTAGEFKRTVTFMGENTEGKGQKFRQLEETHQLFKQFVSENRPQLDIEEVATGEHW					
g005	VDVMTAGEFKRTVTFMGENTEGKGQKFRQLEETHQLFKQFVSENRPGLDIEKIATGEHW					
	250	260	270	280	290	300
	300	310	320	330	340	350
m005.pep	FGRQALALNLIDEISTDDLLLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFACL					
g005	FGRQALALNLIDEISTDDLLLKAFENKQVIEVKYQEKSLIQRIGLQAEASVEKLFACL					
	310	320	330	340	350	360
	360					
m005.pep	VNRRADVMMX					
g005	VNRRADVMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 25>:

g006.seq

```

1  ATGCTGCTGG TGCTggaatt ttggttCGGc gtGtCGGCGG TGGGCatact
51  tgCGTTGTTT TTATGGCttt TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCGG CCTGAACAAC AGCTTGAAC gcgACAACCA CTTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GTACCGCCAT TACGGACTGG TTTCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGCTCGGCG
251 CGGCGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACGGCA GCGCGGGGCA TATTTATTTC GTCCGCACTT ATCTGTGGAT
351 GTTTGCCATG AGTTTGGACG ATGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTCCGAACG GAACATCAAA
451 GCCGGAACCT GA

```

This corresponds to the amino acid sequence <SEQ ID 26; ORF 006.ng>:

g006.pep

```

1  MLLVLEFWFG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51  KGDERQLYRH YGLVSRLRVL ISNREAFGYL CVGAAMGILF GFAFVMMTLK
101 GYGSAGHIYS VGTYLWMFAM SLDDVPRLVE QYSLNKDIGQ RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 27>:

m006.seq

```

1  ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
51  TGCGTTGTTT TTATGGCttt TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCGG CCTGAACAAC AGCTTGAAC GCGACAACCA CTTTATCCGA
151 AAAGGCGACC GCGGCAGCT GTACCGCCAT TACGGACTGC TTGCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGCTCGGCA
251 CGGCGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACAGCA GCGCGGGGCA TGTCTATTTC GTCCGCACTT ATCTGTGGAT

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351 GTTGTCCATG AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
 401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTCGGAACG GAACATCAAA
 451 GCCGGAACCTGA

This corresponds to the amino acid sequence <SEQ ID 28; ORF 006>:

m006.pep
 1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
 51 KGDRRQLYRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK
 101 GYSSAGHVYS VGTYLWMFAM SLDDVPRLVE QYSNLKDIGQ RIEWSERNIK
 151 AGT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 29>:

a006.seq
 1 ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
 51 TGCCTTGT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
 101 TGTATTTCCT CCTGAAGAAC AGCTTGAAC GCGACAACCA CTTTATCCGA
 151 AAAGGCGACG AGCGGCAGCT GGACGCCCAT TACGGACTGC TTGCGCGCCT
 201 CGGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGCTCGGCA
 251 CGCGGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAAA
 301 GGCTACAGCA GCGCGGGGCA TGCTATTTCG GTCGGCACTT ATCTGTGGAT
 351 GTTTGCCATA AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
 401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTCGAAACG GAACATCAAA
 451 GCCGGAACCT GA

This corresponds to the amino acid sequence <SEQ ID 30; ORF 006.a>:

a006.pep
 1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLKN SLERDNHFIR
 51 KGDERQLDRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK
 101 GYSSAGHVYS VGTYLWMFAI SLDDVPRLVE QYSNLKDIGQ RIEWSKRNK
 151 AGT*

m006/a006 96.7% identity over a 153 aa overlap

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGDRRQLYRH					
a006	MLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLKNSLERDNHFIRKGDERQLDRH					
	10	20	30	40	50	60
m006.pep	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSAGHVYSVGTYLWMFAM					
a006	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSAGHVYSVGTYLWMFAI					
	70	80	90	100	110	120
m006.pep	SLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
a006	SLDDVPRLVEQYSNLKDIGQRIEWSKRNKAGTX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 006 shows 95.4% identity over a 153 aa overlap with a predicted ORF (ORF 006.ng) from *N. gonorrhoeae*:

m006/g006

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGDRRQLYRH					

q006-1.seq

1	ATGTGGAAAA	TGTTGAAACA	CATAGCCAAA	ACCCACCGCA	AGCGATTGAT
51	TGGCACATTT	TCCCCGGTCG	GACTGGAAAA	CCTTTTGATG	CTGGGGTATC
101	CGGTGTTTGG	CGGCTGGCGT	ATTAATGCCG	TGATTGCGGG	GAGGGTGTTG
151	CAGCGTGTTC	TGTACGCTTT	GGTTGTATTT	TTGATGTGGC	TGGTCGGTGC
201	GGCACGGCGG	ATTACCGATA	CGCGCACGTT	TACGGCGATT	TATACCGAAA
251	TCGCCGTGCC	GGTTGTGTTG	GAACAACGGC	AGCGGCAAGT	CCCGCATTCA
301	GCGGTAACTG	CACGGGTTGC	CCTGTCGCGT	GAATTGTGCA	GCTTTTTTGA
351	AGAACACCTG	CCGATTGCCG	CGACATCCGT	CGATTCCATA	TTCGGCGCGT
401	GCATCATGCT	GCTGCTGCTG	GAATTTTGGG	TCGGCGTGTC	GGCGGTGGGC
451	ATACTTGCGT	TGTTTTTATG	GCTTTTGCCA	CGTTTTGCCG	CCATCAGCGA
501	AAACCTGTAT	TTCCGCCTGA	ACAAAGCTT	GGAACGCGAC	AACCACTTTA
551	TCCGAAAAGG	CGACGAGCGG	CAGCTGTACC	GCCATTACGG	ACTGTTTTCG
601	CGCCTGCGTG	TGCTGATTTT	CACACGCGAA	GCTTTCGGCT	ATCTGTCGCT
651	CGGCGCGGCG	ATGGGTATTT	TGTTTCGGCT	TGCTTTTGTT	ATGATGACGC
701	TCAAAGGCTA	CGGCAGCGCG	GGGCATATTT	ATTCCGTCGG	CACTTATCTG
751	TGGATGTTTT	CCATGAGTTT	GGACATGTG	CCGCGATTGG	TCGAACAAATA
801	TTCCAATTTC	AAAGACATCG	GACAACGGAT	AGAGTGGTCG	GAACGGAACA
851	TCAAAGCCGG	AACTTGA			

q006-1.ppt

1	MWKMLKHIAK	THRKRIGTF	SPVGLENLLM	LGYPVFGGWA	INAVIAGRUV
51	<u>QALLYALVVF</u>	LMWLGVGAARR	IDATRTFFTRI	YTEAIVPVVL	EQRQVRPHFS
101	AVTARVALSR	EFVFSFEELH	PIAATSVVSI	YGCACIMLLVL	EFWGVGSVAG
151	<u>ILALFLWLLP</u>	RFAAISENLY	FRLNNSLERD	NHFIRKGDGR	QLYRHYGLVS
201	RLRVILSNRE	APFLYLCVGA	MGILFGFAFV	MMTLKGYGSA	GHIYSVGTYL
251	WMFAMSLDDV	PRGVGEYSNL	KDIGORIEVS	ERNIKAGT	

m006-1.seq

1	ATGTGGAAAA	TGTTGAAACA	CATAGCCCAA	ACCCACCGCA	AGCGATTGAT
51	TGGCACATTT	TCCCTGGTCG	GACTGGAAAA	CCTTTTGATG	CTGGTGTATC
101	CGGTGTTTGG	CGCCCGGGCG	ATCAATGCGC	TGATTGCGGG	GGAGGTGTGG
151	CAGCGTTTGC	TGTACGCTTT	GGTTGTGCTT	TATGATGGC	TGGTCGGTGC
201	GGTGCGGCGG	ATTGCCGATA	CGCGCACGTT	TACGCGGATT	TATACCGAAA
251	TCGCCGTGCC	GGTCGTGTTG	GAACAGCGGC	AGCGACAAGT	CCCGCATTCT
301	GCGGTAACTG	CGCGGGTTGC	CCTGTCGCGT	GAGTTTGTCA	GCTTTTTTGA
351	AGAACACCTG	CCGATTGCCG	CGACATCCGT	CGTATCCATA	TTCGGCGCGT
401	GCATCATGCT	GCTGGTGCTG	GAATTTTGGG	TCGGCGTGTC	CGCGGTGGGC
451	ATACTTGCGT	TGTTTTTATG	GCTTTTGCCA	CGTTTTGCCG	CCATCAGCGA
501	AAACCTGTAT	TTCCCGCTGA	ACAACAGCTT	GGAACCGGCAC	AACCACTTTA
551	TCCGAAAAGG	CGACCGGCGG	CAGCTGTACC	GCCATTACGG	ACTGCTTTCG
601	CGCCTCGGTG	TGCTGATTTC	CACCGCGGAA	GCCTTCGGCT	ACTCTCGCGT

651 CGGCACGGCG ATGGGTATTT TGTTCCGGCTT TGCTTTTGTG ATGATGACGC
 701 TCAAAGGCTA CAGCAGCGCG GGGCATGTCT ATTCGGTCGG CACTTATCTG
 751 TGGATGTTTG CCATGAGTTT GGACGACGTG CCGCGATTGG TCGAACATA
 801 TTCCAATTTG AAAGACATCG GACAACGGAT AGAGTGGTCG GAACGGAACA
 851 TCAAAGCCGG AACTGA

This corresponds to the amino acid sequence <SEQ ID 34; ORF 006-1>:

m006-1.pep

1 MWKMLKHIAQ THRKRLIGTF SLVGLENLLM LVYPVFGGRA INAVIAGEVW
 51 QALLYALVVL LMWLVGAVRR IADTRTFTRI YTEIAVPVVL EQRQRQVPHS
 101 AVTARVALSR EFVSFFEEHL PIAATSVVSI FGACIMLLVL EFWVGVSAGV
 151 ILALFLWLLP RFAAISENLY FRLNNSLERD NHFIRKGD RR QLYRHYGLLA
 201 RLRVLISNRE AFGYLCVGT A MGILFGFAFV MMTLKGYSSA GHVYSVGTYL
 251 WMFAMSLDDV PRLVEQYSNL KDIGQRIEWS ERNIKAGT*

m006-1/g006-1 95.5% identity in 288 aa overlap

m006-1.pep	10	20	30	40	50	60
	MWKMLKHIAQTHRKRLIGTFSLVGLENLLMLVYPVFGGRAINAVIAGEVWQALLYALVVL					
g006-1	MWKMLKHIAKTHRKRLIGTFSPVGLENLLMLGYPVFGGWAINAVIAGRNVQALLYALVVF					
	10	20	30	40	50	60
m006-1.pep	70	80	90	100	110	120
	LMWLVGAVRR IADTRTFTRI YTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL					
g006-1	LMWLVGAARR IADTRTFTRI YTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL					
	70	80	90	100	110	120
m006-1.pep	130	140	150	160	170	180
	PIAATSVVSIFGACIMLLVLEFWVGVSAGVILALFLWLLPRFAAISENLYFRLNNSLERD					
g006-1	PIAATSVVSIFGACIMLLVLEFWVGVSAGVILALFLWLLPRFAAISENLYFRLNNSLERD					
	130	140	150	160	170	180
m006-1.pep	190	200	210	220	230	240
	NHFIRKGD RR QLYRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSA					
g006-1	NHFIRKGD RR QLYRHYGLVSRVLISNREAFGYLCVGAAMGILFGFAFVMMTLKGYGSA					
	190	200	210	220	230	240
m006-1.pep	250	260	270	280	289	
	GHVYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
g006-1	GHIYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 35>:

a006-1.seq (partial)

1 ..AGCCAAAACC ACCGCAAGCG ATTGATTGGC ACATTTTTC TGCTCGGACT
 51 GGAAAACCTT TTGATGCTGG TGTATCCGGT GTTTGGCGGC TGGGCGATTA
 101 ATGCCGTGAT TGCGGGGCAG GCGTGGCAGG CGTTGCTGTA CGCTTTGGTT
 151 GTGCTTTTGA TGTGGCTGGT CCGTGCGGCG CCGCGGATTG CCGATACGCG
 201 CACGTTTACG CGGATTATA CCGAAATCGC CGTGCCGGTT GTGTTGGAAC
 251 AGCGGCAGCG GCAAGTCCCG CATTCGGCGG TAAC TGCGCG GGTGCGCTG
 301 TCGCGTGAGT TTGTCAGCTT TTTGAAGAA CACCTGCCGA TTGCCGCGAC
 351 ATCCGTCGTA TCCATATTCG GCGCGTGCAT CATGCTGCTG GTGCTGGAAT
 401 TTTGGGTCGG CGTGTCGGCG GTGGGCATAC TTGCGTTGTT TTTATGGCTT
 451 TTGCCACGTT TTGCCGCCAT CAGCGAAAC CTGTATTTC CCCTGAAGAA
 501 CAGCTTGGA A CGCGACAACC ACTTTATCCG AAAAGGCGAC GAGCGGCAGC
 551 TGGACCGCCA TTACGGACTG CTTGCGCGCC TGCGTGTGCT GATTTCACAC
 601 CGCGAAGCCT TCGGCTATCT CTGCGTCGGC ACGGCGATGG GTATTTTGT
 651 CGGCTTTGCT TTTGTGATGA TGACGCTCAA AGGCTACAGC AGCGCGGGGC

701 ATGTCTATTC GGTCGGCACT TATCTGTGGA TGTTTGCCAT AAGTTTGGAC
 751 GACGTGCCGC GATTGGTCGA ACAATATTCC AATTGAAAG ACATCGGACA
 801 ACGGATAGAG TGGTCGAAAC GGAACATCAA AGCCGGAAC TGA

This corresponds to the amino acid sequence <SEQ ID 36; ORF 006-1.a>:

a006-1.pep (partial)

1 ..SQNHRKRLIG TFFLVGLENL LMLVYPVFGG WAINAVIAGQ AWQALLYALV
 51 VLLMWLVGAA RRIADTRTFT RIYTEIAVPV VLEQRQRQVP HSAVTARVAL
 101 SREFVSFFEE HLPAAATSVV SIFGACIMLL VLEFWGVSA VGILALFLWL
 151 LPRFAAISEN LYFRLKNSLE RDNHFIRKGD ERQLDRHYGL LARLRVLISN
 201 REAFGYLCVG TAMGILFGFA FVMMLKGYG SAGHVYSVGT YLWMFAISLD
 251 DVPRLEQYS NLKDIGQRIE WSKRNIKAGT *

a006-1/m006-1 95.7% identity in 280 aa overlap

	10	20	30	40	50
a006-1.pep	SQNHRKRLIGTFFLVGLENLLMLVYPVFGGWAINAVIAGQAWQALLYALVVL				
m006-1	MWKMLKHIAQTHRKRLLIGTFFSLVGLENLLMLVYPVFGGRAINAVIAGEVWQALLYALVVL				
	10	20	30	40	50
	60	70	80	90	100
a006-1.pep	LMWLVGAAARRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL				
m006-1	LMWLVGAVRRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL				
	70	80	90	100	110
	120	130	140	150	160
a006-1.pep	PIAATSVVSIFGACIMLLVLEFWGVSAVGILALFLWLLPRFAAISENLYFRLKNSLERD				
m006-1	PIAATSVVSIFGACIMLLVLEFWGVSAVGILALFLWLLPRFAAISENLYFRLNNSLERD				
	130	140	150	160	170
	180	190	200	210	220
a006-1.pep	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMLKGYSSA				
m006-1	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMLKGYSSA				
	190	200	210	220	230
	240	250	260	270	280
a006-1.pep	GHVYSVGTYLWMFAISLDDVPRLEQYSNLKDIGQRIEWSKRNIKAGTX				
m006-1	GHVYSVGTYLWMFAMSLDDVPRLEQYSNLKDIGQRIEWSERNIKAGTX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 37>:

g007.seq

1 atgaACACAA CCCGACTGCC GACCGCCTTC ATCTTGTGCT GCCTCTGcgC
 51 CGCcGCTTCT GCCGccgaca acAGCatcat gaCaAAAGGG CAAAAAGTGT
 101 ACGAATCcAa ctGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC
 151 ACTGCGtTTC CTccgctTTT CCggtcgGac tgtattatga acaAACCGCa
 201 cgTCctgctg cacagcatgg tcaaaggcAt cgacgggaca ttcaaagtgg
 251 agcggcaaaa cctacgacgg atttatgCcc gcaaccgcca tcagcgATGC
 301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

This corresponds to the amino acid sequence <SEQ ID 38; ORF 007.ng>:

g007.pep

1 MNTTRLPTAF ILCCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG
 51 TAFPPLFRSD CIMNKPHVLL HSMVKGIDGT FKVERQNLRR IYARNRHQRC
 101 GHCRRRHLYH ERL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 39>:

This corresponds to the amino acid sequence <SEQ ID 40; ORF 007>:

m007.per

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 41>:

a007.seq

This corresponds to the amino acid sequence <SEQ ID 42; ORF 007.a>:

a007.pap.

m007/a007 97.3% identity over a 113 aa overlap

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 007 shows 86.7% identity over a 113 aa overlap with a predicted ORF (ORF 007.ng) from *N. gonorrhoeae*:

m007/g007

```

      10      20      30      40      50      60
m007.pep  MNTRLPTALVLGCFCAASAADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD
          |||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g007      MNTRLPTAFILCCLCAASAADNSIMTKGQKVYESNCIACHGKKGEGRGTAFFPPLFRSD
          10      20      30      40      50      60

          70      80      90     100     110
m007.pep  FIMKKPQVLLHSMVKGINGTIKVRQNLQRIHARNRHQRCGHCRRRHLYHERLX
          ||::|:|||||:|:|:| |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

q007-1.seq (partial)

1	ATGAACACAA	CCCGACTGCC	GACCGCCTTC	ATCTTGTGCT	GCCTCTGCGC
51	CGCGCTTCT	GCCGCGCACA	ACAGCATCAT	GACAAAGGGG	CAAAAAGTGT
101	ACGAATCCAA	CTGCATCGCC	TGCCACGGCA	AGAAAGGGGA	AGGGCGCGGC
151	ACTGCGTTTC	CTCCGCTTTT	CCGGTCGGAC	TATATTATGA	ACAACACGCA
201	CGTCCTGCTG	CACAGCATGG	TCAAAGGCAT	CAACGGTACA	ATCAAAGTCA
251	ACGGCAAAAAC	CTACACACGGA	TTTATCGCCC	CAACCGCCAT	CAGCGATGCG
301	GACATTGCGC	CCGTGCGCC	TTTATCATG	AACCGCTTTG	ACAACGGCGG
351	CGGAAGCGTT	ACCGGAAAAAG	ACGTAATAACA	GGCAAAAGGC	AAAAAAAC.

g007-1.pap (partial)

1 MNTRLPTAF ILCCLCAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG
51 TAFPLFRSD YIMNKPVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVKOAKG KKN...

m007-1.seq

1	ATGAACACAA	CCCGACTGCC	GACCGCCCTC	GTCTTGGGCT	GCTTCTGCGC
51	CGCGCTTCT	GCCGCGACA	ACAGCATCAT	GACAAAAGGG	CAAAAAGTGT
101	ACGAATCCAA	CTCGCTCGCC	TGCCACGGCA	AAAAGGCGCA	AGGCCCGCGA
151	AGCATGTTT	CGCGCTCTA	CCGCTCCGAC	TTCATCATGA	AAAAACCGCA
201	GGTGCTGCTG	CACAGCATGG	TCAAAGGGAT	CAACGGTACA	ATCAAAGTCA
251	ACGGCAAAAC	CTACAACGGA	TTCATGCCCG	CAACCGCCAT	CAGCGATGCG
301	GACATTGCCG	CCGTGCACC	TTATATCATG	AACGCCTTTG	ACAACGGCGG
351	CGGAAGCGTT	ACCGAAAAAG	ACGTAAACA	GGCAAAAGC	AAAAAAACT
401	AA				

m007-1.pap

1 MNTTRLPTAL VLGCFCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVKOAKS KKN*

		10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCFCAAASADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD						
	: : : :						
g007-1	MNTTRLPTAFILCCLCAAASADNSIMTKGQKVYESNCIACHGKKGEGRGTAFPPLFRSD						
		10	20	30	40	50	60
		70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKGINGTIKVNKGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV						
	: : : : : : : : : : : : : : : : :						
g007-1	YIMNKPHVLLHSMVKGINGTIKVNKGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV						
		70	80	90	100	110	120
		130					
m007-1.pep	TEKDVKQAKSKKNX						
	:						
g007-1	TEKDVKQAKGKKN						
		130					

a007-1.seq (partial)

1 ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCCGGGA

```

151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACC GCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CCACTGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAAAACA GGCAAAAAAC AAAAAA..

```

This corresponds to the amino acid sequence <SEQ ID 48; ORF 007-1.a>:

a007-1.pep (partial)

```

1 MNTTRLPTAL VLGC LCA AAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVKQAKN KK..

```

m007-1/a007-1 98.5% identity in 132 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGC	FCA AAS AADNSIMTKG	QKVYESNCVACHGKKGEGRG	TMFPPLYRSD		
a007-1	MNTTRLPTALVLGC	LCA AAS AADNSIMTKG	QKVYESNCVACHGKKGEGRG	TMFPPLYRSD		
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKINGT	IKVNGKTYNGFMPATAISD	AADIAAVATYIMNAFDNGGGSV			
a007-1	FIMKKPQVLLHSMVKINGT	IKVNGKTYNGFMPATAISD	AADIAAVATYIMNAFDNGGGSV			
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVKQAKSKKNX					
a007-1	TEKDVKQAKNKK					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 49>:

g008.seq

```

1 ATGAACAACA GACATTTTGC CGTCatcgCC TTGGGCAGCA ACCTTGACAA
51 CCCCGCACAA CAAATacgcy gcgcattaga cgcgctctcg tcccatcctg
101 acatccggct tgaaCaggtt tcctcactgt aTatgaccgc acctgtcggT
151 tacgAcaaTC agcccgATT CATCaatgcc gTCTgcaccg TTTCCACCAC
201 CtTGGACGGC ATTGcccTGC TTGCCgaACT CAAccgTATC GAAGCCGATT
251 TCGGACGCGA aCGCAGTTTC CGCAATGCAC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCGGCC TTACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAAATACG GAAAGTTGT CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGACA GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 50; ORF 008.ng>:

g008.pep

```

1 MNNRHFAVIA LGSNLDNPAQ QIRGALDALS SHPDIRLEQV SSLYMTAPVG
51 YDNQPDFINA VCTVSTTLDG IALLAELNRI EADFGRRERF RNAPRTL DLD
101 IIDFDGISSD DPLRTLPHPR AHERSFVIRP LAEILPDFIL GKYGKVVELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 51>:

m008.seq

```

1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
51 CCCTGCTCAA CAGGTACGGC CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATT TGTCAATGCC GTCTGCACCG TTTCCACCAC
201 TCTGGACGGC ATTGCCyTGC TTGCCGAAT CAACCGTATC GAGGCTGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GKATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACACsCGAC TcACctTGCC

```

```

351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATCCGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTGTTTTA GGAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGyTGG GCAATCAAGG TATCCGTCTT TTACCGGACA GGTAAAT

```

This corresponds to the amino acid sequence <SEQ ID 52; ORF 008>:

```

m008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFGRRERSF RNAPRTLXLD
101 IIDFDGISSD DTRLTLPHPR AHERSFVIRP LAEILPDFVL GKHGKVAELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 53>:

```

a008.seq
  1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
 51 CCCTGCCCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATACCGCG GCCCGTCGGT
151 TACGACAATC AGCCCGATT CGTCAATGCC GTCTGCACCG TTTCCACCAC
201 CTTGGACGGC ATTGCCCTGC TTGCCGAACT CAACCGTATC GAAGCCGATT
251 TCGGACGCGA ACGCAGCTT CGCAACGCGC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCGAC TCACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATAAGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGATA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 54; ORF 008.a>:

```

a008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFGRRERSF RNAPRTLXLD
101 IIDFDGISSD DPRLTLPHPR AHERSFVIRP LAEILPDFIL GKHGKVAELS
151 KRLGNQGIRL LPDK*

```

m008/a008 97.6% identity over a 164 aa overlap

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHDPDIRLKQASSLYMTAPVGYNQPDFVNA					
a008	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHDPDIRLKQASSLYMTAPVGYNQPDFVNA					
	10	20	30	40	50	60
m008.pep	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
	70	80	90	100	110	120
m008.pep	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
	70	80	90	100	110	120
m008.pep	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
a008	AHERSFVIRPLAEILPDFILGKHGKVAELSKRLGNQGIRLLPDKX					
	130	140	150	160		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 008 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF008.ng) from *N. gonorrhoeae*:

m008/g008

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHDPDIRLKQASSLYMTAPVGYNQPDFVNA					
g008	MNNRHFAVIALGSNLDNPAQQIRGALDALSSHDPDIRLEQVSSLYMTAPVGYNQPDFINA					

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	10	20	30	40	50	60
m008.pep	70	80	90	100	110	120
	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHR					
g008						
	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDPRLTLPHR					
	70	80	90	100	110	120
m008.pep	130	140	150	160		
	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIIRLLPDRX					
g008						
	AHERSFVIRPLAEILPDFILGKYGKVVELSKRLGNQGIIRLLPDRX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 55>:

g009.seq

1	ATGCCCCGCG	CTGCCGTAGC	CTTTGAGCGT	CATCATCACA	AAAGCAAAGC
51	CGAACAAAAT	ACCCATCGCC	GCGCCGACGC	AGAGATAGCC	GAAGGCTTCG
101	CGGTTGGAAA	TCAGCACACG	CAGGCGCGAA	ACCAGTCCGT	AATGGCGGTA
151	CAGCTGCCGC	TCGTCGCCTT	TTCGGATAAA	GTGGTTGTcg	cGTTCCAAGC
201	TGTTGTTTcag	GCGGAAATAC	AGGTTTTCGC	TGATGGCGGC	AAAACGTGGC
251	AaaaGCCATA A				

This corresponds to the amino acid sequence <SEQ ID 56; ORF 009.ng>:

g009.pep

1	MPRAAFAFER	HHHKSKEQN	THRRADAEIA	EGFAVGNQHT	QARNQSVMAV
51	QLPLVAFSDK	VVVAFAQVVQ	AEIQVFADGG	KTWQKP*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 57>:

m009.seq

1	ATGCCCCGCG	CTGCTGTAGC	CTTTGAGCGT	CATCATCACA	AAAGCAAAGC
51	CGAACAAAAT	ACCCATCGCC	GTGCCGACGC	AGAGATAGCC	GAAGGCTTCG
101	CGGTTGGAAA	TCAGCACACG	CAGGCGCGCA	AGCAGTCCGT	AATGGCGGTA
151	CAGCTGCCGC	CGGTGCGCTT	TTCGGATAAA	GTGGTTGTcG	cGTTCCAAGC
201	TGTTGTTTcag	GCGGAAATAC	AGGTTTTCGC	TGATGGCGGC	AAAACGTGGC
251	AAAAGCCATA A				

This corresponds to the amino acid sequence <SEQ ID 58; ORF 009>:

m009.pep

1	MPRAAFAFER	HHHKSKEQN	THRRADAEIA	EGFAVGNQHT	QARKQSVMAV
51	QLPPVAFSDK	VVVAFAQVVQ	AEIQVFADGG	KTWQKP*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 009 shows 97.7% identity over a 86 aa overlap with a predicted ORF (ORF 009.ng) from *N. gonorrhoeae*:

m009/g009

	10	20	30	40	50	60
m009.pep	MPRAAFAFERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
g009						
	MPRAAFAFERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARNQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
m009.pep	70	80				
	VVVAFAQVVQAEIQVFADGGKTWQKPX					
g009						
	VVVAFAQVVQAEIQVFADGGKTWQKPX					
	70	80				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 59>:

```
a009.seq
  1 ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
 51 CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAA TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTC
151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGGTTGTCG CGTTCCAAGC
201 TGTTCCTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A
```

This corresponds to the amino acid sequence <SEQ ID 60; ORF 009.a>:

```
a009.pep
  1 MPRAAVAFAER HHHKSKAEQN THRRADAEIA EGFVGNQHT QARKQSVMAV
 51 QLPLVAFSDK VVVAFAQVLQ AEIQVFADGG KTWQKP*
```

m009/a009 97.7% identity over a 86 aa overlap

	10	20	30	40	50	60
m009.pep	MPRAAVAFAERHHHKSKEQNTTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
a009	MPRAAVAFAERHHHKSKEQNTTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
	70	80				
m009.pep	VVVAFAQVQAEIQVFADGGKTWQKPX					
	:					
a009	VVVAFAQVLQAEIQVFADGGKTWQKPX					
	70	80				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 61>:

```
g010.seq
  1 ATGGGTTTTTC CTGTTGCGAA GTTTGATGCC GTGATTGTCG GCGGTGGCGG
 51 TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTT CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GCGGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTCGC GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTCT TATTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTTGCGC CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGGCGAG GGCGGTATTC TGTGAacgc
801 cgacggcgaa cgcTTTATGG AAcgctatgc GCcgACCGta aAagaCTTGG
851 CTTCTCGCga cgtGGTTTCA CgcgcGatgG CgatggaAat ctatgaaggt
901 cgcggtctgT GtaaaAAcaA agaCCacgtC TTA CTGAAAA TCGACcAtAt
951 cggTGCAGAA AAAATTATGG AAAAAGTACC GGCATCCGC GAGATTTCCTCA
1001 TTCagtttgc cGGTATCGAT CCGATTAAAG ACCCGATTcc ggttgTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTcgc ACCAATTATC ACGGTGAAGT
1101 TGTTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT
1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga
```

This corresponds to the amino acid sequence <SEQ ID 62; ORF 010.ng>:

g010.pep


```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRDWHMY DTVKGSIDLW DDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHAEHGKRA VERACAVADR TGHAMLHTLY
151 QONVRANTQF FVEWTAQDLI RDENGDVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPT V KDLASRDVVS RAMAMEIYEG
301 RGCGKNKDHV LLKIDHIGAE KIMEKLPGR EISIQFAGID PIKDFIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 63>:

m010.seq (PARTIAL)

```

1  ..nTCCAATTAT CCAAATCCGG TCTGAATTGT GCCGTTTTGT CTAAAGTGTT
51  CCCGACCCGT TCGCATACCG TAGCGGCGCA GGGCGGTATT TCCGCTCTn
101 TGGGTAATGT GCAGGAAGAC CGTTGGGACT GGCACATGTA CGATACCCGTG
151 AAAGGTTCCG ACTGGTTGGG CGACCAAGAT GCGATTGAGT TTATGTGCCG
201 CGCCGCGCCT GAAGCCGTAA TTGAGTTGGA ACACATGGGT ATGCCTTTTG
251 ACCGTGTGGA AAGCGGTAAA ATTTATCAGC GTCTTTTCGG CGGCCATACT
301 GCCGAACACG GTAAACGCGC GGTAGAACGC GYCTGTGCCG TTGCCGACCG
351 TACAGGTCAT GCGATGCTGC ATACTTTGTA CCAACAAAAC GTCCGTGCCA
401 ATACGCAATT CTTGTGGAA TGGACGCGAC AAGATTTGAT TCGTGATGAA
451 AACGGCGATG TCGTCGGCGT AACC GCCATG GAAATGGAAA CCGGCGAAGT
501 TTATATTTTC CACGCTAAAG CTGTGATGTT TGCTACCGGC GCGGCGGGTC
551 GTATTTATGC GTCTTCTACC AATGCCTATA TGAATACCGC CGATGGTTTG
601 GGTATTTGTG CGCGTGCAGG TATCCCGTTG GAAGACATGG AATTCTGGCA
651 ATTCCAGCCG ACCGCGGTG CCGGTGCGGG CGTGTGATT ACCGAA....

```

This corresponds to the amino acid sequence <SEQ ID 64; ORF 010>:

m010.pep (PARTIAL)

```

1  ..XQLSKSGLNC AVLKVFPT SHTVAAQGGI SASXGNVQED RWDWHMYDTV
51  KGSDWLGDQD AIEFMCRAP EAVIELEHMG MPFDRVESGK IYQRPFGGHT
101 AEHGKRAVER XCAVADRTGH AMLHTLYQON VRANTQFFVE WTAQDLIRDE
151 NGDVVGVTAM EMETGEVYIF HAKAVMFATG GGGRIYASST NAYMNTGDGL
201 GICARAGIPL EDMFQWQFQ TGVAGAGVLI TE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 65>:

a010.seq

```

1  ATGGGCTTTC CTGTCGCAA GTTTGATGCC GTGATTGTGC GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGGTATT CCGCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCG GCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAA TTTATCAGCG
351 TCCTTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTGTGCG GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCGCA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCGGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CCGGCGCAGAA AAAATTATGG AAAAAGTCCC GGCATCCGC GAGATTTCCT
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCACT ATATGATGGG CCGTATCCG ACCAACTACC ATGGCGAAGT
1101 TGTCGTTTCT CAAGGCGACG AATACGAAGT GCCTGTAATA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCCTGT GCTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCT TTGCCTGCTA

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1301 ATGCCGGCGA ACTGACCCGC CAACGTATCG AGCGTTTGGG CAATCAAAC
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGCGGTTT
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TCGCGACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATGCCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGACGCT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 66; ORF 010.a>:

```

a010.pep
1  MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRDWHMY DTVKGSWDLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNV RANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGGKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPPIVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVFVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVOLHA GVFTDEILS KGVREVMAlA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLSAE ARKESRGAHA SDDHPERDDE
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010/a010 98.7% identity over a 231 aa overlap

```

                                10      20      30
m010.pep                      XQLSKSGLNCVLSKVFPTRSHTVAAQGGISASXGNV
                                |||||
a010      MGFPVRKFDAVIVGGGGAGLRAXLQLSKSGLNCVLSKVFPTRSHTVAAQGGISASLGNV
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m010.pep      QEDRDWHMYDTVKGSDWLDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                |||||
a010      QEDRDWHMYDTVKGSDWLDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m010.pep      GHTAEHGKRAVERXCAVADR TGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVG V
                                |||||
a010      GHTAEHGKRAVERACAVADR TGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVG V
                                130     140     150     160     170     180

                                160     170     180     190     200     210
m010.pep      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                |||||
a010      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                190     200     210     220     230     240

                                220     230
m010.pep      FQPTGVAGAGVLITE
                                |:|||||
a010      FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG
                                250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 010 shows 98.7% identity over a 231 aa overlap with a predicted ORF (ORF 010.ng) from *N. gonorrhoeae*:

m010.pap/g010.pap

m010.pap				10	20	30	
				XQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASXGNV			
g010	MGFPVRKFDAVIVGGGAGLRAALQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV						
	10	20	30	40	50	60	
m010.pap	40	50	60	70	80	90	
	QEDRWDWHMYDTVKGSDDLQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG						
g010	QEDRWDWHMYDTVKGSDDLQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG						
	70	80	90	100	110	120	
m010.pap	100	110	120	130	140	150	
	GHTAEHGKRAVERXCAVADRTGHAMLHTLYQONVRANTQFFVEWTAQDLIRDENGDDVVG						
g010	GHTAEHGKRAVERACAVADRTGHAMLHTLYQONVRANTQFFVEWTAQDLIRDENGDDVVG						
	130	140	150	160	170	180	
m010.pap	160	170	180	190	200	210	
	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ						
g010	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ						
	190	200	210	220	230	240	
m010.pap	220	230					
	FQPTGVAGAGVLITE						
g010	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVSRAAMEIYEG						
	250	260	270	280	290	300	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 67>:

g010-1.seq..

```

1  ATGGGTTTTCTGTTTCGCAA GTTGTATGCC GTGATTGTCG GCGGTGGCGG
51  TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTC
101 CCGTTTTGTC TAAAGTGTC CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GCGGTATTT CCGCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTGCG GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTGCT TATTTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTTGCGC CCGTGGCGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGGCGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTC TGTGTAACGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCGCGGA CGTGGTTTCA CGCGCGATGG CGATGGAAAT CTATGAAGGT
901 CGCGGCTGTG GTAAAAACAA AGACCACGTC TTAAGTAAAA TCGACCATAT
951 CCGTGCAGAA AAAATTATGG AAAAAGTGGC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTTGC CCGTATCGAT CCGATTAAAG ACCCGATTCC GGTGTTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTATC ACGGTGAAGT
1101 TGTTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT

```

1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga

This corresponds to the amino acid sequence <SEQ ID 68; ORF 010-1.ng>:

g010-1.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKV F PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHATAHGKRA VERACAVADR TGHAMLHTLY
151 QQNV RANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RGC GKNDHV LKIDHIGAE KIMEKLP GIR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEV PVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

g010-1 / P10444

sp|P10444|DHSA_ECOLI SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT
 gnl|PID|d1015210 (D90711) Succinate dehydrogenase, flavoprotein [Escherichia coli] gi|1786942
 (AE000175) succinate dehydrogenase flavoprotein subunit [Escherichia coli] Length = 588
 Score = 1073 (495.6 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 191/303 (63%), Positives = 238/303 (78%)

```

Query: 1  MGFPVRKFDAVIVXXXXXXXXXXXXXSKSGLNCVLSKVFPTRSHTVAAQGGISASLGNV 60
      M  PVR+FDVAV++ S+SG CA+LSKVFPTRSHTV+AQGGI+ +LGN
Sbjct: 1  MKLPVREFDAVIGAGGAGMRAALQISQSGQTCALLSKVFPTRSHTVSAQGGITVALGNT 60

Query: 61 QEDRWDWHMYDTVKGSDWLGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG 120
      ED W+WHMYDTVKGSD++GDQDAIE+MC+ PEA++ELEHMG+PF R++ G+IYQRPFG
Sbjct: 61 HEDNWEWHMYDTVKGSDYIGDQDAIEYMCKTGPEAILEHMG LPPSRLLDDGRIYQRPFG 120

Query: 121 GHATAHGKRAVERACAVADRTGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVG V 180
      G + G R A ADRTGHA+LHTLYQQN++ +T F EW A DL+++++G VVG
Sbjct: 121 GQSKNFGGEQAARTAAADRTGHALLHTLYQQNLKNHTTIPSEWYALDLVKNQDGAUVGC 180

Query: 181 TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ 240
      TA+ +ETGEV F A+A + ATGG GRIY S+TNA++NTGDG+G+ RAG+P++DME WQ
Sbjct: 181 TALCIETGEVVYFKARATVLATGGAGRIYQSTTNAHINTGDGVGM AIRAGVPVQDMEMWQ 240

Query: 241 FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG 300
      FHPTG+AGAGVL+TEG RGE G L LN GERFMERYAP KDLA RDVV+R++ +EI EG
Sbjct: 241 FHPTGIAGAGVLVTEGCRGEGGYLLNKHGERFMERYAPNAKDLAGRDVVARSIMIEIREG 300

Query: 301 RGC 303
      RGC
Sbjct: 301 RGC 303

```

Score = 249 (115.0 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 53/102 (51%), Positives = 62/102 (60%)

```

Query: 309 HVLLKIDHIGAEKIMEKLP GIREISIQFAGXXXXXXXXXXXXTTHYMMGGIPTNYHGEVV 368
      H LK+DH+G E + +LPGI E+S FA T HYMMGGIPT G+ +
Sbjct: 310 HAKLKLDHLGKEVLESRLPGILELSRTFAHVDPVKEPIPVIPVPTCHYMMGGIPTKVTTGQAL 369

Query: 369 VPQGEYEV PVKGLYAAGECACASVHGANRLGTNSLLDLVVF 410
      +V V GL+A GE AC SVHGANRLG NSLLDLVVF
Sbjct: 370 TVNEKGEDVVVPG LFAVG E IACVSVHGANRLGGNSLLDLVVF 411

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 69>:

m010-1.seq..

```

1  ATGGGTTTTTC CTGTTTCGCAA GTTGTATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCAGCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTC CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCGGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC

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451 CAACAAACG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGTTCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGGCGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTTC TGTTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTGGC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCC
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTACC ACGGCGAAGT
1101 TGTGTTCCG CAAGGTGAAG ATTACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCTTGT GCTTCCGTAC ACGGTGCGAA CCGCTGGGT
1201 ACCAACTCCC TGTGGACTT GGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCTT TTGCCTGCTA
1301 ATGCAGGTGA GTTGACCCGC CAACGTATCG AGCGTTTGA CAACCAAACC
1351 GATGGTGAAA ACGTTGATGC ATTGCGTCGC GAACTGCAAC GCTCTGTACA
1401 ACTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGCGTTC
1451 GAGAAGTCAT GGCGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTGATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCAGCGCG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATATCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGATGA

```

This corresponds to the amino acid sequence <SEQ ID 70; ORF 010-1>:

m010-1.pep..

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDMHY DTVKGSWDLG DQDAIEFMCR APEAVIELE
101 HMGMPPDRVE SGKIYQRPFG GHAEHKGRA VERACAVADR TGHAMLHTLY
151 QONVRANTQF FVEWTAQDLI RDENGDVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RMERYAPT V KDLSARDVVS RAMAMEIYEG
301 RCGGNKNDHV LKIDHIGAE KIMEKLPGR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVP QGEDYEVVPK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWK LPANAGELTR QRIERLDNOT
451 DGENVDALRR ELQSVQLHA GVFTDEILS KGVREVMIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551 NWMKHTLYHS DINTLSYKPV HTKPLSVEYI KPAKRUVY*

```

m010-1 / g010-1 99.5% identity in 410 aa overlap

```

          10      20      30      40      50      60
m010-1.pep  MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVFPTRSHTVAAQGGISASLGNV
          |||
g010-1      MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVFPTRSHTVAAQGGISASLGNV
          |||

          70      80      90     100     110     120
m010-1.pep  QEDRWDMHYDTVKGSWDLGDQDAIEFMCRAPAEVIELEHMGMPPDRVESGKIYQRPFG
          |||
g010-1      QEDRWDMHYDTVKGSWDLGDQDAIEFMCRAPAEVIELEHMGMPPDRVESGKIYQRPFG
          |||

          130     140     150     160     170     180
m010-1.pep  GHAEHKGRAVERACAVADRTGHAMLHTLYQONVRANTQFFVEWTAQDLIRDENGDVVGCV
          |||
g010-1      GHAEHKGRAVERACAVADRTGHAMLHTLYQONVRANTQFFVEWTAQDLIRDENGDVVGCV
          |||

          190     200     210     220     230     240
m010-1.pep  TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
          |||
g010-1      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
          |||

```

190

	190	200	210	220	230	240
	250	260	270	280	290	300
m010-1.pep	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
g010-1	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m010-1.pep	RGCCKNKHVLLKIDHIGA EKIMKLP GIREISIQFAGIDPIKDPIPVVPTTHYMGGIP					
g010-1	RGCCKNKHVLLKIDHIGA EKIMKLP GIREISIQFAGIDPIKDPIPVVPTTHYMGGIP					
	310	320	330	340	350	360
	370	380	390	400	410	420
m010-1.pep	TNYHGEVVVPQGEDYEVVVKGLYAAGECACASVHGANRLGTNSLLDLVVFGKAAGDSMIK					
g010-1	TNYHGEVVVPQGEDEYEVVVKGLYAAGECACASVHGANRLGTNSLLDLVVFRPTFRK					
	370	380	390	400	410	
	430	440	450	460	470	480
m010-1.pep	FIKEQSDWKPLPANAGELTRQRIERLDNQTDGENVDALRRELQRSVQLHAGVFRTEILS					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 71>:

a010-1.seq..

```

1  ATGGGCTTTC CTGTTGCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTGTATC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTTATGCG TCTTCTACCA ATGCCATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTTC TGTTGAATGC
801 CGACGCGCAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTCTCTCGCA CGTTGTTTCC CGCGCGATGG CGATGGAAT CTACGAAGGT
901 CCGGCTGCG GTAAAAACAA AGACCATGTC TTA CTGAAAA TCGACCATAT
951 CCGCGCAGAA AAAATTATGG AAAAAGTCC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CGGTATTCGG ACCAACTACC ATGGCGAAGT
1101 TGTCGTTTCT CAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 GCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAAACCT TTGCCTGCTA
1301 ATGCCGCGCA ACTGACCCGC CAACGTATCG AGCGTTTGA CAATCAAAC
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGCGTTTC
1451 GAGAAATCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATGCCAATA CTTGTCTCTA
1701 CAAACCGGTG CACACCAAGC CTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 72; ORF 010-1.a>:

a010-1.pep..

```

1  MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKV F PTRSHTVAAQ
51  GGISASLGNV QEDRWDRWHY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101  HMGMPFDRVE SGKIQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY

```

151 QQNVRRANTQF FVEWTAQDLI RDENGDVVGV TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RGCGKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVPK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKPLPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFRTEILS KGVREVMIAA ERVKRTEIKD
501 KSKVWNTARI EAELELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

m010-1 / a010-1 99.3% identity in 587 aa overlap

	10	20	30	40	50	60
a010-1.pep	MGFPVRKFDVAVIVGGGGAGLRAQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV					
m010-1	MGFPVRKFDVAVIVGGGGAGLRAQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a010-1.pep	QEDRWDWHMYDTVKGSDWLGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
m010-1	QEDRWDWHMYDTVKGSDWLGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
	70	80	90	100	110	120
	130	140	150	160	170	180
a010-1.pep	GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENGDVVGV					
m010-1	GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENGDVVGV					
	130	140	150	160	170	180
	190	200	210	220	230	240
a010-1.pep	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ					
m010-1	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
a010-1.pep	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVSRAMAMEIYEG					
m010-1	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVSRAMAMEIYEG					
	250	260	270	280	290	300
	310	320	330	340	350	360
a010-1.pep	RGCGKNKDHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIPVVPTTHYMMGGIP					
m010-1	RGCGKNKDHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIPVVPTTHYMMGGIP					
	310	320	330	340	350	360
	370	380	390	400	410	420
a010-1.pep	TNYHGEVVVPQGDEYEVVPKGLYAAGECACASVHGANRLGTNSLLDLVVFKAAGDSMIK					
m010-1	TNYHGEVVVPQGDEYEVVPKGLYAAGECACASVHGANRLGTNSLLDLVVFKAAGDSMIK					
	370	380	390	400	410	420
	430	440	450	460	470	480
a010-1.pep	FIKEQSDWKPLPANAGELTRQRIERLDNQT DGENVDALRRRELQRSVQLHAGVFRTEILS					
m010-1	FIKEQSDWKPLPANAGELTRQRIERLDNQT DGENVDALRRRELQRSVQLHAGVFRTEILS					
	430	440	450	460	470	480
	490	500	510	520	530	540
a010-1.pep	KGVREVMIAAERVKRTEIKDKSKVWNTARIEAELELDNLIEVAKATLVSAEARKESRGAHA					
m010-1	KGVREVMIAAERVKRTEIKDKSKVWNTARIEAELELDNLIEVAKATLVSAEARKESRGAHA					
	490	500	510	520	530	540
	550	560	570	580		
a010-1.pep	SDDHPERDDENWMKHTLYHS DANTLSYKPVHTKPLSVEYIKPAKRVYX					

m010-1 SDDHPERDDENWMKHTLYHSDINTLSYKPVHTKPLSVEYIKPAKRVYX
550 560 570 580

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 73>:

g011.seq
1 ATGAAGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTGG CTTTTCAGAC
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAC CCGCCTTACC GAAGATATGA AAACCGCGAT GCGCGCCAAA
151 GATCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAATGCCG CCGTCAAACA
201 GTTTGAAGTA GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA
251 TCCTGACCAA AATGGTCAAA CAGCGCAAAG ACGGCGCGAA AATCTACACT
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGACGT
351 GCTGCACCGC TACCTGCCGC AAATGCTCTC CGCCGGCGAA ATCCGCACCG
401 CCGTCGAAGC AGCCGTTGCC GAAACCGGCG CGGCAGGTAT GGCGGATATG
451 GGCAAAGTGA TGGTCGTATT GAAAACccGC CTCGCCGGCA AAGccgATAT
501 GGGCGAAGTC AACAAAATCT TGAAAAccGt aCTGACCGCC tga

This corresponds to the amino acid sequence <SEQ ID 74; ORF 011.ng>:

g011.pep
1 MKTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKTRLT EDMKTAMRAK
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDGAKIYT
101 EAGRQDLADK ENAEIDVLHR YLPQMLSAGE IRTAVEAAVA ETGAAGMADM
151 GKVMVVLKTR LAGKADMGEV NKILKTVLTA *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 75>:

m011.seq (partial)
1 ATGAGGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTGG CTTTTCAGAC
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAT CCGCCTTACC GAAGACATGA AAACCGCGAT GCGCGCCAAA
151 GACCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAACGCCG CCGTCAAACA
201 GTTTGAAGTG GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA
251 TCCTGACCAA AATGGTCAAA CAGCGAAAAG ACAGCGCGAA AATCTACACT
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGAGGT
351 ACTGCACCGC TACCTTCCCC AAATGCTTTC CGCCGGCGAA ATCCGTACCG
401 AGGTCGAAGC TGCCGTTGCC GAAACCGGCG CGGCAGGTAT GGCGGATATG
451 GGTAAGTCA TGGGGCTGCT GAAAACCCGC CTCGCAGGTA AAGCCGA...

This corresponds to the amino acid sequence <SEQ ID 76; ORF 011>:

m011.pep (partial)
1 MRTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKIRLT EDMKTAMRAK
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDSAKIYT
101 EAGRQDLADK ENAEIEVLHR YLPQMLSAGE IRTEVEAAVA ETGAAGMADM
151 GKVMGLLKTR LAGKA.....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 011 shows 95.8% identity over a 165 aa overlap with a predicted ORF (ORF 011.ng) from *N. gonorrhoeae*:

m011/g011

	10	20	30	40	50	60
m011.pep	MRTHRKTCSAVCF	AFQTASKPAVSIR	HPSEDIMSLKIR	LTEDMKTAMRAK	DQVSLGTIRL	
g011	MRTHRKTCSAVCF	AFQTASKPAVSIR	HPSEDIMSLKTR	LTEDMKTAMRAK	DQVSLGTIRL	
	10	20	30	40	50	60
m011.pep	INAAVKQFEVDER	TEADDAKITAIL	TKMVKQRKDSAK	IYTEAGRQDLAD	KENAEIEVLHR	
g011	INAAVKQFEVDER	TEADDAKITAIL	TKMVKQRKDGAK	IYTEAGRQDLAD	KENAEIDVLHR	
	70	80	90	100	110	120

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	70	80	90	100	110	120
	130	140	150	160		
m011.pep	YLPQMLSAGEIRTEVEAAVAETGAAGMADMGKVMGLLKTRLAGKA					
g011	YLPQMLSAGEIRTAEEAAVAETGAAGMADMGKVMVVLKTRLAGKADMGVKNILKTVLTA					
	130	140	150	160	170	180
g011	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 77>:

g012.seq

1	ATGCTCGCCC	GTCGCTATTT	TTTCAATATC	CAACCCGGGG	CGGTTTTTAC
51	TGACAAACTG	CTTGAACAAC	TGATGCGTTT	CCTCCAGTTC	CTGCCGGAAT
101	TTCTGTTTGC	CCTTTTCCGT	ATTTTCACCC	ATAAAAGTAA	CCGTGCGCTT
151	AAATTCGCCC	GCCGTCATCA	CATCCACATC	AATATCATGT	TTTTTCAACa
201	gGcggTGGAT	ATTTCGcact	tccgCcacca	caccacccga	accgatgacc
251	gcaaacggaG	CGGAAACAAT	TTTATCCGCC	acacacgcca	tcatatagcc
301	gcCGCTTGCC	GCGACCTTAT	CGAcggcgac	ggTCAGCGGA	ATATTGCGTT
351	CGCGCAAACG	CCTAAGCTGC	GAAGCCGCCA	AACCGTAACC	GTGAACCACG
401	CCGCCCGGAC	TTTCCAATCT	GAGCAGAAC	TCATCTTCAG	GCTTGCCAAT
451	CAAAAGCACC	GCCGTAATCT	CATGACGCAA	GGATTCTACG	GCGTGTGCAT
501	ACAAATCGCC	GTCAAATCC	AACACAAAAA	GGCGGGATT	TTGCGTTTCG
551	GCAGATTCT	CCCCGCCCTC	CTTCAAACGC	TTTTCTCTG	CTTTGGCTTC
601	CGCCTTTTCC	TTTTTCTTTT	CTTTTCTTTC	CTGATGTTTT	GTCTCTTCTC
651	CGCTTAA				

This corresponds to the amino acid sequence <SEQ ID 78; ORF 012.ng>:

g012.pep

1	MLARRYFFNI	QPGAVETDKL	LEQLMRFLQF	LPEFLFALFR	IFTHKSNRAL
51	KFARRHHIHI	NIMFFQQA	VDIRHFRHHTHR	TDDRKRSGNN	FIRHTRHHIA
101	AACRDLIDGD	GQRNIAFAQT	PKLRSRQTVT	VNHAARTFQS	EQNLIFRLGN
151	QKHRRNLMTQ	GFYGVCIQIA	VKIQHKKAGF	LRFRFLPAL	LQTLFLCFGF
201	RLFLFLFFFF	LMFCLFLA*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 79>:

m012.seq

1	ATGCTCGCCC	GTTGCCACTT	CCTCAATATC	CAATTGAGGG	CGGTTCTCGC
51	TGACAAACTG	CTTGAACAAC	TGATGCGTTT	CCTCCAGTTC	CTGTCCGAAT
101	TTCTGTTTGC	CCTTTTCCGT	ATTTTCACCC	ATAAAAGTAA	CCGTGCGCTT
151	AAATTCGCCC	GCCGTCATCA	CATCCACATC	AATATCATGT	TTTTTCAACA
201	GGCGGTGGAT	ATTTCGCTACT	TCCGCCACCA	CACCCACCGA	ACCGACAATC
251	GCAAACGGAG	CGGAAGCAAT	TTTATCCGCC	ACACACGCCA	TCATATAACC
301	GCCGCTCGCn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn
351	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn
401	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn
451	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn
501	nnnnnnnnnn	nnnnnnnnnC	AACACAAAAA	GGCGTGATT	TTGCGTTTCG
551	GCAGATTCT	CCCCACCCTC	CTTCAAACGT	TTTTCTCTG	CTTTGGCTTC
601	CGCCTTTTCC	TTTTTCTTTT	CCTCTTTTTC	CTGATGTTGT	GCCTCTTCCC
651	CGCTTAA				

This corresponds to the amino acid sequence <SEQ ID 80; ORF 012>:

m012.pep

1	MLARCHFLNI	QLRAVLADKL	LEQLMRFLQF	LSEFLFALFR	IFTHKSNRAL
51	KFARRHHIHI	NIMFFQQA	VDIRYFRHHTHR	TDRKRSGSN	FIRHTRHHIT
101	AARXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX
151	XXXXXXXXXX	XXXXXXXXXX	XXXQHKKAF	XRFRFLPTL	LQTFFLCFGF
201	RLFLFLFLFF	LMLCLFLPA*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 81>:

```
a012.seq
1   ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTGCGAAT
101 TTCTGTTTGC CTTTTCCTGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGGTGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTCAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATT TCGCGTTTCG
551 GAAGATTCTT CCCCACCTCT CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 82; ORF 012.a>:

```
a012.pep
1   MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRYFRYNTHR TDNRKSGNN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKHRNLMTO GFYGVCIQIA VKIQHKKAGF LRFRFLPTL LQTLFLCFGF
201 RLEFLFLFF LMFCLEPA*
```

m012/a012 64.2% identity over a 218 aa overlap

m012.pep	10	20	30	40	50	60
	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
a012	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
m012.pep	70	80	90	100	110	120
	NIMFFQQA VDIRYFRHHTHRTDNRKSGSNFIRHTRHHITAARXXXXXXXXXXXXXXXXXX					
a012	NIMFFQQA VDIRYFRYNTHRTDNRKSGNNFIRHTRHHITTARRHLIDGDGQRNIAFAQT					
	70	80	90	100	110	120
m012.pep	130	140	150	160	170	180
	XXXQHKKAXF					
a012	PKLRSRQTVT VNHAARTFQSKQNLIFRLGNQKHRNLMTOGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
m012.pep	190	200	210	219		
	XRFRFLPTLLQTFFLCFGRFLFLFLFFLMLCLFPAX					
a012	LRFRFLPTLLQTLFLCFGRFLFLFLFFLMLCLFPAX					
	190	200	210			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 012 shows 58.7% identity over a 218 aa overlap with a predicted ORF (ORF 012.ng) from *N. gonorrhoeae*:

m012/g012

m012.pep	10	20	30	40	50	60
	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
g012	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					

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	10	20	30	40	50	60
m012.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHTHRTDNRKRSGSNFIRHTRHHITAARXXXXXXXXXXXXXXXXXX					
g012	: : : : : : :					
	70	80	90	100	110	120
	NIMFFQQAVDIRHFRHHTHRTDDRKRSGNNFIRHTRHHIAAACRDLIDGDGQRNIAFAQT					
m012.pep	130	140	150	160	170	180
	XXXQHKKAXF					
g012	:	:	:	:	:	
	130	140	150	160	170	180
	PKLRSRQTVTVNHAARTFQSEQNLIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
m012.pep	190	200	210	219		
	XRFGRFLPTLLQTFFLCFGRFLFLFLFLFFLMLCLFPAX					
g012	: : : : : :					
	190	200	210			
	LRFGRFLPALQLTFLCFGRFLFLFLFFFLMFLCLFLAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 83>:

m012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CTTTTCCTGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGCTGGAT ATTCGGTACT TCCGCCACCA CACCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCC GCCACCTTAT CGACGGCGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CyTAAGCTGC GAAGCCGCCA AACCCTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT GAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAATCC AACACAAAAA GGCGGGATT TCGCGTTTCG
551 GCAGATTCTC CCCACCCCTC CTTCAAACGC TTTTCTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 84; ORF 012-1>:

m012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALER IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRHHTHR TDNRKRSGSN FIRHTRHHIT
101 AARRHLIDGD GQRNIAFAQT XKLRSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKHRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRFLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCLEPA*

```

m012-1/g012 91.7% identity in 218 aa overlap

	10	20	30	40	50	60
m012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALERIFTHKSNRALKFARRHHIHI					
g012	: : : : : :					
	10	20	30	40	50	60
	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALERIFTHKSNRALKFARRHHIHI					
m012-1.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHTHRTDNRKRSGSNFIRHTRHHITAARRHLIDGDGQRNIAFAQT					
g012	: : : : : :					
	70	80	90	100	110	120
	NIMFFQQAVDIRHFRHHTHRTDDRKRSGNNFIRHTRHHIAAACRDLIDGDGQRNIAFAQT					
m012-1.pep	130	140	150	160	170	180
	XKLRSRQTVTVNHAARTFQSEQNLIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
g012	: : : : : :					
	PKLRSRQTVTVNHAARTFQSEQNLIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					

196

	130	140	150	160	170	180
	190	200	210	219		
m012-1.pep	LRFGRLPTLLQTLFLCFGRFLFLFLFLFLMFLCLFPAX					
	: : : :					
g012	LRFGRLPALQLTLFLCFGRFLFLFLFLFLMFLCLFLAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 85>:

a012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTGCGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTGCGCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGTGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTCAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GCGGGGATT TTGCGTTTCG
551 GAAGATTCTC CCCCACCCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 86; ORF 012-1.a>:

a012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRYFRYNTHR TDNRKRSNN FIRHTRHHIT
101 TARRHLIDGD QORNIAFAQT PKLRSRQVT VNHAARTFQS KQNLIFRLGN
151 QKRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFLCLFPA*

```

a012-1/m012-1 97.2% identity in 218 aa overlap

	10	20	30	40	50	60
a012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	: : : :					
m012-1	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a012-1.pep	NIMFFQQAVIDIRYFRYNTHRTDNRKRSNNFIRHTRHHITTARRHLIDGDGQORNIAFAQT					
	: : : :					
m012-1	NIMFFQQAVIDIRYFRHHTHRTDNRKRSNSNFIRHTRHHITAARRHLIDGDGQORNIAFAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a012-1.pep	PKLRSRQVTVNHAARTFQSKQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	: : : :					
m012-1	XKLRSRQVTVNHAARTFQSEQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
	190	200	210	219		
a012-1.pep	LRFGRLPTLLQTLFLCFGRFLFLFLFLFLMFLCLFPAX					
	: : : :					
m012-1	LRFGRLPTLLQTLFLCFGRFLFLFLFLFLMFLCLFPAX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 87>:

g013.seq

```

1  aTgcctttga ccatgctgtg cagcaGGAcy tGCGGTTtgt tcataatata
51  gtCcgaccgG AAAagcgag GAAaCGCAGT GCCGCGCCCT TCCCTTTCT
101 TGCCGTGGCA GGCGATGCag tTgATTTCGT ACACTTTTTG CCCTTTtGtc

```

```

151 atgatGCTgt tgtcggCGGC AGAAGCgGCG GcgCAGAGGC AGCACAAGAT
201 GAAGGCGGTC GGCAGTCGGG TTGTGTtcat tGgcgTTTCC cctaattgtt
251 tgaaaccttg ttttttgatt Ttgcctttac ggggtgaaaa gtttttTtgg
301 cccaaatccg gaatttag

```

This corresponds to the amino acid sequence <SEQ ID 88; ORF 013.ng:

g013.pep

```

1 MPLTMLCSRT CGLFIIQSDR KSGGNAVPRP SPFLPWQAMQ LDSYTFCPFV
51 MMLLSAAEAA AQRQHKMKAV GSRVVFIVGS PNVLKPCFLI LPLRGEKFFW
101 PKSGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 89>:

m013.seq

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TCGGGTTTTT TCATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
101 TGCCGTGGCA GGCACGCAG TTGGATTCGT ACACTTTTTC CCCTTTTGTC
151 ATGATGCTGT TGTCCGCGGC AGAAGCGGCG GCGCAGAAGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTCAT TGGTGTTCCT TTCATGTTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT TTTGCCGAAT
301 CAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 90; ORF 013>:

m013.pep

```

1 MPLTMLCSST CGFFMMKSER XSGGNMVRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQRQPKTRAV GSRVVFIVGS FMFETLLLL L RSGXKIFLPN
101 Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 91>:

a013.seq

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TCGGGTTTTT TCATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
101 TGCCGTGGCA GGCACGCAG TTGGATTCGT ACACTTTTTC CCCTTTTGTC
151 ATGATGCTGT TGTCCGCGGC AGAAGCGGCG GCGCAGAGGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTCAT TGGTGTTCCT TTAATGTTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT CTTGCCGAAT
301 CGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 92; ORF 013.a>:

a013.pep

```

1 MPLTMLCSST CGFFMMKSER *SGGNMVRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQRQPKTRAV GSRVVFIVGS LMFETLLLL L RSG*KIFLPN
101 R*

```

m013/a013 97.0% identity over a 101 aa overlap

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
a013	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQRQPKTRAVGSRVVFIVGSFMFETLLLLILRSGXKIFLPNQX					
	: :					
a013	AQRQPKTRAVGSRVVFIVGSLMFETLLLLILRSGXKIFLPNRX					
	70	80	90	100		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 013 shows 73.3% identity over a 101 aa overlap with a predicted ORF (ORF 013.ng) from *N. gonorrhoeae*:

m013/g013

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	: : :: :					
g013	MPLTMLCSRTCGLFIIQSDRKSGGNVPRPSPFLPWQAMQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQKQPKTRAVGSRVVFVIGVSF-MFETLLLILR-SGXKIFLPNQX					
	: : :: : : :					
g013	AQRQHKMKAVGSRVVFVIGVSPNVLPKPCFLILPLRGEKFFWPKSGIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 93>:

g015.seq

```

1 ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51 CATTTTGGTA TTCAACATCC GTTTTTTCCT ACTTTGGAAA AATCCAGAAA
101 AGCCCTTGGT CGGCTTTTGG AAAGCACTGC CCCACCTCAA CGACACGATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAG ATTACCCATT TCTCCCCGTT
201 CAACGCGCCT TGGCTCGGCA CAAAATCCT GCTCCTGTTT GCCTACATCG
251 CACTGGGCAT GGTAATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCTAT GTGTTGCATC GCCTGCATCG TTTACCTTGC
351 CAAAACCAA GTCCTGCCAT TCTGA
```

This corresponds to the amino acid sequence <SEQ ID 94; ORF 015.ng>:

g015.pep

```

1 MQYLIVKYSH QIFVTITILV FNIRFFLLWK NPEKPLVGFW KALPHLNDTM
51 LLFTGLWLMK ITHFSPFNAP WLGTKILLLF AYIALGMVMM RARPRSTKFY
101 TVYLLAMCCI ACIVYLAKTK VLPF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 95>:

m015.seq (partial)

```

1 ..AAAATCAGAA AAGCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA
51 CGACACCATG CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT
101 TCTCCCCGTT CAACGCGCCT TGGCTCGGTA CAAAATCCT GCTTCTGCTC
151 GCCTATATCG CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC
201 CAAGTTCTAC ACCGTTTACC TGCTCGCCAT GTGTTGCGTC GCCTGCATCG
251 TTTACCTTGC CAAAACCAA GTCCTGCCTT TCTGA
```

This corresponds to the amino acid sequence <SEQ ID 96; ORF 015>:

m015.pep (partial)

```

1 ..KIRKALAGFW KALPHLNDTM LLFTGLWLMK ITHFSPFNAP WLGTKILLLL
51 AYIALGMMM RARPRSTKFY TVYLLAMCCV ACIVYLAKTK VLPF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 97>:

a015.seq

```

1 ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51 CATTTTGGTA TTCAACATCC GTGTTTCNT ACTTTGGAAA AATCCAGAAA
101 AGCCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA CGACACCATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT TCTCCCCGTT
201 CAACGCGCCT TGGCTCGGTA CAAAATCCT GCTTCTGCTC GCCTATATCG
251 CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCCAT GTGTTGCCTC ACCTGCATCG TTTACCTTGC
351 CAAAACCAA GTCCTGCCTT TCTGA
```

This corresponds to the amino acid sequence <SEQ ID 98; ORF 015.a>:

a015.pep

1 MQYLIVKYSH QIEVTITILV FNIRVFXLWK NPEKPLAGFW KALPHLNDTM
 51 LLFTGLWLMK ITHFSPFNAP WLGTKILLLL AYIALGMMM RARPRSTKFY
 101 TVYLLAMCCL TCIVYLAKTK VLPF*

m015/a015 96.7% identity over a 91 aa overlap

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
a015	LIVKYSHQIFVTITILVFNIRVFXLWKNPEKPLAGFWKALPHLNDTM	LLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep		40	50	60	70	80
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYT	TVYLLAMCCVACIVYLAKTKVLP			
a015	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYT	TVYLLAMCCLTCIVYLAKTKVLP			
	70	80	90	100	110	120
m015.pep	FX					
a015	FX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 015 shows 94.5% identity over a 91 aa overlap with a predicted ORF (ORF 015.ng) from *N. gonorrhoeae*:

m015/g015

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
g015	LIVKYSHQIFVTITILVFNIRFFLLWKNPEKPLVGF	WKALPHLNDTM	LLFTGLWLMKITH			
	10	20	30	40	50	60
m015.pep		40	50	60	70	80
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYT	TVYLLAMCCVACIVYLAKTKVLP			
g015	FSPFNAPWLGTKILLLLFAYIALGMVMRRARPRSTK	FYT	TVYLLAMCCVACIVYLAKTKVLP			
	70	80	90	100	110	120
m015.pep	FX					
g015	FX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 99>:

g018.seq

1 atGCAGCAGG GGCagttggt tggacgcgtc gcccgcaata AAGATATGCG
 51 GAATgctggt CTGCATggtC AGCGGATCGG CAACGGGtac gccgcgcgcg
 101 tctttgTCGA TATTGATGTT TTCCAAACCG ATATTgTCAA CGTTCGGACG
 151 GCgACCTACG GCTGCCAACA TATATTCGGC AACAAATACG CCTTTTCGC
 201 CATCCTGCTC CCAATGGACT tctACATTGC CGTCTGCGTC GAGTTTGACC
 251 TCGGTTTtag CATCCAGATG CAGTTTCAAT tctTCTCCGA ACACGGCTTT
 301 CGCCTCGTCT GA

This corresponds to the amino acid sequence <SEQ ID 100; ORF 018.ng>:

g018.pep

1 MQQGQLVGRV ARNKDMRNAG LHGQRIGNGY AARVFVDIDV FQTDIVNVRT
 51 ATYGCOHIFG NKYAFAILL PMDFYIAVCV EFDLGFSIQM QFQFFSEHG

101 RLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 101>:

```
m018.seq
1 ATGCAGCAGA GGCAGTTGGT TGGACGCATC GCCTGCGATG AAGATATGCG
51 GAATACTGGT CTGCATGGTC AGCGGGTCGG CAACAGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATATT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCATC GAGTTTGACC
251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT TCTTCGCCGA ACACGGCGTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 102; ORF 018>:

```
m018.pep
1 MQQRQLVGRI ACDEDMRNTG LHGQRVGNRY AARIFFDIDI FQTDIVNVRT
51 AAHGCGHIFG NKYAFAILL PMDFYIAVCI EFDLGFSIQM QFQFFAEHGV
101 RLV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 103>:

```
a018.seq
1 ATGCAGCAGG GGCAGTTGGT TGGACGCGTC GCCGCAATA AAGATATGCG
51 GAATACTGGT CTGCATAGTC AGCGGATCGG CAACGGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATGTT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCTACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCGTC GAGTTTGACC
251 TCGGTTTTAG CATCCAAATG CAGTTTCAAT TCTTCACCGA ACACGGCTTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 104; ORF 018.a>:

```
a018.pep
1 MQQGQLVGRV ARNKDMRNTG LHSQRIGNGY AARIFFDIDV FQTDIVNVRT
51 AAYGCGHIFG NKYAFAILL PMDFYIAVCV EFDLGFSIQM QFQFFTEHGF
101 RLV*
```

m018/a018 86.4% identity over a 103 aa overlap

	10	20	30	40	50	60
m018.pep	MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCGHIFG					
			:		:	
a018	MQQGQLVGRVARNKDMRNTGLHSQRIGNGYAARIFFDIDVFTQTDIVNVRTAAYGCGHIFG					
	10	20	30	40	50	60
	70	80	90	100		
m018.pep	NKYAFAILLPMDFYIAVCIEFDLGFSIQMQFQFFAEHGVRLVX					
			:		:	
a018	NKYAFAILLPMDFYIAVCVEFDLGFSIQMQFQFFTEHGFRLVX					
	70	80	90	100		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 018 shows 84.5% identity over a 103 aa overlap with a predicted ORF (ORF 018.ng) from *N. gonorrhoeae*:

```
m018/g018
10 20 30 40 50 60
m018.pep MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCGHIFG
||| ||||| :| ||||| ||||| :| ||||| ||||| :| |||||
g018 MQQGQLVGRVARNKDMRNAGLHGQRIGNGYAARVFVDIDVFTQTDIVNVRTATYGCQHIFG
10 20 30 40 50 60
```


	70	80	90	100
m018.pep	NKYAFFAILLPMDFYIAVCIEFDLGFSIQMQFQFFAEHGVRLVX			
	: : :			
g018	NKYAFFAILLPMDFYIAVCVEFDLGFSIQMQFQFFSEHGFRVLX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 105>:

g019.seq (partial)

```

1 ..ctgctggcgg cccgtggtgct tgccgcgtgt tcttcgACAA ACacacTGCC
51 AGCCGGCAAG ACCCCGGCAG ACAATATAGA AActgcCgAC CTTTCGGCAA
101 GCGTTCCAC cgcCCTGCC GAACCGAAG GAAAAACGCT GGCAGATTAC
151 GCGCGTACC CGTCCGACT GGATGCAGTG AAACAGAACA ACGATGCGGC
201 AGCCGCCGCC TATTTGAAA Acgcaggaga cagCGcgatg gcGGAAtg
251 tccgaagga gtgGCTGa

```

This corresponds to the amino acid sequence <SEQ ID 106; ORF 019.ng>:

g019.pep (partial)

```

1 ..LLAALVLAAC SSTNTLPAGK TPADNIETAD LSASVPTRPA EPEGKTLADY
51 GGYPSALDAV KQNDAAAAA YLENAGDSAM AENVKLEWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 107>:

m019.seq (partial)

```

1 ATGTACCTAC CCTCTATGAA GCATTCCCTG CCGCTGCTGG CGGCCCTGGT
51 GCTTGCCGCG TGTTCCTCGA CAAACACACT GCCAGCCGGC AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTC CACCCGCCCT
151 CCCGAACCCG AAAGAAAAAC GCTGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCACGCAG ACAGTGGACG CTGTTTGCAC AGGAATACGC
351 CAAACTCGAA CCGGCAGGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCTG AACTGGTCAA AAATACGGGC
451 AACTGCGCTT CCGGCTGCAC CAAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGCGCCGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAAGAA GCACGCAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAGCGG TTTAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CTTGCCGCTT TGGACTATTA
801 CGGCAAGGTT GCCGACCGCC GCCAATGAC CGACGACCAA ATCGAGTGGT
851 AGCCCGCGC CGCCTTGCGC GCCCGACGTT GGGACGAGCT GGCCTCGGTT
901 ATCTCGCATA TGCCCGAAAA ACTGCAAAAA AGCCCGACCT GGCTCTACTG
951 GCTGGCACGC AGCCCGCGCG CAACGGGCAA CACGCAAGAG GCGGAAAAAC
1001 TTTACAAACA GCGGCGAGCG ACGGGCAGGA ATTTTATGCG GGTGCTGGCA
1051 GGGGAAGAAT TGGGTCGGAA AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAAAC AGCGTCCGCC GCATGGCGGA AGACGGTGCA GTCAAACCGC
1151 CACTGGTACT GTTCCAAAAC AGCCAATCTG CCGGTGATGC AAAAATGCGC
1201 CGTCAGGCTC AGGCGGAATG GCGTTTTGCC ACACGCGGCT TTGACGAAGA
1251 CAAGCTGCTG ACCGCGCGC AAACCGCGTT CGACCACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCAGC GCAAACTCAA CTACACCTTG
1351 CGCTATATTT CGCCGTTTAA AGACACGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCTTGGG TTTATGGGCT GATTCGTCAG GAAAGCCGCT
1451 TCGTTATAGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCTGCCA CCGCGCGGA AATCGCCGCG AAAATCGGTA TGGATGCCCG
1551 ACAACTTTAC ACCGCGGACG GG...

```

This corresponds to the amino acid sequence <SEQ ID 108; ORF 019>:

m019.pep (partial)

```

1 MYLPSMKHSL PLLAALVLA CSSTNTLPAG KTPADNIETA DLSASVPTRP

```

```

51  AEPERKTLAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARRQWT LFAQEYAKLE PAGRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSTGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDYYGKV ADRRQLTDDQ IEWYARAALR ARRWDELASV
301 ISHMPEKLQK SPTWLYWLAR SRAATGNTQE AEKLYKQAAA TGRNIFYAVLA
351 GEELGRKIDT RNNVPDAGKN SVRRMAEDGA VKRALVLFQN SQSAGDAKMR
401 RQAQAEWRFA TRGFDEKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYYL
451 RYISPFKDTV IRHAQNVNVD PAWVYGLIRQ ESRFVIGAQS RVGAQGLMQV
501 MPATAREIAG KIGMDAAQLY TADG...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 109>:

a019.seq

```

1  ATGTACCCAC CCTCTCTGAA GCATTCCCTG CCGCTGCTGG TGGNCCTGGT
51  GCTTGCCCGC TGTCTTNGA CAAACACACT GTCAGCCGAC AAGACCCCGG
101 CAGACAATAT AGAACTGCC GACCTTTCGG CAAGCGTTCC CACCGCCCTT
151 GCGGAACCCG AANGAAAAAC GTNGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTGTTG
251 AAAACGCCCG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGCTTG
301 AAGTCTTTGG GCGCGCGCAG ACAGTGGACG CTGTNTGCAC ANGAATATGC
351 NAAACTCGAA CCGGCANGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCGG AACTGGTCAA AAATACGGGC
451 AAACTGCCTT CGGGCTGCAC CAAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCACGACG CCTGGAGGCG CGTGCGCGGA CTGCTGGCCG
551 GCCGCCAACC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAGAGG GCACGCAAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTTAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CCTGCCGCTT TGGACTATTA
801 NGGCAAGGTT GCCGACCGCC GCCAACTGAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC GCNNTNNGC NNNCGNNGTT NGNANGANN TGGCNCNNNN
901 ANCNCGNNNN TGCNNGANAA ACNNNNNNAN AGNCNNANNT NGNTNNANTG
951 NNTGGCACGC AGCCGCGCCG CNACGGGCAA CACGCAANAN GCGGANAACC
1001 TNTACAAACA GCGCGCAGCA NCGGGCANGA ATTTTATATG NGTGCTGN CN
1051 GGGGAAGAGT TGGGGCGCAN AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAANC AGCGTCCTCC GTATGGCGGA AGACGGCGCG ATTAAGCCGC
1151 CGCTGGTGCT GTTCCGAAAC AGCCGAACCG CCGGCGATGC GAAAATGCGC
1201 CGTCNGGCTC AGGCGGAATG GCGTTTCGCC ACACGGGCTT TCGATGAAGA
1251 CAAGCTGCTG ACCGCCGCGC AAACCGCGGT CGACCACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACTCAA CTACACCTTG
1351 CGCTACATTT CGNNNNNTNA NGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCGTGGG TTTACGGGCT GATTGCTCAG GAAAGCCGCT
1451 TCGTTATGGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCTGCGCA CCGCGCGCGA AATCGCCGGC AAAATCGGTA TGGATGCCCG
1551 ACAACTTTAC ACCGCCGACG GCAATATCCG TATGGGGACG TGGTATATGG
1601 CGGACACCAA ACGCGCGCTG CAAAACAACG AAGTCCTCGC CACCGCAGGC
1651 TATAACGCCG GTCCCGGCAG GCGCGCCGGA TGGCAGGCGG ACACGCCCTT
1701 CGAAGGCGCG GTATATGCCG AAACCATCCC GTTTTCCGAA ACGCGCGACT
1751 ATGTCAAAAA AGTGATGGCC AATGCCGCTC ACTACGCTC CCTCTTCGGC
1801 GCGCCGCA CA TCCCGCTCAA ACAGCGTATG GGCATTGTCC CCGCCCGCTG
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 019.a>:

a019.pep

```

1  MYPPSLKHSL PLLVXLVLAA CSXTNTLSAD KTPADNIETA DLSASVPTXP
51  AEPEKTXAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARRQWT LXAXEYAKLE PAXRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSTGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDXXGKV ADRRQLTDDQ IEWYARAAXX XXXXXXXXXX
301 XXXXXXXXXX XXXXXXXXAR SRAATGNTQX AXKLYKQAAA XGXNIFYAVLX
351 GEELGRXIDT RNNVPDAGKX SVLRMAEDGA IKRALVLFN SRTAGDAKMR
401 RXAQAEWRFA TRGFDEKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYYL

```

451 RYISXXXTDV IRHAQNVNVD PAWVYGLIRQ ESRFVMAQS RVGAQGLMQV
 501 MPATAREIAG KIGMDAAQLY TADGNIRMGW WYADTKRRL QNNEVLATAG
 551 YNAGPGRARR WQADTFLEGA VYAETIPFSE TRDYVKKVMA NAAYASLFG
 601 APHIPLKQRM GIVPAR*

m019/a019 88.9% identity over a 524 aa overlap

m019.pep	10	20	30	40	50	60
	MYLPSMKHSLPLLAALVLAACSSTNTLPAGKTPADNIETADLSASVPTRPAPERKTLAD					
a019	MYPPSLKHSLPLLVLVLAACSXTNTLSADKTPADNIETADLSASVPTXPAPPEXKTXAD					
m019.pep	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKS LGARRQWTLFAQEYAKLE					
a019	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKS LGARRQWTLXAXEYAKLE					
m019.pep	130	140	150	160	170	180
	PAGRAQEVECYADSSRNDYTRAAELVKNTGKLP SGCTKLLEQAAASGLLDGNDAWRRVRG					
a019	PAXRAQEVECYADSSRNDYTRAAELVKNTGKLP SGCTKLLEQAAASGLLDGNDAWRRVRG					
m019.pep	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSFFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
a019	LLAGRQTTDARNLAAALGSFFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
m019.pep	250	260	270	280	290	300
	EQRSFAWGV LGHYQSQNLNVPAALDYGKVADRRQLTDDQIEWYARAALRARRWDELASV					
a019	EQRSFAWGV LGHYQSQNLNVPAALDYXGKVADRRQLTDDQIEWYARAAXXRXRXRXAXX					
m019.pep	310	320	330	340	350	360
	ISHMPEKLQKSPTWLYWLARSRAATGNTQAEKLYKQAAATGRNFYAVLAGEELGRKIDT					
a019	XXXXXXXXXXXXXXXXXARSRAATGNTQAXKLYKQAAAXGXNFYAVLXGEEELGRXIDT					
m019.pep	370	380	390	400	410	420
	RNNVPDAGKNSVRRMAEDGAVKRALVLFQNSQSAGDAKMRRQAQAEWRFATRGFDEDKLL					
a019	RNNVPDAGKXSVLRMAEDGAIKRALVLFNRSRTAGDAKMRRXAQAEWRFATRGFDEDKLL					
m019.pep	430	440	450	460	470	480
	TAAQTAFDHGFYDMAVNSAERTDRKLNYYTLRYISPFKDTVIRHAQNVNVDPAWVYGLIRQ					
a019	TAAQTAFDHGFYDMAVNSAERTDRKLNYYTLRYISXXXTDVIRHAQNVNVDPAWVYGLIRQ					
m019.pep	490	500	510	520		
	ESRFVIGAQS RVGAQGLMQVMPATAREIAGKIGMDAAQLYTADG					
a019	ESRFVMAQS RVGAQGLMQVMPATAREIAGKIGMDAAQLYTADGNIRMGWYADTKRRL					
a019	550	560	570	580	590	600
	QNNEVLATAGYNAGPGRARRWQADTFLEGA VYAETIPFSETRDYVKKVMANAAYASLFG					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 019 shows 95.5% identity over a 89 aa overlap with a predicted ORF (ORF 019.ng) from *N. gonorrhoeae*:

g019/m019

		10	20	30	40	49
g019.pep		LLAALVLAACSSSTNTLPAGKTPADNIETADLSASVPTRPAEPEGKTLAD				
m019	MYLPSMKHSLPLLAALVLAACSSSTNTLPAGKTPADNIETADLSASVPTRPAEPEKTLAD					
		10	20	30	40	50
		50	60	70	80	89
g019.pep	YGGYPSALDAVKQNNDAAAAYLENAGDSAMAENVRKEWL					
m019	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSLGARRQWTLFAQEYAKLE					
		70	80	90	100	110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 111>:

g023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCCAT TACGGTTTGC GCGATTGGGT
51  AATGCAGCGT GCGACTGCGG TTATTATGTT GATTATATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCCCTG CCTAAAGAAT ATCCGGCATG GCAGGCATTT
151 TTTAGTCAAG CTTGGGTAAA AGTATTTACC CAAGTGAGCT TTATCGCCGT
201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCTTCGG CGTGCCTTTG TTTTTCAGG TTGCCACCAT TGctctGGCTG
301 GTCGGCTGCC TCGTGTATTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 023.ng>:

g023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVVLFEAL PKEYPAWQAF
51  FSQAWVKVFT QVSFIQVFLH AWVGIRDLWM DYIKPFGVRL FLQVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

m023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCCAT TACGGTTTGC GCGATTGGGT
51  GATGCAACGT GCGACTGCGG TTATTATGTT GATTATATACC GTTGCACTTT
101 TAGTGGTTCT ATTTCCCTG CCTAAAGAAT ATCCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT
201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCTTCGG CGTGCCTTTG TTTTTCAGG TTGCCACCAT CGTTTGGCTG
301 GTCGGCTGTC TCGTGTATTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 023>:

m023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVVLFSL PKEYSAWQAF
51  FSQTWVKVFT QVSFIQVFLH AWVGIRDLWM DYIKPFGVRL FLQVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

a023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCCAT TACGGTTTGC GGGATTGGGC
51  GATGCAACGT GCGACCGCGG TTATTATGTT GATTATATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCTCTG CCTAAAGAAT ATCCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT

```

201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATNA
 251 AACCCCTTCG CGTGCGTTTG TTTTTCAGG TTGCCACCAT CGTCTGGCTG
 301 GTCGGCTGCT TGGTGTATTC AATTAAAGTA ATTTGGGGGT AA

This corresponds to the amino acid sequence <SEQ ID 116; ORF 023.a>:

a023.pep
 1 MVERKLTGAH YGLRDWAMQR ATAVIMLIYT VALLVVLFA L PKEYSAWQAF
 51 FSQTWVKVFT QVSFIAVFLH AWVGIRDLWM DYXKPFVRL FLQVATIVWL
 101 VGCLVYSIKV IWG*

m023/a023 96.5% identity over a 113 aa overlap

	10	20	30	40	50	60
m023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFSLPKEYSAWQAFFSQTWVKVFT					
	: : : : :					
a023	MVERKLTGAHYGLRDWAMQRATAVIMLIYTVALLVVLFA L PKEYSAWQAFFSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
m023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
	: : : : :					
a023	QVSFIAVFLHAWVGIRDLWMDYXKPFVRLFLQVATIVWLVGCLVYSIKVIWGX					
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 023 shows 97.3% identity over a 113 aa overlap with a predicted ORF (ORF 023.ng) from *N. gonorrhoeae*:

g023/m023

	10	20	30	40	50	60
g023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFA L PKEYPAWQAFFSQA WVKVFT					
	: : : : :					
m023	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFSLPKEYSAWQAFFSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
g023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
	: : : : :					
m023	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 117>:

g025.seq

1 ATGTTGAAAC AAACgACACT TTTGGCAGCT TGTACCGCCG TTGCCGCTCT
 51 GTTGGGCGGT TGcgCCACCC AACAGCCTGC TccTGTcATT GCAGGCAATT
 101 CAGGTATGCA GACCGTATCG TCTGCGCCGG TTTACAATCC TTATGGCGCA
 151 ACGCCGTACA ATGCCGCTCC TGCCGCCAac gatgcGCCgT ATGTGCCGCC
 201 CGTGCAAact gcgcgggttT ATTCGCTCTC TGCTTATGTT CCGCcgTCTG
 251 CACCTGCCGT TTCGggtaca tatgtTCCTT CTTACGCACC CgtcgACATC
 301 aacgCGGCGa cgCataCTAT TGTGCGTGGC GACACgGtgt acaACATTTc
 351 caaAcgCtac CATATCTCTC AAGACGATTT CCGTGCCTGG AACGGCATGA
 401 CCGACAATAC GTTGAGCATC GGTCAGATTG TTAAAGTCAA ACCGGCaggA
 451 TATGCCGCAC CGAAAACCGC AGCCGTAGAA AGCAGGCCCG CCGTACCGGC
 501 TGCCGCGCAA ACCCTGTGA AACC CGCCGc gcaACCGCCC GTTCAGTCCG
 551 CGCCGCAACC TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCCCCC
 601 CGCCCGCCC CGCAATCTCC TGCCGCTTCG CCTTCCGCA CGCGTTCGGT
 651 CGCGGCATT GTTTGGCAGC GTCCGACCCA AGGTAAAGTG GTTGCCGATT

```

701 TCGGCGGCGG CAACAAGGGT GTCGATATTG CCGGCAATGC CGGACAACCC
751 GTTTTGGCGG CGGCTGACGG CAAAGTGGTT TATGCCGGTT CAGGTTTGAG
801 GGGATACGGA AACTTGGTCA TCATCCAGCA CAATTCCTCT TTCCTGACCG
851 CGTACGGGCA CAACCAAAAA TTGCTGGTTCG GCGAAGGTCA GCAGGTCAAA
901 CGCGGTGAGC AGGTTGCTTT GATGGGTAAT ACCGATGCTT CCAGAACGCA
951 GCTTCATTTT GAGGTGCGTC AAAACGGCAA ACCGGTTAAC CCGAACAGCT
1001 ATATCGCGTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 025.ng>:

```

g025.pep
  1 MLKQTTLLAA CTAVAALLGG CATQPPAPVI AGNSGMQTVS SAPVYNPYGA
 51 TPYNAAPAAN DAPYVPPVQT APVYSPPAYV PPSAPAVSGT YVPSYAPVDI
101 NAATHTIVRG DTVYNISKRY HISQDDFWAN NGMTDNTLSI GQIVKVKPAG
151 YAAPKTAAVE SRPAVPAAQ TPVKPAAQPP VQSAPQPAAP AAENKAVPAP
201 APAPQSPAAS PSGTRSVGGI VWQRPTQGV VADFGGNGK VDIAGNAGQP
251 VLAADGKVV YAGSGLRGY NLVIIQHNS FLTAYGHNQK LLVGEGQQVK
301 RGQQVALMGN TDASRTQLHF EVRQNGKPVN PNSYIAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

```

m025.seq (partial)
  1 ..GTGCCGCGG TGCAAAGCGC GCCGGTTTAT ACGCCTCCTG CTTATGTTCC
 51 GCCGTCTGCA CCTGCCGTTT CGGGTACATA CGTTCCTTCT TACGCACCCG
101 TCGACATCAA CGCGGCGACG CATACTATTG TCGCGGCGCA CACGGTGTAC
151 AACATTTCCA AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA
201 CGGCATGACC GACAATACGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC
251 CGGCAGGATA TGCCGCACCG AAAGCCGCG CCGTAAAAAG CAGGCCCGCC
301 GTACCGGCTG CCGCGCAACC GCCCGTACAG TCGCACCCG TCGACATTAA
351 CGCGGCGACG CATACTATTG TGCGCGGCGA CACGGTGTAC AACATTTCCA
401 AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA CGGCATGACC
451 GACAATATGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC CGGCAGGATA
501 TGCCGCACCG AAAACCGCAG CCGTAGAAAG CAGGCCCGCC GTACCGGCTG
551 CCGTGCAAAC CCTGTGAAA CCCGCCGCGC AACCGCCTGT GCAGTCCGCG
601 CCGCAACCTG CCGCGCCCGC TGCGGAAAAT AAAGCGGTT CCGCGCCCGC
651 CCCGCAATCT CCTGCCGCTT CGCCTTCCGG CACGCGTTC GTCGGCGGCA
701 TTGTTTGGA GCGTCCGACG CAAGGTAAAG TGGTTGCCGA TTTCGGCGGC
751 AACAACAAGG GTGTGCATAT TGCCGGTAAT GCGGGACAGC CCGTTTGGC
801 GGCGGCTGAC GGCAAAGTGG TTTATGCCGG TTCAGTTTG AGGGGATACG
851 GAAACTTGGT CATCATCCAG CATAATTCTT CTTTCCTGAC CGCATACGGG
901 CACAACCAAA AATTGCTGGT CGGCGAGGGG CAGCAGGTCA AACCGGTCA
951 GCAGGTTGCT TTGATGGGCA ATACCGATGC TTCCAGAACG CAGCTTCATT
1001 TCGAGGTGCG TCAAACGGC AAACCGGTTA ACCCGAACAG CTATATCGCG
1051 TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 025>:

```

m025.pep (partial)
  1 ..VPPVQSAPVY TPPAYVPPSA PAVSGTYVPS YAPVDINAAT HTIVRGDTVY
 51 NISKRYHISQ DDFRAWNGMT DNTLSIGQIV KVKPAGYAAP KAAAVKSRPA
101 VPAAAQPPVQ SAPVDINAAT HTIVRGDTVY NISKRYHISQ DDFRAWNGMT
151 DNMLSIGQIV KVKPAGYAAP KTAAVESRPA VPAAVQTPVK PAAQPPVQSA
201 PQPAAPAAEN KAVPAPAPQS PAASPSGTRS VGGIVWQRPT QGKVADFGG
251 NNKGVDIAGN AGQPVLAAD GKVVYAGSL RGYGNLVIIQ HNSSF LTAYG
301 HNQKLLVGEG QQVKRQQVA LMGNTDASRT QLHFVQRNG KPVNPNSYIA
351 F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

a025.seq
  1 ATGTTGACAC CAACAACACT TTAGGTAGCT TGTACCGCCC TGCCGCTCA
 51 GTTGGGCGGA TGCCCCACCC AACACCCTTC TCCTGTCATT GCAGGCAATT
101 CAGGTATGCA GACCGTACCG TCTGCGCCGG TTTACAATCC TTATGGCGCA

```

```

151 ACGCCGTACA ATGCCGCTCC TGCCGCCAAC GATGCGCCGT ATGTGCCGCC
201 GGTGCAAAGC GCGCCGTTTT ATANGCCTCC TGCTTATGTT CCGCCGTCTG
251 CACCTGCCGT TTCGGGTACA TACGTTCCCTT CTTACGCANC CGTCGACATC
301 AACGCGGCGA CCCATACTAT TGTGCGCGGC GACACCGTGT ACAAGATTTC
351 CAAATGCTAC CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA
401 CCGACAATAC GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCAGGA
451 TATGCCGCAC CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCCGC
501 TGCCGCGCAA CCGCTCGTAC AGTCCGCACC CGTCGACATC AACGCGGCGA
551 CGCATACTAT TGTGCGCGGC GACACGGTGT ACAACATTTC CAAACGCTAC
601 CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA CCGACAATAC
651 GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCAGGA TATGCCGCAC
701 CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCCGC TGCCGTGCAA
751 ACCCCTGTGA AACCCTCCGC GCAACCGCCT GTGCAGTCCG CGCCGCAACC
801 TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCGCGCGCC GCCCGCAAT
851 CTCTGCCGC TTCGCTTCC GGCACGCGTT CGGTGCGCGG CATTGTTTGG
901 CAGCGTCCGA CGCAAGGTAA AGTGGTTGCC GATTTCGGCG GCAACAACAA
951 GGTGTGCGAT ATTGCAGGAA ATGCGGGACA GCCCGTTTTG GCGGCGGCTG
1001 ACGGCAAAGT GGTATTATGCA GGTTCGGTT TGAGGGGATA CGGCAATTG
1051 GTCATCATCC AGCATAATTC TTCCTTCCTG ACCGCATACG GGCACAACCA
1101 AAAATTGCTG GTCGCGGAAG GCCAGCAGGT CAAACGCGGG CAGCAGGTCG
1151 CTTTGATGGG CAATACCGAG GCTTCTAGAA CGCAGCTTCA TTTGAGGTG
1201 CGGCAAAACG GCAAACCGGT TAATCCGAAC AGCTATATCG CGTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 025.a>:

a025.pep

```

1 MLTP TTL*VA CTALAAQLGG CPTQHPSPVI AGNSGMQTVP SAPVYNPYGA
51 TPYNAAPAAAN DAPYVPPVQS APVYXPPAYV PPSAPAVSGT YVPSYAXVDI
101 NAATH TIVRG DTVYKISKCY HISQDD FRAW NGMTDNTLSI GQIVKVKPAG
151 YAAPKAAAVK SRPAVPAAAQ PLVQSAPVDI NAATH TIVRG DTVYNI SKRY
201 HISQDD FRAW NGMTDNTLSI GQIVKVKPAG YAAPKAAAVK SRPAVPAAVQ
251 TPVKPAAQPP VQSAPQPAAP AAENKAVPAP APQSPAASPS GTRSVGGIVW
301 QRPTQGVVVA DFGGNNKGVD IAGNAGQPVL AAADGKV VYA GSGLRGYGNL
351 VLIQHNSFL TAYGHNQKLL VEGEQQVKRG QQVALMGNTE ASRTQLHFEV
401 RQNGKPVNPN SYIAF*

```

m025/a025 97.4% identity over a 351 aa overlap

```

                                10      20      30
m025.pep                      VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
                                |||:|||||:|||||:|||||:|||||
a025      GMQTVPSAPVYNPYGATPYNAAPAANDAPYVPPVQSAPVYXPPAYVPPSAPAVSGTYVPS
              40      50      60      70      80      90

              40      50      60      70      80      90
m025.pep    YAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMTDNTLSIGQIVKVKPAGYAAP
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a025      YAXVDINAATH TIVRGDTVYKISKCYHISQDD FRAWNGMTDNTLSIGQIVKVKPAGYAAP
              100     110     120     130     140     150

              100     110     120     130     140     150
m025.pep    KAAAVKSRPAVPAAAQPPVQSAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMT
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a025      KAAAVKSRPAVPAAAQPLVQSAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMT
              160     170     180     190     200     210

              160     170     180     190     200     210
m025.pep    DNMLSIGQIVKVKPAGYAAPKTAAVESRPAPVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a025      DNTLSIGQIVKVKPAGYAAPKAAAVKSRPAVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
              220     230     240     250     260     270

              220     230     240     250     260     270
m025.pep    KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQGVVADFGGNNKGVDIAGNAGQPVLAAAD
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

m025/q025

```

m025.pep                                10          20          30
                                VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
                                |||||:||||:|||||
g025    GMQTVSSAPVYNPHYGATPYNAAPAANDAPYVPPVQTAPVYSPPAYVPPSAPAVSGTYVPS
          40          50          60          70          80          90

          40          50          60          70          80          90
m025.pep    YAPVDINAATHTIVRGDTVYNISKRYHISQDDFRANGMTDNTLSIGQIVKVKPAGYAAP
          |||||
g025    YAPVDINAATHTIVRGDTVYNISKRYHISQDDFRANGMTDNTLSIGQIVKVKPAGYAAP
          100         110         120         130         140         150

          100         110         120         130         140         150
m025.pep    KAAAVKSRPAVPAAQPPVQSAPVDINAATHTIVRGDTVYNISKRYHISQDDFRANGMT
          |
g025    K-----

          160         170         180         190         200         210
m025.pep    DNMLSIGQIVKVKPAGYAAPKTAAVESRPAPVAAVQTPVKPAAQPPVQSAPQPAAPAAEN
          |||||
g025    -----TAAVESRPAPVAAQTPVKPAAQPPVQSAPQPAAPAAEN
          160         170         180         190

          220         230         240         250         260
m025.pep    KAVPAPAP--QSPAASPSGTRSVGGIIVQWRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
          |||||
g025    KAVPAPAPAPQSPAASPSGTRSVGGIIVQWRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
          200         210         220         230         240         250

          270         280         290         300         310         320
m025.pep    ADGKVYVYAGSLRGYGNLVIIQHNSFLTAYGHNQKLLVGEQQVKRGQQVALMGNTDAS
          |||||
g025    ADGKVYVYAGSLRGYGNLVIIQHNSFLTAYGHNQKLLVGEQQVKRGQQVALMGNTDAS
          260         270         280         290         300         310

          330         340         350
m025.pep    RTQLHFEVRQNGKPVNPNPSYIAFX

```


9025 |||||
 RTQLHFEVRONGKPVNPNSYIAFX
 320 330

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 113>:

g031.seq
 1 ATGGTGTCCC TCCGCTTCAG ATTCGGCAAC CACTTTAAAC GCCGACATTC
 51 TGACAATTTC CTTTCCGCC AGCCAAATAT CATGCGTATC TTTCCGTTTCG
 101 GGCTTGTTGG GCATGGCAAC CTCAACAGC CGCGCCATCA CAGGAATCGT
 151 CGTTCCCTGA ATCAGCAGCG ACAGCACCAC CACGGCAAAC GCCACATCAA
 201 ACAGCAGGTG CGAATTGGGA ACGCCCATCA CCAGCGGCAT CATCGCCAGC
 251 GAAATCGGTA CGGCTCCTCG CAAGCCCAAC CAACTGATAT ACGCCTTTTC
 301 ACGCAGGCTG TAATTGAATT TCCACAAACC GCCGAACACT GCCAGCGGAC
 351 GCGCGACCAG CATCAGGAAC GCCGCAATCG CCAAGGCTTC CGCGCCCTG
 401 TCCAACACGC CGGCGGGAGA AACCAGCAGA CCGAGCATGA CGAACAAAGT
 451 TGCCTGCGCC AGCCAAGCCA AACCGTCCAT CACACGCAA ACCTGTTCG
 501 TcgcACGGTT GCGTGTTA CCGACAATGA TGCCGGCAAG GTAAACCGCC
 551 AAAAAGCCGC TGCCGCTAT GGTATTGGTA AACGCAACA CAAGCAGCCC
 601 GCCCGACACA ATCATCAGCG CGTACAGACC TTCCGTacac acctccaatt
 651 cccaatcaac gtcatactgt tctcccggtg taaaatgttc ttcacttcag
 701 aatccccccc ttcttcccag cccgaaacct tcatgtgtta naccctgggg
 751 tgccccaacg gatttagtaa cctcccaatg actctgcttg tcgccccctt
 801 cgcccgcttt ctccttcg gaaaacttgt tgtcccgctc ttacattaa

This corresponds to the amino acid sequence <SEQ ID 114; ORF 031.ng>:

g031.pep
 1 MVSLRFRFGN HFKRRHSDNF LFRQPNIMRI FRFLVGHGN LQPRHRNR
 51 RSLNQQRQHH HGKRHIKQV RIGNAHQHR HRQRNRYGSS QAQPTDIRLF
 101 TOAVIEFPOT AEHCQTRDQ HQERRNRQGF RRPVQHAGGR NQQTEDHDEQS
 151 CLRQPSQTVH HTQNVFRRTV ALVTDNDAGK VNRQKAAAY GIGKRKHQKP
 201 ARHNHQRVQT FRTHLQFPIN VIAVSRVKMF FTSESPSSQ PETFMCXTLG
 251 CPNGFSNLEP TLLVAPFARF LLPGKLVVFP LH*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

m031.seq (partial)
 1 ...CGCCTGAAGC ACGGTGTCGG ACTGCATTTT TATTCGGCTA TACGCCTTTT
 51 CACGCAGGCT GTAATTGAAT TTCCACAAAC CGCCGAACAC TGCCGACGGA
 101 CGCGCGACCA GCATCAGGAA CGCCGCAATC GCCAAGGCTT CGCCGCCCCT
 151 GTCCAACACG TTGGCAGGAG AAACCAGCAG CAAAGGCATT CCCAAACGTG
 201 CGGACAAAGT GGTGAAACC ACGCTCAGAA ACAACAGTGC GCCACCCGGC
 251 AG....

This corresponds to the amino acid sequence <SEQ ID 116; ORF 031>:

m031.pep (partial)
 1 ...RLKHGVLHF YSAIRLFTQA VIEFPQTAEH CRRTRDQHQE RRNRQGFRFP
 51 VQHVGRNRQQ QRHSQTCGQS GRNHAQKQOC ATRO....

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

a031.seq
 1 ATACGCCTTT TCACGCAGGC TGTAATTGAA TTCCACAAA CCGCCGAACA
 51 CTGCCGGGGG ACGCGCGACC AGCATCAGGA ACGCCGCAAT CGCCAAGGCT
 101 TCCGCCGCCC CGTCCAACAC GTTGCCAGGA GAAACCAGCA GCAAAGGCAT
 151 TCCCAAACGT GCGGACAAAG TGGTCGAAAC CACGCTCAGA AACAACAGTG
 201 CGCCACCCGG CAG

This corresponds to the amino acid sequence <SEQ ID 118; ORF 031.a>:

a031.pep (partial)
 1 IRLFTQAVIE FPQTAEHCRN TRDQHQERRN RQGFRFPVQH VGRNRQQQRH
 51 SQTCCGQSGRN HAQKQOCATR Q

210

m031/a031 100.0% identity over a 71 aa overlap

	10	20	30	40	50	60
m031.pep	RLKHGVLH	FYSAIRLFTQ	AVIEFPQTAEH	CRRTDQHQ	ERRNRQGF	RRPVQHVGRNRQ
a031		IRLFTQAVIEFPQTAEH	CRRTDQHQ	ERRNRQGF	RRPVQHVGRNRQ	
		10	20	30	40	
	70	80				
m031.pep	QRHSQTCGQSGRNHAQKQ	QCATRQ				
a031	QRHSQTCGQSGRNHAQKQ	QCATRQ				
	50	60	70			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 031 shows 60.0% identity over a 85 aa overlap with a predicted ORF (ORF 031.ng) from *N. gonorrhoeae*:

m031/g031

		10	20	30
m031.pep		RLKHGVLH	FYSAIRLFTQ	AVIEFPQTAEH
g031	NQQRQHHHGKRHIKQQVRIGNAHHRQRRNRYGSSQAQPTDIRLFTQAVIEFPQTAEH			
	60	70	80	90
	40	50	60	70
m031.pep	CRRTDQHQERRNRQGFRRPVQHVGRNRQQRHS-QTCGQSGRNHAQKQQCATRQ			
g031	CQRTDQHQERRNRQGFRRPVQHAGGRNQTEHDEQSCLRQPSQTVHHTQNVFRTVALV			
	120	130	140	150
	180	190	200	210
g031	TDNDAGKVNROKAAAAYGIGKRKHKQPARHNRQVQTFRTHLQFPINVIASRVKMFFTS			
	180	190	200	210
	220	230		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 119>:

g032.seq

```

1  ATGCGGCGAA  ACGTGCCTGC  CGTCGCCGTA  TTGCGCCGCC  CACGATTCTGA
51  GGCCTTTTTG  GATTTGCGGT  TGGCTCAGGC  GCGTGCCGTT  CCTGCCGGTA
101 AACAGGGCTT  TGCCGTCCGA  TGCCTCTGA  CGCAGCGGCA  GATAGTTTTT
151 CAAGGCTTCC  ACGCTTTTGC  CGGTCAGCGG  AACCTGACGC  TGCTTGCGCC
201 CTTTGCCGGT  AACGTGTACC  CACGCTTCGT  CCAAATATAC  ATCATCTGCA
251 TTCAAGCCGT  GTATCTCGCT  CACGCGCAAA  CCGCTGCCGT  ACATCAGCTC
301 GAACAGCGCG  TGGTCGCGCA  CCGCCAGCGG  GTCGCCGCCG  TCCACGGGCA
351 AATCCAACAT  CCGTTTCAGC  CATTCCTGCG  GCAGGGCTTT  GGGTACGCGC
401 TCGGGCTGCT  TCGGCGGTTT  GATGTCGGCG  GTCGGGTCGG  CGCGCATCAG
451 CCCGCGTTTG  ACCAGCCAGG  CGCAATACTG  CCGCCACGCC  GACAGCTTGC
501 GCGCCAGCGT  CCGACCGTCC  AAACCGCGCT  GCGACAGCCG  CCGCAACGCC
551 GccgTAAAT  CGCGCCGCGA  CAAGTCCTGC  GGCACGCgc  ctgcATCTTC
601 AGACGGCATT  TGTGCCAACA  GTGCAAACAG  TTCTTCCAAA  TCGCGCCGGT
651 ATGCCGCAAC  CGTGTGCTCC  GACTTGCCCT  CGCGCACGAT  GTTTTCCAAA
701 TAAGCGTCAA  AATacgcgc  AAACccgTCC  AAAACCATAA  CCGTCCCACA
751 CAAATATCAA  AAAACCACTG  A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 032.ng>:

g032.pep

```

1  MRRNVPAAV  LRRPRFEAF  L  DLALAAQAV  PAGKQGFVR  CRLTORQIVF
51  QGFHAFAGQ  R  NLTLAPFAG  N  VYPRFVQIY  IICIQAVYLA  HAQTAAVHQL

```

```

101 EQRVVAHRQR VAAVHGQIQH PVQPFRLRQGF GYALGLLRRF DVGGRVGAHQ
151 PAFDQPGAIL PRRRLARQR PTVQTALRQP PRRRKIAPR QVLRHAACIF
201 RRHLCQQCKQ FFQIAPVCRN RVLRLALAH DVFQISVKIRR KPVQNHNRPT
251 QISKNQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

m032.seq (partial)
  1 ATGCGGCGAA ACGTGCmTGC mGTGCGCGTT kTGCGCCGCC CATTGCGCCA
 51 AACGTTTTTG GATTTGGCGT TGGCTCAGGC GCGTGCCGTT CCTGCCGGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAGGGCTTCC ACGCTTTTGC CGACCAGCGG CACCTGCCGC TgTT.GCGCC
201 CTTTGCCGAT AACGTGTACC CACGCTCGT CCAAATAGAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAA CCGTGCCGT ACATCAGTTC
301 GAACAGGGCG TGGTCGCGCA CCGCAGCGG GTCGCCGCCG TCCACGGGCA
351 AATCCAGCAT CCGGTTTCAGC CATTCCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGGCG GTCGGGTCGG CGTGCATCAG
451 GCCGCGCTTT ACCAGCCAAA CGCAATACTG CCGCCAAGAC GAAAGCTTGC
501 GAGCCAGCGT CCGTTCCCCC AAACCGCG...

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 032>:

```

m032.pep (partial)
  1 MRRNVXAVAV XRRPLRQTFL DLALAQARAV PAGKQGFVR CRLTORQIVF
 51 QGFHAFADQR HLPLXAFAD NVYPRXVOID IICIQAVYLA HAQTAAVHQF
101 EQGVVAHRQR VAAVHGQIQH PVQPFRLRQGF GYALGLLRRF DVGGRVGVHQ
151 AALYQFNAIL PRRKLASQR PFPQTA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

```

a032.seq
  1 ATGCGGCGAA ACGTGCCTGC CGTCGCGGTT TTGCGCCGCC CATTGCGCCA
 51 AACGTTTTTG GATTTGGCGT TGGCTCAGGC GCGTGCCGTT CCTGCCGGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAGGGCTTCC ACGCTTTTGC CGGTCAGCGG AACCTGCCGC TGCTTGCGTC
201 CTTTGCCGGT AACGTGTACC CACGCTCGT CCAAATATAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAA CCGTGCCGT ACATCAGTTC
301 GAACAGCGCG TGATCGCGCA CCGCAGCGG GTCGCCGCCG TCCACGGGCA
351 AATCCAGCAT CCGGTTTCAGC CATTCCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGGCG GTCGGGTCGG TATGCAGCAG
451 ACCGCGTTTG ACCAGCCAGG CGCAATACTG CCGCCAAGAC GACAGTTTGC
501 GCGCCAGCGT CCGCGCATTC AAACCGCGCT GCGACAGCCG CCGCAACGCC
551 GCCGTAAAT CGCGCTGCGA CAAGCCCTGC GGCACGCCGC CTGCATCTTC
601 AGACGGCATT TGTGCCAACA GCGCAAACAG TTCTTCCAAA TCGCGCCGGT
651 ATGCCGCCAC CGTGTGCTCC GACTTGCCCT CGCGCAGCAT GTTTTCCAAA
701 TAAGCGTCAA AATGCGCCGC AAACCCGTCC AAAACCATAA CCGCCCCACA
751 CAAATATCAA AAAACAGTG A

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 032.a>:

```

a032.pep
  1 MRRNVPAVAV LRRPLRQTFL DLALAQARAV PAGKQGFVR CRLTORQIVF
 51 QGFHAFAGQR NLPLASFAG NVYPRLVQIY IICIQAVYLA HAQTAAVHQF
101 EQRVIAHRQR VAAVHGQIQH PVQPFRLRQGF GYALGLLRRF DVGGRVGMQQ
151 TAFDQPGAIL PRRRLARQR PRIQTALRQP PRRRKIALR QALRHAACIF
201 RRHLCQQRKQ FFQIAPVCRH RVLRLALAH DVFQISVKMRR KPVQNHNRPT
251 QISKKQ*

```

m032/a032 88.1% identity over a 176 aa overlap

```

m032.pep      10      20      30      40      50      60
MRRNVXAVAVXRRPLRQTFLDLALAQARAVPAGKQGFVRCRLTORQIVFQGFHAFADQR
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a032          10      20      30      40      50      60
MRRNVPAVAVLRRPLRQTFLDLALAQARAVPAGKQGFVRCRLTORQIVFQGFHAFAGQR

```

212

	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQRVAAVHGGIQH					
a032	NLPLASFAGNVYPRVQIYIICIQAVYLAHAQTAAVHQFEQRVIAHRQRVAAVHGGIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFLLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPPRRKLASQRPFPQTA					
a032	PVQPFLLRQGFYALGLLRRFDVGGVMQQTAFDQPGAILPPRRQLARQRPRIQTALRQP					
	130	140	150	160	170	180
a032	PQRRRKIALRQALRHAACIFRRHLCCQQRKQFFQIAPVCRHRVLRLLALAHDFQISVKMRR					
	190	200	210	220	230	240

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 032 shows 86.4% identity over a 176 aa overlap with a predicted ORF (ORF 032.ng) from *N. gonorrhoeae*:

m032/g032

	10	20	30	40	50	60
m032.pep	MRRNVXAVAVXRRPLRQTFDLALAQARAVPAGKQGFVRCRLTQRQIVFQGFHAFADQR					
g032	MRRNVPAVAVLRRPRFEAFDLALAQARAVPAGKQGFVRCRLTQRQIVFQGFHAFAGQR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQRVAAVHGGIQH					
g032	NLTLAPFAGNVYPRFVQIYIICIQAVYLAHAQTAAVHQLEQRVVAHRQRVAAVHGGIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFLLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPPRRKLASQRPFPQTA					
g032	PVQPFLLRQGFYALGLLRRFDVGGVGAHQPAFDQPGAILPPRRQLARQRPVQTALRQP					
	130	140	150	160	170	180
g032	PQRRRKIAPRQVLRHAACIFRRHLCCQCKQFFQIAPVCRNRVLRLLALAHDFQISVKIRR					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 115>:

g033.seq

```

1  ATGGCGGCGG CGGACAACT CTTGGGCGGC GACCGCCGCA GCGTCGCCAT
51  CATCGGAGAC GCGCGGATGA CGGCGGGGCA GCGGTTTGAA GCCTTGAATT
101 GCGCGGGCGA TATGGATGTG GATTGTCTGG TCGTCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAAGCT CGGCGCGTTG CCCAAATATC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAA GCGCAAAcgg
251 GCAAGGTATT AGACAAAATA CCCGGCGCGA TGGagtTTGC CCAAAAAGTC
301 GAACaCaAaA TCAAAACCTT TGCCGAAGAA GCCGAACACG CCAAACAGTC
351 GCTGTCGCTG TTTGAAAATT TCGGCTTCCG CTACACCGGC CCCGTGGACG
401 GACACAACGT CGAGAACTCT GTGACGTAT TGAAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCcg tCaAATACCA CGCCGTGCGc aACCTGCcta
551 AAGAAGGCGG GCGCAAAATg ccGTCTGAAA AAGAACCcAA GCCCGCGcCc
601 aaaccgACCT ATACCCAAGT ATTCGGCAAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG

```

```

701 GACTGGTGGA GTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT tacCTTTGCC GCGGTTTGG CGTGCGAAGG
801 CATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTGCCCCG TTTGTTTGCC
901 GTCGACCGTG CGGGCATCGT CGGCGCGGAC GGTCCGACCC ATGCCGGCTT
951 GTACGATTTG AGCTTCTTGC GCTGTGTGCC GAACATGATT GTTGCCGCGC
1001 CGAGCGATGA AAACGAATGC CGCCTGCTGC TTTCGACCTG CTATCAGGCG
1051 GATGCGCCCG CCGCGTCCG CTATCCGCGC GGCACGGGTA CGGGCGCGCC
1101 GGTTCAGAC GGCATGAAA CCGTGGAAT CCGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCC TtcatTGCCT TCGGCAGTAT GGTGCGCCACC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTCGCGG ATATGCGCTt
1251 cgtcaaacCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCAcg
1301 accGCATCGT TACCTTGAA GAAAACGCGG AACAGGGCGG CGCAGGCGGC
1351 GCGGTCTTGG AAGTGTGGC GAAACACGGC ATCTGCAAA CCGTTTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGAACA CGGCGATCCG AAAAACTTT
1451 TGGACGATT GGGTTGAGT GCCGAAGCGG TGGAACGCGG GGTGCGCGAG
1501 TGGCTGCCCG ACCGTGATGC GGCAAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 116; ORF 033.ng>:

```

g033.pep
1 MAAADKLLGG DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVLNDNE
51 MSISPNVGAL PKYLASNVVR DMHLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDLKDLRSR
151 KGPQLLHVIT KKGNGYKLA E NDPVKYHAVA NLPKEGGAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGKTA FIAFGSMVAT
401 ALAVAEKLNA TVADMRVFKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLLLV ADTVTEHGDP KKLLDDLGLS AEAVERVRRE
501 WLPDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

```

m033.seq
1 ATGGCGGCGG CAGACAACT CTGCGGCAGC GACCGCCGCA GCGTCGCCAT
51 CATCGGCGAC GCGCGGATGA CCGCGGGGCA GCGGTTTGAA GCCTTGAATT
101 GCGCaG.CGA TATGGATGT GATTGTCTrG TCGTCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAAGT CCGCGCGCTG CCGAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GCCTGTTGAG TACCGTCAA GCGCAACGG
251 GCAAGGTATT AGACAAAATA CCGGCGCGCA TGGAGTTTGC CCAAAAAGTC
301 GAACACAAA TCAAAACCCT TGCCGAAGAA GCCGAACAG CCAACAGTC
351 GCTGTCTTTG TTTGAAAAC TCGGCTTCG CTACACGGC CCCGTGGAGC
401 GACACAACGT CGAAAATCTG GTGGACGTAT TGAAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCG TCAAATACCA CGCCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGCAATG CCGTCTGAAA AAGAACCCTA GCCCGCCGCC
601 AAACCGACCT ATACCCAAGT GTTCGGCAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTACCGT TTTGTTTGCC
901 GTCGACCGCG CGGGCATCGT CCGCGCGGAC GGCCCCACCC ATGCCGGTCT
951 GTACGATTTG AGCTTTTTCG GCTGCGTGCC GAACATGATT GTCGCCGCGC
1001 CGAGCGATGA AAACGAATGC CGCCTGTTGC TTTCGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCGTCCG CTATCGCGC GGCACGGGTA CGGGCGCGCC
1101 GGTTCAGAC GGCATGAAA CCGTGGAAT CCGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACGCA TTCATTGCCT TCGGCAGTAT GGTGCGCCCC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTCGCGG ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCAGC

```

```

1301 ACCGCATCGT TACCTTGAA GAAACGCGG AACAGGGCGG CGCAGGCGGG
1351 GCGGTGCTGG AAGTATTGGC GAAACACGGC ATCTGCAAAC CCGTTTGTCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTG GGGCTTGAGT GCCGAAGCGG TGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 033>:

```

m033.pep
1  MAAADKLLGS DRRSVAIIGD GAMTAGQAFE ALNCAXDMDV DLLVVLNDNE
51  MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDLKDLRSR
151 KGPQLLHVIT KKGNGYKLAE NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLO RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPETHAGLYDL SFLRCVPNMI VAAPSDENEC RLLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGEKTA FIAFGSMVAP
401 ALAVAELKNA TVADMRFVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLLGV ADTVTGHGDP KKLLDDLGLS AEAVERRVRA
501 WLSDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

```

a033.seq
1  ATGGCGGCGG CGGACAAACA GTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51  CATCGGCGAC GCGCGCATGA CGGCGGGTCA GCGGTTTGAA GCCTTGAAC
101 GCGCGGCGCA TATGGATGTG GATTGCTGG TCGTCCTCAA CGACACGAA
151 ATGTCGATTT CCCCAACGT CGGTGCGTTG CCCAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAAA GCGCAAACGG
251 GCAAGGTATT AGACAAATA CCCGGCGCGA TGGAGTTTGC CCAAAAGTTC
301 GAACATAAAA TCAAAACCTT TGCCGAAGAA GCCGAACACG CCAACAGTTC
351 ACTGCTTTTG TTTGAAACT TCGGCTTCG CTATACCGGC CCCGTGGACG
401 GACACAACGT CGAAATCTG GTCGATGTAT TGAAGACCT GCGCGGACGC
451 AAAGGCCCGC AGCTTCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGATCCCG TCAAATACCA CGCCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGCAAATG CCGTCTGAAA AAGAACCCTA GCCCGCCGCC
601 AAACCGACCT ATACCCAAGT GTTCGGCAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCAGCCCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAA ACCTGCCCGT TTTGTTGCC
901 GTCGACCGCG CGGCATCGT CGGCGCGGAC GGCCCGACCC ATGCCGTTT
951 GTACGATTTA AGCTTTTTC GCTGCATTCC GAATATGATT GTCGCCGCGC
1001 CGAGCGATGA AAATGAATGC CGCCTGCTGC TTTCGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCCGTCG CTATCCGCGC GGCACGGGTA CGGGCGTGCC
1101 GGTTCAGAC GGCATGGAAA CCGTGGAAAT CGGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCA TTCATTGCCT TCGGCAGTAT GGTGCCCCCT
1201 GCATTGGCGG TCGCCGAAA ACTGAACGCC ACCGTCGCCG ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCTTGCC CGAAGCCAGC
1301 ACCGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCAGC
1351 GCGGTGCTGG AAGTGTGGC GAAACACGGC ATCTGCAAAC CCGTCTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTG GGGCTTGAGT GCCGAAGCGG TGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 120; ORF 033.a>:

```

a033.pep
1  MAAADKQLGS DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51  MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDLLEDLRGR
151 KGPQLLHVIT KKGNGYKLAE NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLO RAYDQLVHDI ALQNLPLVFA

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301 VDRAGIVGAD GPTHAGLYDL SFLRCIPNMI VAAPSDENEC RLLSTCYQA
 351 DAPAAVRYPR GTGTGVPVSD GMETVEIGKG IIRREGKTA FIAFGSMVAP
 401 ALAVAGKLNA TVADMRVVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGS
 451 AVLEVLAKHG ICKPVLLLGV ADTVTGHGDP KKLLDDLGLS AEAVERRVRA
 501 WLSDRDAAN*

m033/a033 98.4% identity over a 509 aa overlap

m033.pep	10	20	30	40	50	60
	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVLLVVLNDNEMSISPNGAL					
a033	MAAADKQLGSDRRSVAIIGDGAMTAGQAFEALNCAGDMDVLLVVLNDNEMSISPNGAL					
	10	20	30	40	50	60
m033.pep	70	80	90	100	110	120
	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQVEHKIKTLAEAEHAKQSLSL					
a033	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQVEHKIKTLAEAEHAKQSLSL					
	70	80	90	100	110	120
m033.pep	130	140	150	160	170	180
	FENFGFRYTGPDVGHNVENLVDVLKDLRSRKGPLLHVITKKNGYKLAENDPVKYHAVA					
a033	FENFGFRYTGPDVGHNVENLVDVLEDLRGRKGPLLHVITKKNGYKLAENDPVKYHAVA					
	130	140	150	160	170	180
m033.pep	190	200	210	220	230	240
	NLPKESAAQMPSEKEPKPAKPTYTQVFGKWLCDRAAADSRLVAITPAMREGSGLVEFEQ					
a033	NLPKESAAQMPSEKEPKPAKPTYTQVFGKWLCDRAAADSRLVAITPAMREGSGLVEFEQ					
	190	200	210	220	230	240
m033.pep	250	260	270	280	290	300
	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA					
a033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA					
	250	260	270	280	290	300
m033.pep	310	320	330	340	350	360
	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
a033	VDRAGIVGADGPTHAGLYDLSFLRCIPNMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
	310	320	330	340	350	360
m033.pep	370	380	390	400	410	420
	GTGTGAPVSDGMETVEIGKGIIRREGKTAFAFGSMVAPALAVAEKLNATVADMRVVKP					
a033	GTGTGVPVSDGMETVEIGKGIIRREGKTAFAFGSMVAPALAVAGKLNATVADMRVVKP					
	370	380	390	400	410	420
m033.pep	430	440	450	460	470	480
	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTGHGDP					
a033	IDEELIVRLARSHDRIVTLEENAEQGGAGSAGVLEVLAKHGICKPVLLLGVADTVTGHGDP					
	430	440	450	460	470	480
m033.pep	490	500	510			
	KKLLDDLGLSAEAVERRVRAWLSRDAANX					
a033	KKLLDDLGLSAEAVERRVRAWLSRDAANX					
	490	500	510			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 033 shows 98.4% identity over a 509 aa overlap with a predicted ORF (ORF 033.ng) from *N. gonorrhoeae*:

m033/g033

m033 . pep	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSI SPNVGAL	60
g033	MAAADKLLGGDRRSVAIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSI SPNVGAL	60
m033 . pep	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQKVEHKIKTLAEAEHAKQSLSL	120
g033	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQKVEHKIKTLAEAEHAKQSLSL	120
m033 . pep	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGQPLLHVITKKGNKYKLAENDPVKYHAVA	180
g033	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGQPLLHVITKKGNKYKLAENDPVKYHAVA	180
m033 . pep	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRVAITPAMREGSGLVEFEQ	240
g033	NLPKEGGAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRVAITPAMREGSGLVEFEQ	240
m033 . pep	RFPDRYFDVGIAEQHAVTFAGGLACEGMPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA	300
g033	RFPDRYFDVGIAEQHAVTFAGGLACEGMPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA	300
m033 . pep	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLLSTCYQADAPAAVRYPR	360
g033	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLLSTCYQADAPAAVRYPR	360
m033 . pep	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAGSMVAPALAVAEKLNATVADMR FVKP	420
g033	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAGSMVATALAVAEKLNATVADMR FVKP	420
m033 . pep	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTGHGDP	480
g033	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTEHGDP	480
m033 . pep	KKLLDDLGLSAEAVERRVRWLSDRDAANX	510
g033	KKLLDDLGLSAEAVERRVREWLPRDAANX	510

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 121>:

g034 . seq

```

1  ATGAGCCGTT TATGGTTTTT TGCCGTAAAA AACATTATAA TCCGCCTTAT
51  TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGACCA CGCCGCCGAA AACAGCTACG GCCTGCCCGC GTTCAACGTC
151 AACAACTCG AACAAATGCG CGCCATTATG GAAGCCGCCG ACCAAGTCAA
201 CGGCCCCGTC ATCGTACAGG CGAGCGCAGG TGCGCGCAAA TACGcgGCG
251 CGCCGTTTTT GCGCCACCTG ATTCTGGCGG CAGTCGAAGA ATTTCCGCAC
301 ATCCCCGTCG TGATGCACCA AGACCACGGC GCATCGCCCG ACGTgtgCCA
351 ACGCTCCATC CAACTGGGCT TCTCTCCGT GATGATGGAC GGCTCTTGC
401 TCGAAGACGG CAAAACCCCT TCTTCTTACG AATACAACGT CAACGCCACC
451 CGTACCGTCG TCAACTTCTC CCACGCCTGC GCGGTGTCCG TCGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAAACCGG CGAAGCAGGC GAAGAAGACG
551 GAGTGGGCGC GGCAGGCAAA CTCTCACAG ACCAAATGCT CACCAGCGTT
601 GAAGATGCCG TGCCTTTCGT TAAAGATACC GCGGTTGACG CATTGGCGAT
651 TGCCGTCGGC ACCAGCCAGC GGCATACAA ATTCACCCGT CCGCCACAG

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701 GCGACGTATT GCGTATCGAC CGCATCAAGG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGgtCCAGC TCCGTTCCGC AAGAatgGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CGGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG CAAAGTCAAC
901 ATCGATACCG ACCTGCGCCT CGCTTCCACC GGCGCGGTAC GCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TTGATCCGCG CAAATACTTG GGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GTTATCTTGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAAT CAAACCTGTT TCGTTGGAAA AAATGGCAAG
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 122; ORF 034.ng>:

g034.pep

```

1 MSRLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EADQVNAIPV IVQASAGARK YAGAPFLRHL ILAAVEEFPFH
101 IPVVMHQDHG ASPDVCQRSI QLGFSSVMMD GSLEDGKTP SSYEYNVNAT
151 RTVVNFSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAAGK LSHDQMLTSV
201 EDAVRVFKDT GVDALAIIVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKI NEYGGNIGET YGVFVEEIVE GIKHGVKRVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL GKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMASRYA KGELNQIVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 123>:

m034.seq (partial)

```

1 ATGAGCTGTT TATGGTTTTT TGCTGTAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA WACAGCTACG GCyTGCCGGC GTTCAACGTC
151 AACAACTCG WACAGATGCG CGCCATCATG GAGGCTGCAG ACCAAGTCGA
201 CGCCCCCGTC ATCGTACAGG CGAGTGCCGG TGCGCGCAA TATGCGGGTG
251 CGCCGTTTTT ACGCCACCTG ATTTTGGCGG CTGTCGAAGT ATTTCCACAC
301 ATCCCCGTCG TCATGCACCA AGACCACGGC GCATCACCCG ACGTGTGCCA
351 ACGCTCCATC CAACTGGGCT TCTCCTCTGT AATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTACG AATACAACGT CAACGCCACA
451 CGTACCGTGG TTAACCTTCTC CCACGCTTGC GGCGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAAACCGG CGATGCAGGC GAAGAAGACG
551 GTGTAGCGC AGTGGGCAAA CTTTCCACG ACCAAATGCT GACCAGCGTC
601 GAAGATGCCG TATGTTTCGT TAAAGATACC GGCGTTGACG CATTGGCTAT
651 TGCCGTCGGC ACCAGCCACG GCGCATACAA ATTCACCCGT CCGCCACAG
701 GCGATGTATT ACGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA C...

```

This corresponds to the amino acid sequence <SEQ ID 124; ORF 034>:

m034.pep (partial)

```

1 MSCLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE XSYGLPAFNV
51 NNLXQMRAIM EADQVDAIPV IVQASAGARK YAGAPFLRHL ILAAVEVFPFH
101 IPVVMHQDHG ASPDVCQRSI QLGFSSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFSHAC GVSVEGEIGV LGNLETGDAG EEDGVGAVGK LSHDQMLTSV
201 EDAVCFVKDT GVDALAIIVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMH...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 125>:

a034.seq

```

1 ATGAGCCGTT TATGGTTTTT TGCCGCAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA AACAGCTACG GCCTGCCCGC GTTCAACGTC
151 AACAACTCG AACAAATGCG CGCCATTATG GAAGCCGCGC ACCAAGTCAA
201 CGCGCCCGTC ATCGTACAGG CGAGCGCAGG TGCGCGCAA TACGCGGGCG
251 CGCCGTTTTT GCGCCACCTG ATTTTGGCGG CTGTCGAAGA ATTTCCGCAC
301 ATCCCCGTCG TGATGCACCA AGACCACGGC GCATCGCCCG ACGTGTGCCA
351 ACGTCCATC CAACTGGGCT TTTCTCTCGT GATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTATG AATACAACGT CAACGCCACC

```

```

451 CGTACCGTGG TTAATTTCTC CCACGCCTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAACTGG CGAAGCCGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAAA CTTTCCACG ACCAAATGCT CACCAGCGTC
601 GAAGATGCCG TCGTTTTCTG TAAAGATACC GCGTTGACG CATTGGCGAT
651 TGCCGTCGGC ACCAGCCACG GCGCGTACAA ATTCACCCGT CCGCCCACAG
701 GCGACGTGTT GCGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGGCTCCAGC TCCGTTCCGC AAGAATGGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CGGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG TAAAGTCAAC
901 ATCGATACCG ACTTGCGCCT TGCTTCCACC GCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TCGATCCGCG CAAATATTG AGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GCTACCTCGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAAT CAAACCGGTT TCCTTGAAA AAATGGCAAA
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 126; ORF 034.a>:

```

a034.pep
1  MSRLWFFAAK NIIIRLIYLL PKETQMALVS MRQLLDHAAE NSYGLPAFNV
51  NNLEQMRRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFHSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAVGK LSHDQMLTSV
201 EDAVRFVKDT GVDALAIAGV TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKV NEYGGNIGET YGVPVEEIVE GIKHGVKRVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL SKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMANRYA KGELNQIVK*

```

m034/a034 96.9% identity over a 257 aa overlap

```

m034.pep      10      20      30      40      50      60
MSCLWFFAVKNIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRRAIM
|| |||||:|||||||||||||||||||||||||||||||||||||||||||
a034          10      20      30      40      50      60
MSRLWFFAAKNIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRRAIM

m034.pep      70      80      90      100     110     120
EAADQVDAPVIVQASAGARKYAGAPFLRHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI
|||||:|||||||||||||||||||||||||||||||||||||||||||
a034          70      80      90      100     110     120
EAADQVNAPVIVQASAGARKYAGAPFLRHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI

m034.pep      130     140     150     160     170     180
QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHSHACGVSVEGEIGVLGNLETGDAG
|||||||||||||||||||||||||||||||||||||||||||||||||
a034          130     140     150     160     170     180
QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHSHACGVSVEGEIGVLGNLETGEAG

m034.pep      190     200     210     220     230     240
EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID
|||||||||||||||||||||||||||||||||||||||||||||||||
a034          190     200     210     220     230     240
EEDGVGAVGKLSHDQMLTSVEDAVRFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID

m034.pep      250
RIKEIHQALENTHIVMH
||||||||||||||
a034          250     260     270     280     290     300
RIKEIHQALENTHIVMHGSSSVPQEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVKRVN

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 034 shows 96.5% identity over a 257 aa overlap with a predicted ORF (ORF 034.ng) from *N. gonorrhoeae*:

m034/g034

m034 . pep	MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNVLXQMRAIM	60
g034	MSRLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNLEQMRAIM	60
m034 . pep	EAADQVDAPVIVQASAGARKYAGAPFLRHLILA AVEVFPHIPVVMHODHGASPDVCQRSI	120
g034	EAADQVNAPVIVQASAGARKYAGAPFLRHLILA AVEEFPHIPVVMHODHGASPDVCQRSI	120
m034 . pep	QLGFSSVMDGSLMEDGKTPSSYBYNVNATRTTVNFSHACGVSVEGEIGVLGNLETGDAG	180
g034	QLGFSSVMDGSLLEDGKTPSSYBYNVNATRTTVNFSHACGVSVEGEIGVLGNLETGEAG	180
m034 . pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID	240
g034	EEDGVGAAGKLSHDQMLTSVEDAVRFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID	240
m034 . pep	RIKEIHQALPNTHIVMH	257
g034	RIKEIHQALPNTHIVMHGSSSVPEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVRKVN	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 127>:

g036 . seq

```

1  ATGCTGAAGC CGTGTGTTGGT ATACAGTGCC TGTGCGGCGG cgttgccTGC
51  GCGGACTTCG AGCAGCAGGC GTTGCGTGCC TTCGGGCAGA TGTGCGTACC
101 AATATTCGAG CAGGGCGGAC GCAACGCCCC GTCGGGCGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCTGCCGT CTTTTCGCGC AAGGAAAACC TGTTCGGACG
251 GCGAAACAAG CGCGGACTCA AATTGGCGTT GCGTCCACGC GGACGGGTTG
301 CAGACGGTAT CGAGCGCGGC CAGTGCAGCG CAGTCCGACG GTGAGGCTGG
351 GCGGATGTTT ATGTTTCGTGC CTTCCGTTCC GCCTGTTCTT TGGCAGTCAG
401 GGCGATTTTG TTGCGGACGT AGAGCAGTTC GCGGTGTGCC GCGCCAGTTG
451 CGGGATAGCC GCCGCCGAGG GCGAGCGCGA GAAAATCGGC GGCGGTCCGC
501 ATATCGGGTT TGCCTGAGAA GGGCGGACGG TTTTCCAGTG CGAACGCACT
551 GCCGATGCCG TCTGAAAGA CGTACCCCTC GGGGAGGGCA ATGTCTGCCG
601 CCCTACCGAC TTGATAATCG CTCAAACGGC GGCGGTTTCA CGTGTGCAAC
651 CACGCATAAA ACACCTCGCC CATACGCGCG TCCGACGCGG CGAGTATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCAGAGCGT GGGATGCCGA
751 TTAAGGCGT  GTCGAACGGC GTTGCCAAAC CTTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 128; ORF 036.ng>:

g036 . pep

```

1  MLKPCLVYSA CAAALPARTS SSRRCVPSGR CAYQYSSRAD ATPRRRHSGA
51  VAIRCSSDSS GRFCQTIKAA ILPSFSARKT CSDGETSADS NWRCVHADGL
101 QTSSAASAA QSDGEAGRMF MFVPSVPPVL WQSGRFCCGR RAVRRVPRQL
151 RDSRRRGRAR ENRRRSAYRV CLRRADGFPV RTHCRCLKR RTFRGGQCLP
201 PYRLDNRSNG GGSACRTHK TLRPYARPQR RVCSFAAAAA RRRHRAWGCR
251 LKACRTALPN LAPRRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 129>:

m036 . seq

```

1  ATGCTGAAGC CGTGCAGCGT GTACAGTGCC TGTGCGGCGG TGTGCTGTC
51  ACGGACTTCG AGCAGCAGGC GTTGCGTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCCg.CGT CTTTTCGCGC AAGGAAAACC TGTTCGGACG
251 CGGAAACAG TCGGACTCA AATTGGCGTT GCGTCCATGC GGACGGGTTG
301 CAGACGGCAT CGAGTGCAGC CAGCTCCTCA CAATCGGCAC AAACGGCAGC

```

```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401 GCGGATTTTG TTGCGGACGT AGAGCAAACC GCGGTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGCTT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CCGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA ACACTTCGCC CATAAGAGCG TCCGTAGCGG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGGGGT ATCAAACGGC GTTGCCAAAC CCTGAGCTAC ACCGATGCCG
801 ATACGCAGTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 130; ORF 036>:

```

m036.pep
1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPXSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLPMR ESRQSAYPV CLRTAELLPA RTRCLCRLKR RIPPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*R QGCSFAAAAA RRRHRARVRR
251 LRGYQTALPN PELHRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 131>:

```

a036.seq
1 ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTGCGCTGC
51 ACGGACTTCG AGCAGCAGGC GTTGCGTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GGCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCCGCCGT CTTTTTCGCG AAGGAAAACC TGTTCGGACG
251 GCGAAACCAG TGCGGACTCA AATTGGCGTT GCGTCCACGC GGACGGGTTG
301 CAGACGGCAT CGAGCGCGGC GAGTGCAGCG CAATCGGCAT AAACGGCGCG
351 GCGGATGTTT ACAGCGCGCG CCTCCGTTCC GCCTGTTCTT TGGCAGTCAA
401 GCGGATTTTG TTGCGGACGT AGAGCAGCTC GCGGTGTGCC GCAGCGACGG
451 CGGGAAAACC GCCTTCAGCC GCCAGATTGA GGAAGTCGCG GGCGGTCCGG
501 ATATCGGGTT TGCCTGAGAA GGGCGGACGG TTTTCCAGCG CGAACGCATT
551 GCCGATGCCG TCTGAAAAGG CGCATCCTTC CGGCAGCCGG ATGTCTGCCG
601 CCGGACCGAC CTGATAATCG CTCAAACGGC GCGGTTTCAG CGTGTGCAAC
651 CATGCATAAA ACACTTCGCC CATAAGTGCG TCCGACGCGG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGAGT ATCAAACGGC GTTGCCAAAC CTTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 132; ORF 036.a>:

```

a036.pep
1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPPSFSARKT CSDGETSADS NWRCVHADGL
101 QTASSAASAA QSA*TARRMF TGAPSVPPVL WQSRRFCCGR RAARRVPQRR
151 RENRLQPPD* GSRRRSAYRV CLRRADGFPA RTHCRCLKR RILPAAGCLP
201 PDRPDNRSNG GGSACRTMHK TLRPYVRPQR QGCSFAAAAA RRRHRARVRR
251 LKEYQTALPN LAPRRCRYAV P*

```

m036/a036 85.6% identity over a 270 aa overlap

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIRCSSDSS					
a036	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIRCSSDSS					
	10	20	30	40	50	60
m036.pep	GRFCQTIKAAIPXSFSAKRTCSNWRVHADGLQTASSAASSSQSAQTARRMF					
a036	GRFCQTIKAAIPPSFSARKTCSNWRVHADGLQTASSAASAAQSAXTARRMF					
	70	80	90	100	110	120

Homology with a predicted ORF from *N. gonorrhoeae*

m036/g036

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACA	AVLPARTSSSR	RCVSSGR	CVNQYSS	RADAI	PWRRHSGAVAIR
g036	MLKPCLVYSACA	AAALPARTSS	SRRCVPSGR	CAYQYSS	RADATPR	RRHSGAVAIR
	10	20	30	40	50	60
	70	80	90	100	110	120
m036.pep	GRFCQTIKAAI	PXSFSARK	TCS	DGETS	ADSNWRC	VHADGLQTASSA
g036	GRFCQTIKAAI	LPXSFSARK	TCS	DGETS	ADSNWRC	VHADGLQTVSSA
	70	80	90	100	110	120
	130	140	150	160	170	180
m036.pep	TGALS	VRPVLWQ	SGRFCCG	RANRRV	RHGRQD	NRPWLP
	:				:	:
g036	MEFVPS	VPPVLWQ	SGRFCCG	RRAVRR	VPRLR	DSRRRGR
	130	140	150	160	170	180
	190	200	210	220	230	240
m036.pep	RTRCL	RCLKRR	IPFAAG	CLPFAR	PDNRS	NGGSSAY
	:		:			
g036	RTHCR	RCLKRR	T	PRGGQ	CLPFYR	LDNRS
	190	200	210	220	230	240
	250	260	270			
m036.pep	RRRHR	ARVRRL	RGYQTAL	PNPEL	HRCRY	AVRX
		:		:		
g036	RRRHR	AWGCR	LKACRTAL	PNLAP	RRCRY	AVRX
	250	260	270			

m036-1.seq

1	ATGCTGAAGC	CGTGCGCCGT	GTACAGTGCC	TGTGCGGCGG	TGTTGCCTGC
51	ACGGACTTCG	AGCAGCAGGC	GTTGCGTGTC	TTCGGGCAGA	TGTGTGAACC
101	AATATTCGAG	CAGGGCGGAC	GCAATTCTCT	GGCGGCGGCA	TCGGGCGCGG
151	GTGGCAATCA	GGTGCAAGTC	GGATTGCTCG	GGCAGGTTCT	GCCAAACGAT
201	AAAGGCGGCA	ATCCCGCCGT	CTTTTTCGCG	AAGGAAAACC	TGTTTCGGAC
251	GCAGAAACCA	TGCGGAGCTA	AATTGGCGTT	CGCTCCGATG	GGACGGGTTG
301	CAGACGGCAT	CGAGTGCGGC	CAGTCTCTCA	CAATCGGCAC	AAACGGCACG

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```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401 GGCATTGTTT TTGCGGACGT AGAGCAAACC GGCCTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGGCT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA ACACTTCGCC CACACGAGCG TCCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 134; ORF 0036-1>:

```

m036-1.pep
  1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
 51 VAIRCSSDSS GRFCQTIKAA IPPSFSARKT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLPMR ESRRQSAYPV CLRTAELLPA RTRCLRLKR RIPPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*

```

m036-1/g036 76.8% identity in 228 aa overlap

```

              10      20      30      40      50      60
m036-1.pep  MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIRCSSDSS
              ||||| |||||:||||| ||||: ||||| | ||||| |||||
g036         MLKPCLVYSACAAALPARTSSSRRCVPSGRCAVQYSSRADATPRRRHSGAVAIRCSSDSS
              10      20      30      40      50      60

              70      80      90      100     110     120
m036-1.pep  GRFCQTIKAAIPPSFSARKTCS DGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g036         GRFCQTIKAAILPSFSARKTCS DGETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMF
              70      80      90      100     110     120

              130     140     150     160     170     180
m036-1.pep  TGALSVRPVLWQSGRFCCGRANRRVRHGRQDNRPWLPMRESRRQSAYPVCLRTAELLPA
              : || ||||| ||||| ||| : :||| ||||| ||||| ||| : ||
g036         MFVPSVPPVLWQSGRFCCGRRAVRRVPRQLRDSRRRGRARENRRRSAYRVCLRRADGFPV
              130     140     150     160     170     180

              190     200     210     220     229
m036-1.pep  RTRCLRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERPX
              ||:| ||||| | :| ||||| ||||| ||| ||||| |||
g036         RTHCRCLKRRTPRGGQCLPPYRLDNRSNGGSACRTHKTLRPYARPQRRVCSFAAAAA
              190     200     210     220     230     240

g036         RRRHRAWGCRLKACRTALPNLAPRRCRYAVRX
              250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 135>:

```

g038.seq
  1 ATGACTGATT TCCGCCAAGA TTTCCTCAAA TTCTCCCTCG CCCAAAATGT
 51 TTTGAAATTC GGCGAATTTA CCACCAAAGC CGGACGGCGG TCGCCCTATT
101 TCTTCAATGC CGGCTCTTTC AACGACGGCG CGTCCACGCT GCAACTGGCA
151 AAATTCTATG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201 GTTCGGCCCC GCCTACAAAG GCATTATTTT GCGGGCGGCA ACCGCGATGA
251 TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301 GCCAAAGACC GCGGCGAAGG CGGCGTGTG GTGCGGCGCG CGCTTAAAGG
351 GCGCGTGTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401 AATCAATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGCG CGGTGTGCGC
451 ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTAAATTGT CCGCCGTCTCA
501 GGAAGTGGAA AAACAATACG GCCTGCCCGT CGCCCCATC GCCAGCCTGA
551 ACGATTGTG TATCCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601 GAACCCGTCC GCACCTACCG CCGGCAGTAC GCGTAGAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 136; ORF 038.ng>:

```
g038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGASTLQLA
 51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDRGEGGVL VGAPLKGRVL IIDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GKLSAVQVEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRTYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 137>:

```
m038.seq
  1  ATGACCGATT TCCGCCAAGA TTTCTCTCAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GCGCAATTTA CCACCAAGGC AGGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGTCCC GCCTACAAAG GCATTATTTT GCGGCGCGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGGCGCGC CGCTTAAAGG
351  GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
451  ATCGCGCTCG ATCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501  GGAAGTGGAA AAACAATACG GkCTGCCCGT CGCCCCATC GCCAGCCTGA
551  ACGATTGTGT TATTCTGTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 138; ORF 038>:

```
m038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDHGEGGVL VGAPLKGRVL IIDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GELSAVQVEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRAYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 139>:

```
a038.seq
  1  ATGACCGATT TCCGCCAAGA TTTCTCTCAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GCGCAATTTA CCACCAAGC CCGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGCCCC GCCTACAAAG GCATTATTTT GCGGCGGGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGGCGCGC CGCTTAAAGG
351  GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
451  ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501  GGAAGTGGAA AAACAATACG GCCTGCCCGT CGCCCCATC GCCAGCCTGA
551  ACGATTGTGT TATTCTGTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 140; ORF 038.a>:

```
a038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDHGEGGVL VGAPLKGRVL IIDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GELSAVQVEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRAYRRQY GVE*
```

m038/a038 100.0% identity over a 213 aa overlap

```

              10      20      30      40      50      60
m038.pep    MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
```

```

|||||
a038      MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQAKFYAQSIIES
           10      20      30      40      50      60

           70      80      90      100     110     120
m038.pep  GIRFDMFLGFPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
           |||||
a038      GIRFDMFLGFPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
           70      80      90      100     110     120

           130     140     150     160     170     180
m038.pep  IIDDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQVEVEKQYGLPVAPI
           |||||
a038      IIDDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQVEVEKQYGLPVAPI
           130     140     150     160     170     180

           190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
           |||||
a038      ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
           190     200     210

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 038 shows 98.1% identity over a 213 aa overlap with a predicted ORF (ORF 038.ng) from *N. gonorrhoeae*:

m038/g038

```

           10      20      30      40      50      60
m038.pep  MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQAKFYAQSIIES
           |||||
g038      MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGASTLQAKFYAQSIIES
           10      20      30      40      50      60

           70      80      90      100     110     120
m038.pep  GIRFDMFLGFPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
           |||||
g038      GIRFDMFLGFPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDRGEGGVLVGAPLKGRVL
           70      80      90      100     110     120

           130     140     150     160     170     180
m038.pep  IIDDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQVEVEKQYGLPVAPI
           |||||
g038      IIDDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGKLSAVQVEVEKQYGLPVAPI
           130     140     150     160     170     180

           190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
           |||||
g038      ASLNDLFILLQNNPEFGQFLEPVRTYRRQYGVEX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 141>:

g039.seq

```

1  ATGCCGTC CG AACCACCTGC CGCTTCAGAC GGCATCAAAC CGACACACAC
51  CGAGAAAACA TCATGCCCGC CTGTTTCTGT CCGCACTGCA AAACCCGCCT
101 CTGGGTCAAA GAAAcccagC TCAAcgtCgC ccaagGCTTC GTCGTCTgcc
151 aaAAAtgcga agGGCTgttt aaAgccaaaG accAtctggc aaGcacGAAA
201 gaacctatat tcaacgattg gcccgaaget gtttcgggat gTcaaaCTCG

```



```

251 TCaccgcaT cggcacgcac gccattagca aGAaacagat gtccccgcgac
301 gaaatCgccg atatcctcaa cggcgggtaca acCCTGCACG ATACGCCGCC
351 CGCAACCGCC GCTGCCGCac ctGCCGCCGC ACCGcaggTT TCCGTACCGC
401 CCGCCCGTCA GGAAGGGCTC AACTGGACTA TTGCAACCTT GTTCGCACTT
451 ATCGTCCTCA TTATGCAGCT TTCCTACCTC TTCATCCTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 142; ORF 039.ng>:

g039.pep

```

1 MPSEPPAASD GIKPTHTEKT SCPPVSVRTA KPASGSKKPS STSPKASSSA
51 KNAKGCLKPK TIWQARKNLY STIGPKLFRD VKLVHRIGTH AISKQMSRD
101 EIADILNGGT TLHDTTPATA AAPAAAPQV SVPPARQEGT NWTIATLFAL
151 IVLIMQLSYL FIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 143>:

m039.seq

```

1 ATGCCGTCCTG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCACTGCA AAACCGTCT
101 CTGGGTCAAA GAAACCCAAC TCAATGTCGC CGnnnnnnnnn nnnnnnnnnn
151 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
201 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnCCC GAGGCTGTTT
251 CGGATGTCAA ACTCGTTCAC CGTATCGGCA CGCGCGCCAT CGGCAAGAAA
301 CAGATTTCCT GTGACGAAAT CGCCGGCATC CTCAACGCGG GTACAACCCA
351 GCCGATATT CCGCCGCAA CCGCCGCCAC CCCTGCTGCC GCACCGCAGG
401 TTACCGTACC GCCCGCCGCG CCCGCCGCTC AGGATGGGTT CAACTGGACG
451 ATTGCAACCC TGTTCGCCCT TATCGTCCTC ATTATGCAGC TTTCTACCT
501 CGTCATCCTA TGA

```

This corresponds to the amino acid sequence <SEQ ID 144; ORF 039>:

m039.pep

```

1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPXXXXXX
51 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXP EAVSDVKLVH RIGTRAIGKK
101 QISRDEIAGI LNGGTTQPD I PPATAATPAA APQVTVPPAA PARQDGFNWT
151 IATLFALIVL IMQLSYLVIL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 145>:

a039.seq

```

1 ATGCCGTCCTG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCACTGCA AAACCGTCT
101 CTGGGTCAAA GAAACCCAAC TCAATGTCGC CCAAGGCTTC GTCGTCTGCC
151 AAAATGCGA AGGAATGTTT AAAGCCAAAG ACCATCTGGC AAGCACGAAA
201 GAACCATAT TCAACGATT. TGCCCGAAGC TGTTCGGAT GTCAAACCTCG
251 TTCACCGCAT CGGCACGAGC GCCATCGGCA AGAAACAGAT TTCCCGTGAC
301 GAAATCGCCG GCATCCTCAA CGGCGGCACA ACCCAGCCCG ATATTCGCC
351 CGCAACCGCC GCCACCCCTG CTGCCGCACC GCAGGTACC GTACCGCCCG
401 CCGCGCCCGC CCGTCAGGAT GGGTTCAACT GGACGATTGC AACCTGTTT
451 GCCCTTATCG TCCTCATTAT GCAGCTTTC TACCTCGTCA TCCTATGA

```

This corresponds to the amino acid sequence <SEQ ID 146; ORF 039.a>:

a039.pep

```

1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPKASSSA
51 KNAKECLKPK TIWQARKNPY STIXPEAVSD VKLVHRIGTS AIGKKQISR
101 EIAGILNGGT TQPDIPPATA ATPAAAPQV VPPAAPARQD GFNWTIATLF
151 ALIVLIMQLS YLIVL*

```

m039/a039 79.4% identity over a 170 aa overlap

	10	20	30	40	50	60
m039.pep	MPSEPPYASDGIKPDTHEEIPC					
a039	MPSEPPYASDGIKPDTHEEIPC					

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	10	20	30	40	50	60
m039.pep	70	80	90	100	110	120
	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIGTRAIGKKQISRDEIAGILNGGTTQPD				
a039	:	:	:	:	:	:
	TIWQARKNPYSTIX----	PEAVSDVKLVHRIGTSAIGKKQISRDEIAGILNGGTTQPD				
	70	80	90	100	110	
m039.pep	130	140	150	160	170	
	PPATAATPAAAPQVTVP	PAAPARQDGFNWTIATLFALIVLIMQLSYLVILX				
a039	PPATAATPAAAPQVTVP	PAAPARQDGFNWTIATLFALIVLIMQLSYLVILX				
	120	130	140	150	160	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 039 shows 60.8% identity over a 171 aa overlap with a predicted ORF (ORF 039.ng) from *N. gonorrhoeae*:

m039/g039

	10	20	30	40	50	60
m039.pep	MPSEPPYASDGIKPD	THEEIPCPVVSAPTAKPVSGSKKPNMS	PXXXXXXXXXXXXXXXXXXXX			
g039	MPSEPPAASDGIKPTHTEKTSCPPVSVRTAKPASGSKKPSSTSPKASSSAKNAKGCLKPK					
	10	20	30	40	50	60
m039.pep	70	80	90	100	110	120
	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIGTRAIGKKQISRDEIAGILNGGTTQPD				
g039	:	:	:	:	:	:
	TIWQARKNLYSTIG----	PKLFRDVKLVHRIGTHAISKKQMSRDEIADIILNGGTTLHDT				
	70	80	90	100	110	
m039.pep	130	140	150	160	170	
	PPATAAT-PAAAPQVTVP	PAAPARQDGFNWTIATLFALIVLIMQLSYLVILX				
g039	PPATAAAAPAAAPQVSVP	PA---RQEGLNWTIATLFALIVLIMQLSYLFILX				
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 147>:

g040.seq

```

1   ATGAACGCGC CCGACAGCTT TGTCGCCCAC TTCCGCGAAG CCGCCCCCTA
51  CATCCGCCAA ATGCGCGGCA CGACACTGGT CGCCGGCATA GAcggCCGCC
101 TGCTCGAAGG CGGCACCTTA AATAAGCTCG CCGCCGACAT CGGGCTGTTG
151 TCGCAACTGG GCATCCGACT CGTCCTCATC CACGGCGCGT ACCACTTCCT
201 CGAcggCCTC GCCGCCGCGC AAGgccGCAC GCCGCATTAT TGCCGgggtt
251 tGCGCGTTAC CGACGaAACc tcGctcgGAC AGGCGCAGCA GtttGCCGGC
301 AccgTCCGCA GCCGTTTTGA agcCGCATTG tgcggcagCG tttcaggatt
351 cgcgCGCGCG CCTTCCGTCC CGCTCGTAtc gggcaacttc ctgacCGCCC
401 GTCcgatggg cgtgattgac ggaACCGata tggaaatacgc gggggttatc
451 cgcaaaaccg ACACCGCCGC CCTCCGTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGATG CCGCCGCTCG GGCATTCTTA CGGCGGCAAA ACCTTCAATC
551 TCGATATGGT GCAGGCCGCC GCTTCCGTCT CCGTCTCGCT TCAGGCCGAA
601 AAACCTGTTT ACCTGACCCT TTCAGACGGC ATTCCCCGCC CCGACGGCAC
651 GCTCGCCGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGCCAGCGA AACCCGACGA CTGATTTCGT CCGCCGTTGC CGCGCTCGAA
751 GCGGGCGTGC ATCGCGTCCA AATCCTCAAC GGGGCGCGCG ACGGACGCTT
801 GCTGCAAGAA CTCTTCACCC GCAACGGCAT CGGCACGTCC ATTGCCAAG
851 AAGCCTTCGT CTCCATCCGG CAGGCGCACA GCGGCGACAT CCCGCACATC
901 GCCGCCCTCA TCCGCCCGCT GGAAGAACAG GCGGTCCTAT TGCACCGCAG
951 CCGGAATAC CTCGAAAACC ACATTTCCTG ATTTTCATC CTCGAACACG

```

```

1001 ACGGCGACCT GTACGGCTGT GCCGCACTCA AAACCTTTGC CGAAGCCGAT
1051 TCGGGCGAAA TCGCCTGCCT TGCCTGCTCG CCGCAGGCAC AGGACGGCGg
1101 ctACGGCGAA CGCCTGCTTG CCCACATTAT CGATAAGGCG CGCGGCATAG
1151 GCATAAGCAG GCTGTTCGCA CTGTCCACAA ATACCGGCGA ATGGTTTGCC
1201 GAACGCGGCT TTCAGACGGC ATCGGAAGAC GAGCTGCCCG AAACGCGGCG
1251 CAAAGACTAC CGCAGCAACG GACGAAACCC GCATATTCTG GTGCGTCGCC
1301 TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 148; ORF 040.ng>:

g040.pep

```

1 MNAPDSFVAH FREAAPYIRQ MRGTTLVAGI DGRLLGGTLL NKLAADIGLL
51 SQLGIRLVLI HGAYHFLDRL AAAQGRTPHY CRGLRVTDET SLGQAQGFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPMGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWM PPLGHSYGGK TFNLDMVQAA ASVAVSLQAE
201 KLVYLTLSDG ISRPDGTAE TLQAQEAQSL AEHAASETRR LISSAVAALAE
251 GGVHRVQILN GAADGSLQAE LFTRNGIGTS IAKEAFVSIR QAHSGDIPHI
301 AALIRPLEEQ GVLLHRSREY LENHISEFSI LEHDGDLYGC AALKTFAEAD
351 CGEIACLAVS POAQDGGYGE RLLAHIIDKA RGIGISRLFA LSTNTGEWFA
401 ERGFQTASED ELPETRRKDY RSNGRNPHIL VRRLLHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 149>:

m040.seq

```

1 ATGAGCGCGC CCGACCTCTT TGTCGCCCAC TTCCGCGAAG CCGTCCCCTA
51 CATCCGCCAA ATGCGCGGCA AAACGCTGGT CGCCGGCATA GACGACCGCC
101 TGCTCGAAGG TGATACCTTA AACAAAGCTCG CCGCCGACAT CGGGCTGTTG
151 TCGCAACTGG GCATCAGGCT CGTCCTCATC CACGGCGCGC GCCACTTCCT
201 CGACCGCCAC GCCGCGGCTC AAGGCCGCAC GCCGCATTAT TGCCGGGGCT
251 TGCGCGTTAC CGACGAAACC TCGCTCGAAC AGGCGCAGCA GTTTGCCGGC
301 ACCGTCCGCA GCCGTTTGA AGCCGCATTG TGCGGCAGCG TTTCCGGGTT
351 CGCGCGCGCG CCTTCCGTCG CGCTCGTATC GGGCAACTTC CTGACCCGCC
401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGAATACGC GGGCGTTATC
451 CGCAAAACCG ACACCGCCGC CCTCCGTTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGCTG CCGCCGCTCG GACATTCTTA CAGCGGCAAG ACCTTCTATC
551 TCGATATGCT TCAAACCGCC GCCTCCGCGC CCGTCTCGCT TCAGGCCGAA
601 AAACCTCGTT ACCTGACCTT TTCAGACGGC ATTCCCGCC CCGACGGCAC
651 GCTCGCCGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGGCGGGCA AACCGGACGG CTGATTTCTG CCGCGAATC CTTACCCGCG
751 AACGGCATCG GCACGTCCAT TGCCAAAGAA GCCTTCGTCT CCATCCGGCA
801 rGCCAaywg G.CGACATCC CGCACATCGC CGCCCTCATC CGCCCGCTGG
851 AAGAACAGGG CATCCTGCTG CACCGCAs.c GCGAATACCT CGAAAAACAC
901 ATTTCCGAAT TTTCCATCCT CGAACACGAC GGCAACCTGT ACGGTTGCGC
951 CGCCCTGAAA ACCTTTGCCG AAGCCGATTG CGGCGAAATC GCCTGCCTTG
1001 CCGTCTCGCC GCag.cACAG GACGGCGGCT ACGGCGAATC CnTGCTTGCC
1051 CACATTATCG ATAAGGCGCG CGGCATAGGC ATAAGCAGGC TGTTCGCACT
1101 GTCCACAAAT ACCGGCGAAT GGTTTGCCGA ACGCGGCTTT CAGACGGCAT
1151 CGGAAGACGA GTTGCCCGAA ACGCGGCGCA AAGACTACCG CAGCAACGGA
1201 CGGAACTCGC ATATTCTGGT ACGTCGCTG CACCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 150; ORF 040>:

m040.pep

```

1 MSAPDLFVAH FREAVPYIRQ MRGKTLVAGI DDRLLGGDTL NKLAADIGLL
51 SQLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVTDET SLEQAQGFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFYLDMLQTA ASAAVSLQAE
201 KLVYLTLSDG ISRPDGTAE TLQAQEAQSL AEHAGGQTRR LISSAELEFTR
251 NGIGTSIAKE AFVSIRQAHX XDIPHIAALI RPLEEQGILL HRXREYLENH
301 ISEFSILEHD GNLYGCAALK TFAEADCGEI ACLAVSPQXQ DGGYGERXLA
351 HIIDKARGIG ISRLFALSTN TGEWFAERGF QTASEDELPE TRRKDYRSNG
401 RNSHILVRRL HR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 151>:

a040.seq

a040.pap

1	MIVPDLFVAH	FREAAPYIRQ	MRGKTLVAGI	DDRLEGDTL	NKFAADIGLL
51	<u>SQLGRLVL</u>	HGARVGLDRH	AAQQGRTPHY	CRGLRPTVDET	SLEQAQQFAG
101	TVRSRFEAAH	QGSVSGFARA	PSVPLVSGNF	LTARPIGVID	GTDMEYAGVI
151	RKTDFAALRF	CLDAGNIWVL	PPLGHSYSGK	TFHLDMLQTA	ASVAVSLQAE
201	KLVYLTLSDG	ISRPDGT LAV	TLSAQEAQSL	AEHAGGETTR	LISSAVA ALE
251	GGVHRVQILN	GAADGSLLQE	LFTNRNGTGS	IAKEAFVSIR	QAHSGDIPHI
301	AALIRPLEEQ	PQLLHRSREY	LENHISEFSI	LEHGDNLGYC	AALKTF AEAD
351	CGEIACLAVS	GQAQDGSYGE	RLLAHITDKA	RGISIRSLFA	LSTNTGEWFA
401	ERGFQTASED	ELPETRRKDY	RSNGRNSHIL	VRRLHR*	

	10	20	30	40	50	60
m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLEGDTLNKLAAIDIGLLSQLGIRLVLI	:	:	:	:	:
a040	MIVPDLFVAHFREAAPYIRQMRGKTLVAGIDDRLLEGDTLNKFADIGLLSQLGIRLVLI	:	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m040.pep	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA	:	:	:	:	:
a040	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA	:	:	:	:	:
	70	80	90	100	110	120
	130	140	150	160	170	180
m040.pep	PSVPLVSGNFLTARPIGVIDGTMDEYAGVIRKTDTAALRFQLDAGNIWVLPPLGHSSYSGK	:	:	:	:	:
a040	PSVPLVSGNFLTARPIGVIDGTMDEYAGVIRKTDTAALRFQLDAGNIWVLPPLGHSSYSGK	:	:	:	:	:
	130	140	150	160	170	180
	190	200	210	220	230	240
m040.pep	TFYLDMLQTAASAAVSLSQAEKLVYLTLSDGISRPDGTLAETLSAQEAQSLSAEHAGGQTRR	:	:	:	:	:
a040	TFHLDMLQTAASVAVSLSQAEKLVYLTLSDGISRPDGTLAETLSAOEAOSSLAEHAGGETRR	:	:	:	:	:

	190	200	210	220	230	240
m040.pep	LISSA-----250 260 270					
	ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI					
a040	LISSAVAALEGGVHRVQILNGAAGSLLQELFTRNGIGTSIAKEAFVSIRQAHSGDIPHI					
	250	260	270	280	290	300
m040.pep	280	290	300	310	320	330
	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS					
a040	AALIRPLEEQGILLHRSREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS					
	310	320	330	340	350	360
m040.pep	340	350	360	370	380	390
	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY					
a040	PQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY					
	370	380	390	400	410	420
m040.pep	400	410				
	RSGRNSHILVRRRLHRX					
a040	RSGRNSHILVRRRLHRX					
	430					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 040 shows 88.3% identity over a 436 aa overlap with a predicted ORF (ORF 040.ng) from *N. gonorrhoeae*:

m040/g040

m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLLEGDTLNKLAADIGLLSQLGIRLVLI	60
g040	MNAPDSFVAHFREAPYIRQMRGTTLVAGIDGRLLLEGDTLNKLAADIGLLSQLGIRLVLI	60
m040.pep	HGARHFLDRHAAQGRTPHYCRGLRVTDTSLEQAQQFAGTVRSRFEALCGSVSGFARA	120
g040	HGAYHFLDRLAAQGRTPHYCRGLRVTDTSLGQAQQFAGTVRSRFEALCGSVSGFARA	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK	180
g040	PSVPLVSGNFLTARPMGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWMPPLGHSYGGK	180
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTLSDGISRDPDGLAETLSAQEAQSLAEHAGGQTRR	240
g040	TFNLDMVQAAASVAVSLQAEKLVYLTLSDGISRDPDGLAETLSAQEAQSLAEHAASETRR	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI	276
g040	LISSAVAALEGGVHRVQILNGAAGSLLQELFTRNGIGTSIAKEAFVSIRQAHSGDIPHI	300
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS	336
g040	AALIRPLEEQGVLLHRSREYLENHISEFSILEHDGDLGCAALKTFAEADCGEIACLAVS	360
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	396
g040	PQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	420
m040.pep	RSGRNSHILVRRRLHRX	413
g040	RSGRNPILVRRRLHRX	437

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 153>:

```
g041.seq
1   ATGAGTTCGC CCAAACACAT CGGCTTGCGG GCGGCGAGCA ACGGCGGCCT
51  GATTACCGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATC GGTGCGCTGG
101 TGTGCGAAGT ACCGCTGACC GATATGATCC GTTATCCGCT GCTGTCCGCC
151 GGTTCAGATT GGACGGACGA ATACGGCAAT CCGCAGAAAT ACGAAGCCTG
201 CAAACGCCCG CTGGGCGAAT TGTCGCCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCACTC ATTACCACCA GCCTCAGCGA CGACCGCGTC
301 CATCCCGCCC ACGCGCTCAA ATTCTACGCC AAACCTGCGG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCAACGCGA ATCCGCCGAC AAACCTGCCT GCGTGTGCT GTTTTGTAAA
451 GAATTTTGG GATAA
```

This corresponds to the amino acid sequence <SEQ ID 154; ORF 041.ng>:

```
g041.pep
1   MSSPKHIGLO GGSNGGLITA AAFVREPOSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEACKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSPOSW LYSPDGGGHT NGTQRESAD KLACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 155>:

```
m041.seq
1   ATCAGTTCGC CCGAACACAT CGGCTTGCGG GCGGCGAGCA ACGGCGGACT
51  GATTACTGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATC GCGCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGACT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCCG TTGGGCGAAT TGTCGCCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAACCTGCGG AAACCTCCGC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCAACGCGA ATCCGCCGAC GAACTCGCCT GCGTCTTGCT GTTTTGTAAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 156; ORF 041>:

```
m041.pep
1   ISSPEHIGLO GGSNGGLITA AAFVREPOSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEVCKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSQSW LYSPDGGGHT NGTQRESAD ELACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 157>:

```
a041.seq
1   ATCAGTTCGC CCGAACACAT CGGCTTGCGG GCGGCGAGCA ACGGCGGACT
51  GATTACTGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATA GCGCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGACT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCCG TTGGGCGAAT TGTCGCCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAACCTGCGG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CGCAGCGCGA AGCCGCCGAC GAACTCGCCT GCGTGTGCT GTTTTGTAAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 158; ORF 041.a>:

```
a041.pep
1   ISSPEHIGLO GGSNGGLITA AAFVREPOSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEVCKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSPOSW LYSPDGGGHT NGTQREAAD ELACVLLFLK
```

151 EFLG*

m041/a041 98.7% identity over a 154 aa overlap

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPOSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
a041	ISSPEHIGLQGGSNGLITAAAFVREPOSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCKRRRLGELSPYHNLSGDIDYPPALITTSLSDDRHPAHALKFYAKLRETSAQSW					
a041	PQKYEVCKRRRLGELSPYHNLSGDIDYPPALITTSLSDDRHPAHALKFYAKLRETSAQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
a041	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 041 shows 96.8% identity over a 154 aa overlap with a predicted ORF (ORF 041.ng) from *N. gonorrhoeae*:

m041/g041

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPOSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
g041	MSSPKHIGLQGGSNGLITAAAFVREPOSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCKRRRLGELSPYHNLSGDIDYPPALITTSLSDDRHPAHALKFYAKLRETSAQSW					
g041	PQKYEVCKRRRLGELSPYHNLSGDIDYPPALITTSLSDDRHPAHALKFYAKLRETSAQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
g041	LYSPDGGGHTGNGTQRESADKLACVLLFLKEFLGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 159>:

g041-1.seq

1	ATGAAATCCT	ACCCGACCC	CTACCGCCAT	TTTGAAAACC	TCGATTCCGC
51	CGAAACGCAA	AACCTCGCTG	CTGAAGCGAA	TGCCGAAAACG	CGCGCGCGTT
101	TTTTAAACAA	CGACAAGGCG	CGCGCACTTT	CAGACGGCAT	TTTGAATCAA
151	ATGCAGGACA	CGCGGCAGAT	TCCGTTTGT	CAGGAACACC	GCGCGCGGAT
201	GTACCATTTT	CATCAGAATG	CGGAATATCC	GAAGGGCGTG	TACCGCATGT
251	GTACGGCGGC	GACCTACCGT	TCCGGCTATC	CCGAGTGGAA	AATCCTGTTT
301	TCCGTTGCGG	ATTTGATGA	GTTGCTCGGC	GACGATGTGT	ATTGGGCGG
351	CGTGTGCGAC	TTGGTGGAGC	AGCCCAACCG	CGCGCTGCTG	ACTTTGAACA
401	AATCGGGCGG	CGATACGGCG	TATACGCTGG	AAGTGGATTT	GGAAGCAGGG
451	GAATTGGTAG	AGGGCGGTTT	TCACTTTCCG	GCAGGCAAAA	ACCATGTGTC
501	GTGGCGCGAT	GAAAACAGCG	TGTGGGTGTG	TCCGGCTTGG	GACGAACGCC
551	AGTTGACCGA	ATCGGGCTAT	CCGCGGAAG	TGTGGCTGGT	GGAACGCGGC

```

601 AAGAGTTTCG AGGAAAGCCT GCCGGCGTAC CAAATCGATA AAGGCGCGAT
651 GATGGTAAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AGACGTATTT GCAGGTGTCG
751 TCCGAAGGCG GGGCGAAACC GTTGAACCTG CCTAATGATT GCGATGTGGT
801 CGGCTATCTG GCGGGACATC TTTTGCTGAC GCTGCGCAAG GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCGT TGGTGGCGGT GAAACTGAAT
901 CGGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGGTG GCAAGCCTGC
1001 TGGAGAAATGT ACRAAGCCGT CTGAAAGCGT GCGGTTTTCG CGACAGCAAA
1051 TGGCAGGAAG CCGAGTTGCC GCACCTGCCC TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGCGGCG ACGTGGTTTA TCTTGCCGCC AGCGATTTCa
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAACGACC
1201 GTCATGCGCC TCCAGCCGCA GCAGTTTGTG TCAGACGGCA TCGAAGTGCG
1251 GCAGTTTTCG GCGGTGTCTG CCGACGGCGA ACGCATTTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACACGCCGA CCTTAGTCTA TGCTTACGGA
1351 GGTTCGCGCA TTCCTGAATT GCCGCATTAT CTGGGCAGCG TCGGCAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GGCAAAATC CGCGGCGGCG
1451 GAGAATTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAC
1501 AAAAGCGTTG ATGATTTGTT GGCAGTCGTG CGTGATTTGT CCGAACGCGG
1551 CATGAGTTCG CCCAAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGCC
1601 TGATTACCGC CGCCGCTTC GTGCGCGAAC CGCAAAGCAT CCGTGCGCTG
1651 GTGTGCGAAG TACCGCTGAC CGATATGATC CGTTATCCGC TGCTGTCCGC
1701 CGGTTCAAGT TGGACGGACG AATACGGCAA TCCGCAGAAA TACGAAGCCT
1751 GCAAACGCCG GCTGGGCGAA TTGTGCGCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCACT CATTACCACC AGCCTCAGCG ACGACCGCGT
1851 CCATCCCGCC CACGCGCTCA AATTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CAAACTCGCC TCGTGTGTTG TGTTTTGA
2001 AGAATTTTGG GGATAA

```

This corresponds to the amino acid sequence <SEQ ID 160; ORF 041-1.ng>:

g041-1.pep

```

1 MKSYDPYRHH FENLDSAEQ NFAAEANAET RARFLNNDKA RALSDGILNQ
51 MQDTRQIPFC QEHRARMYHF HQNAEYPKGV YRMCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLNKSOGDTA YTLEVDLEAG
151 ELVEGGFHFH AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPAY QIDKGAMMVN AWRYLDPOGS PIDLIEASDG FYTKTYLQVS
251 SEGGAAPLNL PNDVDVGYL AGHLLLTLRK DWHRANQSYP SGALVAVKLN
301 RGEAGAAQLL FAPDETQALE SVETTKRFV ASLLENVQGR LKAWRFADSK
351 WQEAELPHLP SGALEMTDQP WGGDVVYLA SDFTTPTLTF ALDLNVMELT
401 VMRLQPPQFV SDGIEVRQFW AVSSDGERIP YFHVGNKNAAP DTPTLVYAYG
451 GFIPELPHY LGSVGYKYLE EGNFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAVV RDLSEGMSS PKHIGLQGS NGGLITAAAF VREPQSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEACKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQRESADKLA CVLLFLKEFL G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 161>:

m041-1.seq

```

1 ATGAAATCCT ACCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51 CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAGAAAA CGACAAGGCG CGCGCGCTTT CAGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAGAT TCCGTTTGTG CAGGAACACC GCGCGCGGAT
201 GTACCATTTC CATCAGGACG CGGAGTATCC GAAGGGCGTG TACCGCGTGT
251 GTACCGCGGC GACGTATCGT TCCGCTATC CCGAGTGGA AATCCTGTTT
301 TCGGTGGCGG ATTCGACGA ATTGCTTGGC GACGATGTGT ATTGGGCGG
351 CGTGTCGCAC TTGGTGGAAC AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATTGGGCGA CGATACGGCG TACACGCTGG AAGTGGATTG GGAAGCAGGG
451 GAGTTGGTCG AAGGCGGTTT TCACTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG AACGAACGCC
551 AGTTGACCCA ATCGGGCTAT CCGCGCGAAG TATGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCTGTGTAT CAAATCGGCG AAGACGGCAT
651 GATGTGAAC GCGTGGCGTT ATCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AAACCTATTT GCGGGTCTCA

```


m041-1.pgp

1	MKSYDPDYR	FENLDSAETQ	NFAAEANAET	RARFLENDKA	RALSDGILAQ
51	LQDTRQIFPC	QEHARMYHF	HQDAEYPKGV	YRVCTAATYR	SGYPEWKILF
101	SVADFDELLG	DDVYLGVGVH	LVEQPNRALL	TLSKLGSQDTA	YTLVEDLEAG
151	ELVEGQFHFP	AGKNHVSWRD	ENSVMWCPAW	NERQLTQSGY	PREWVLVRG
201	KSFEESLPVY	QIGEDGMVN	AWRYLDPQGS	PIDLIEASDG	FYTKTYLVRG
251	AEGEAKPLNL	PNDCDVVGJL	AGHLLTLFRK	DMWNRANQSP	SGALVAVKLN
301	RGELGAQQLL	FAPDETQALE	SVETTKRFVY	ASLLENVOQR	LKAWRFADGK
351	WQEVELPRLP	SGALEMTDQP	WGGDVVYLA	SDFPTPLTLF	ADDLNVMLT
401	VMRROQPOFD	SDGINVGQFW	TTSADGERLP	YFHVKGNAAP	DMPTLVYAYG
451	GFGIPELPHY	LGSIGKYWLE	EGNAFVLANI	RGGEFGPNRW	HQAQAGQSKH
501	KSVDDLLAVV	RDLSERGISS	PEHIGLGGGS	NGGLITAAAF	VREPOQIGAL
551	VCEVPLTDMI	RYPLLSAGSS	WTDEYGNPQK	YEVCKRRLGE	LSPYHNLSDG
601	IDYPPALITL	SLSDRRVHPA	HALKFYAKLR	ETSAQSWLYS	PDGGGHTGNG
651	TQRESADETA	CULLFLKEFL	G*		

m041-1/g041-1 94.6% identity in 671 aa overlap

	10	20	30	40	50	60
m041-1.pep	MKSYDPYRHFENLDSAETQNFAAEANAETRARFLENDKARALSDGILAQLQDTRQIPFC					
g041-1	MKSYDPYRHFENLDSAETQNFAAEANAETRARFLNNDKARALSDGILNQMDTRQIPFC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041-1.pep	QEHRARMYHFFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
g041-1	QEHRARMYHFFHQNAEYPKGVMCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m041-1.pep	LVEQPNRALLTLSKLGSOTAYTLEVLDLEAGELVEGGGFHFPAGKNHVSWRDENS VWCPAW					
g041-1	LVEQPNRALLTLNKSGGDYATYLEVDLEAGELVEGGGFHFPAGKNHVSWRDENS VWCPAW					
	130	140	150	160	170	180
	190	200	210	220	230	240
m041-1.pep	NERQLTSQSGYPREVWLVERGKSFEESLPVYQIGEDGMVNNAVRYLDPQGSPIDLIEASDG					
	:	:	:	:	:	:

sp|P55577|Y4NA_RHISN PROBABLE PEPTIDASE Y4NA >gi|2182536 (AE000086) Y4nA [Rhizobium sp. NGR234] Length = 726
Score = 370 bits (940), Expect = e-101
Identities = 217/682 (31%), Positives = 331/682 (47%), Gaps = 22/682 (3%)

Query: 121 LVEQPNRALLTSLKLGSDTAYTLEVDLEAGELVEGGFHFPGAKNHVSWRDENSVMVCPAW 180
L N L+ LS G D E D+ GE V+ GF P GK V+W DEN+++V W

Sbjct: 162 LPPTSNLCLIRLSGGKDADVREFDIAKGEFVKEGFVLPEGRQSVTWVDENTIIYVTREW 221

Query: 181 NERQLTQSGYPREVWLVERGKSFEESLPVYQ-----IGEDGMM--VNAWRYLDPQGSPI 232
 ++T SGY +V+RG+S ++++ +++ E G++ ++ +D +

Sbjct: 222 TPG EVTSSGYAYVTKVVKRQSLDQAVEIFRGQKKDVSAERGVLRLDIDGKYVMDTSYRGL 281

Query: 233 DLIEASDGFYTKTYLRVSAEGEAKPLNLPNDCDVVGYLAGHLLTLRKDNWRANQS-YPS 291
 D FY + + L LP GY G + L+ DW A + + +

Sbjct: 282 DFFNTELA FYPNGH----PDTRKVVLPLPTTAVFSGYYKGQAIYWLKSDWTSAGKTVFHN 337

Query: 292 GALVAVKLNREGELGAAQL----LFAPDETOALESVETTKRFVVASLLENVQGRKAWRFA 347
 GA++A L A++ LF P+E Q++ TK +V S+L NV ++++ F

Sbjct: 338 GAIIAFDLKAALADPARVEPLVLFMPNEHQSVAGTTQTKNRLVLSILSNVTSEVRSFDFG 397

Query: 348 DGKWQEVLEPRLPSGALEMTDQPWGGDVVYLAASDFTTPTLTFALDNLVMEITVMRRQPQ 407
 G W +L + L +T D +++ + F P TLF D ++ + P

Sbjct: 398 KGGWSSFKLALPENSTLSLTSSDDESQDLVFSEGFLEPSTLFCADAATGQVEKITSTPA 457

Query: 408 QFDSGGINVQQFWTTSADGERIPYFHVGNKNAAP---DMPTLVYAYGGFGIPELPHYL GSI 464
 +FD+ G+ QQFW TS DG ++PYF V + PT++YAYGGF IP P Y +

Sbjct: 458 RFDAGGLQAQQFWATSKDGT KVPYFLVARKDVKLDGNTPTILYAYGGFQIPMQPSYSAVL 517

Query: 465 GKYWLEEGNAFVLANIRGGGEFGPRWHQAAQGISKHKSVDDLLAVVRDLSEGRISSEPHI 524
 GK WLE+G A+ LANIRGGGEFGP+WH A ++ + DD AV +DL + ++S H+

Sbjct: 518 GKLWLEKGGAYALANIRGGGEFGPKWH DAGLKTNRQRYDDFQAVQDLIAKKVTSTPHL 577

Query: 525 GLOGGSNGGLITAAAFVREPQSIGALVCEVPLTDMIRYPLL SAGSSWTDEYGNPQKYEVC 584
 G+ GGSNGGL+ ++ P A+V +VPL DM+ + +SAG+SW EYG+P V

Sbjct: 578 GIMGGSNGGLLMGVQMIQRPDLWNAVVIQVPLLDVNFTRMSAGASWQAEYGS PDD-PVE 636

Query: 585 KRLGELSPYHNLSGDIDYPPALITTSLSDDRVP HPAHALKFYAKLRETS AQSWLYSPDGG 644
 L +SPYHN+ G+ YP TS DDRV P H A K A + + Y G

Sbjct: 637 GAFLRISISPYHNKAGVAYPEFFETSTKDDRVPVHARKMAALFEDMGLPFFYYENIEG 696

Query: 645 GHTGNGTQRESADELACVLLFL 666
 GH +E A A +++

Sbjct: 697 GHAAAANLQEHARRYALEYIYM 718

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 163>:

a041-1.seq

```

1  ATGAAATCCT ACCCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCA CGCGCATTGT CTGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAAAAT TCCGTTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTC CATCAAGATG CGGAATATCC GAAAGGCGTG TACCGCGTGT
251 GTACCGCGGC GACTTACCGT TCGGGCTATC CTGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTCGACGA ATTGCTCGGT GACGATGTAT ATCTAGGCGG
351 CGTGTGCGAC CTGTTGGAAC AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATCGGGCGG CGATACCGCG TACACGCTGG AAGTGGATT TGAAGCAGGG
451 GAGTTGGTAG AAGCGGTTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAAACAGC TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAGG TGTGGCTGGT GGAACCGCGC
601 AAGAGTTTCG AGGAAAGCCT GCCGGTGTAC CAAATTGCTG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCTGACGGT TTTTACACCA AAACCTATTT GCAGGTCTCA
751 GCCGAAGGCG AAGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTAGT
801 CGGCTATCTG GCCGGACATC TTTTGTGAC CTGCGTAAA GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCAT TGGTAGCAGT AAAATTAAAC
901 CGCGGCGAAT TGGGCGCGGC GCAGCTTTTG TTGCGGCCA ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGCTG GCGAGCCTGC
1001 TGGAAAACGT ACAGGGTCGT CTGAAAGCGT GGCGTTTAC TGATGGCAAA
1051 TGGCAGGAAA CCGAGTTGCC GCGCCTGCCT TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGGGGCG ACGTAGTTTA CCTTGCCGCC AGCGATTTC
1151 CCACGCCGCT GACGCTGTTT GCATTGGATT TGAACGTGAT GGAACGTGAC
1201 GTCATGCGCC GCCAGCCGCA GCAGTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCCT TATTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGGCA TCCCGAATT GCCGATTAT CTGGGCAGCA TTGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTGTATT GGCGAACATC CGCGCGCGCG

```

```

1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAT
1501 AAAAGCGTTG ATGATTTATT GGCAGTCGTG AGCGATTTGT CCGAACGCGG
1551 TATCAGTTCG CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACCGCGGAC
1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT AGGCGCGCTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAA TACGAAGTCT
1751 GCAAACGCCG GTTGGGCGAA TTGTCGCCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCGCGCT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CCGCAACGGC
1951 ACGCAGCGCG AAGCCGCCGA CGAACTCGCC TGCGTGTTC TGTTTTGA
2001 AGAGTTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 164; ORF 041-1.a>:

a041-1.pep

```

1  MKSYDPYRHF FENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKGV YRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TSKSGGDTA YTLEVDLEAG
151 ELVEGGFHFH AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPVY QIAEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 AEGEAKPLNL PNDCDVVGYL AGHLLTLRKL DWHRANQSYF SGALVAVKLN
301 RGELGAAQLL FAPNETQALE SVETTKRFV VASLLENVQGR LKAWRFTDGR
351 WQETELPRLP SGALEMTDQP WGGDVVYLAA SDFTPLTLF ALDLNVMELT
401 VMRRQPQFDF SDGINVQFV TTSADGERIP YFHVGNKNAAP DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNAFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLAVV SDLSERGISS PEHIGLQGS NGGLITAAF VREPOSIGAL
551 VCEVPLTDRI RYPLLSAGSS WTDEYGNPQK YEVCKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQREAADELA CVLLFLKEFL G*

```

a041-1/m041-1 97.9% identity in 671 aa overlap

a041-1.pep	10	20	30	40	50	60
m041-1	10	20	30	40	50	60
a041-1.pep	70	80	90	100	110	120
m041-1	70	80	90	100	110	120
a041-1.pep	130	140	150	160	170	180
m041-1	130	140	150	160	170	180
a041-1.pep	190	200	210	220	230	240
m041-1	190	200	210	220	230	240
a041-1.pep	250	260	270	280	290	300
m041-1	250	260	270	280	290	300
a041-1.pep	310	320	330	340	350	360
m041-1	310	320	330	340	350	360

a041-1.pep	370	380	390	400	410	420
	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQQFSDSGINVQQFW					
m041-1	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQQFSDSGINVQQFW					
	370	380	390	400	410	420
a041-1.pep	430	440	450	460	470	480
	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
m041-1	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
	430	440	450	460	470	480
a041-1.pep	490	500	510	520	530	540
	RGGGEFGPRWHQAAQGISKHKSVDLLAVVSDLSEGISSEPHIGLQGGSNGLITAAAF					
m041-1	RGGGEFGPRWHQAAQGISKHKSVDLLAVVRDLSEGISSEPHIGLQGGSNGLITAAAF					
	490	500	510	520	530	540
a041-1.pep	550	560	570	580	590	600
	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSPYHNLSDG					
m041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSPYHNLSDG					
	550	560	570	580	590	600
a041-1.pep	610	620	630	640	650	660
	IDYPPALITTSLSDDRVPFAHALKFYAKLRETSQSWLYSPDGGGHTGNGTQREAADELA					
m041-1	IDYPPALITTSLSDDRVPFAHALKFYAKLRETSQSWLYSPDGGGHTGNGTQREADELA					
	610	620	630	640	650	660
a041-1.pep	670					
	CVLLFLKEFLGX					
m041-1	CVLLFLKEFLGX					
	670					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 165>:

g042.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAagcG TTCGTGCCGC ATACCAGCGC
51  GTTATCCAAC ACTTCCACGG CAGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TGCGGTCGAT GATGAAAATC CAGCCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACGG GCTGCCCGTG CCCTTCGTTG CGTAAAGATT CGTCCACGGG
201 CGGCAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GATTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCTGTAACCG ACAGCACCAG CCCGCGTCTT
301 TTGCCTTTGG cggCTTCGCG CTTTGGGCG AACAGCGCGT CAATCTGCGC
351 ATTCAATTCC GCCACGCGCG CTTCTTACC GAAAATCCGC GACAGGGTCT
401 CCATCTGCTT CTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAAA
451 TCTATGgtgG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCACCCGG
501 CCCGCCGTA ATGACAAACT GCGGATTGTG GCGGTGCAGG GATTGCGCAAT
551 CGGGCTCAA CAGCGTCCCC ACCGTTGCCG CTTGTCAAA TGCAGGCTGC
601 AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 166; ORF 042.ng>:

g042.pep

```

1  MTMICLRFOA FVPHTSALSN TSTAAGPSCP MAAVRSMKI QPGFFSLMYS
51  KETGCPCLSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDTSPRP
101 LPLAASRFA NSASICAFNS ATRASLPKIR DRVSICFSPL VRILPLSTVK
151 SMVVAFFANC SYASAPGPV MTNCLWRRC DSQSGSNSVP TVAALSNAGC
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 167>:

m042.seq

```

1 ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAmT ACTTCGACAG CCGcCGGCCy TTCyTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCCGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 168; ORF 042>:

m042.pep

```

1 MTMICLRFOA FVPRTSALSX TSTAAGXSCP MAAVRSMMKI QSGFFSLMYS
51 KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVDSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTSXGLXRCR ASXSGSNSVP TVAALSNAAG
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 169>:

a042.seq

```

1 ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCCGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCCAACGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 170; ORF 042.a>:

a042.pep

```

1 MTMICLRFOA FVPRTSALSX TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51 KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVDSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*GL*RCR AS*SGSNSVP TVAALSNAAG
201 K*

```

m042/a042 99.0% identity over a 201 aa overlap

	10	20	30	40	50	60
m042.pep	MTMICLRFOAFVPRTSALSXTSTAAGXSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
a042	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVDSTSPRPLPLAASRVWANSASICAFNS					
a042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVDSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m042.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					

```

a042      |||||
          AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          130      140      150      160      170      180

          190      200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          |||||
a042      ASXSGSNSVPTVAALSNAGCKX
          190      200

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 042 shows 93.0% identity over a 201 aa overlap with a predicted ORF (ORF 042.ng) from *N. gonorrhoeae*:

m042/g042

```

          10      20      30      40      50      60
m042.pep  MTMICLRFQAFVPRTSALSXTSTAAGXSCPMMAVRSMMKIQSGFFSLMYSKETGCPCPSL
          |||||
g042      MTMICLRFQAFVPRTSALSNTSTAAGPSCPMMAVRSMMKIQPGFFSLMYSKETGCPCPSL
          10      20      30      40      50      60

          70      80      90      100     110     120
m042.pep  RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS
          |||||
g042      RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRFWANSASICAFNS
          70      80      90      100     110     120

          130     140     150     160     170     180
m042.pep  AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          |:||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g042      ATRASLPKIRDRVSICFSPLVRILPLSTVKS MVVAFFANC SYASAPGPPVMTNCGLWRCR
          130     140     150     160     170     180

          190     200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          | |||||
g042      DSQSGSNSVPTVAALSNAGCKX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 171>:

m042-1.seq

```

1   ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGCGGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCTT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 172; ORF 042-1>:

m042-1.pep

```

1   MTMICLRFQA FVPRTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMY
51  KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVT DSTSPR
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTV
151 SMVVAFFANC SYASAPGPPV MTS*

```

m042-1/g042 95.4% identity in 173 aa overlap

240

	10	20	30	40	50	60
m042-1.pep	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	:					
g042	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQPGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDTSTSPRPLPLAASRVWANSASICAFNS					
g042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDTSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
	: :					
g042	ATRASLPKIRDVSICFSPLVRILPLSTVKSMVVAFFANC SYASAPGPPVMTNCGLWRCR					
	130	140	150	160	170	180
g042	DSQSGSNSVPTVAALSNAGCKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 173>:

a042-1.seq

```

1   ATGACGATGA   TTTGCTTGCG   CTTCCAAGCG   TTCGTGCCGC   GTACCAGCGC
51  GTTATCCAAT   ACTTCGACAG   CCGCCGGGCC   TTCCTGCCCG   ATGGCGGCGG
101 TACGGTCGAT   GATGAAAATC   CAATCGGGGT   TTTTCTCTTT   GATGTATTCT
151 AAGGAAACAG   GCTGCCCGTG   CCCCTCGTTG   CGTAAAGATT   CGTCTACAGG
201 CGGTAGGCCG   ATGTCGCCGT   GTATCCAAC   TGCCAACCGC   GACTGCGTGC
251 CGAAGGCGGA   CACCTTGTTG   CCCGTAACCG   ACAGCACCAG   CCCGCGTCTT
301 TTGCCTTTGG   CGGCTTCGCG   CGTTTGGGCG   AACAGCGCGT   CAATCTGCGC
351 CTTCATTCC   GCCGCGCGCG   CTTCTTGCC   GAAAATCCGC   GCCAAGGTCT
401 CCATCTGCTT   TTCGCCGCTG   GTGCGGATAT   TGCCGTTGTC   CACCGTCAGA
451 TCTATGGTGG   TCGCGTTTTT   CGCCAAC   TCATACGCTT   CCGCGCCCGG
501 CCCGCCGTA   A

```

This corresponds to the amino acid sequence <SEQ ID 174; ORF 042-1.a>:

a042-1.pep

```

1   MTMICLRFOA   FVPRTSALSN   TSTAAGPSCP   MAAVRSMMKI   QSGFFSLMYS
51  KETGCPCPSL   RKDSSTGGRP   MSPCIQLANR   DCVPKADTLL   PVTDTSTSPR
101 LPLAASRVWA   NSASICAFNS   AARASLPKIR   AKVSICFSPL   VRILPLSTVR
151 SMVVAFFANC   SYASAPGPPV   MTS*

```

m042-1/a042-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
m042-1.pep	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
a042-1	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDTSTSPRPLPLAASRVWANSASICAFNS					
a042-1	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDTSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
a042-1	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 175>:

g043.seq

```

1 ATGGTTGTTT CAAATCAAAA TATCTATGCC GTCGGCCCAT CAGCACTTTT
51 TCACATCCGA AGGCAAAAAT CCGTAATGCC GCCTGAACGC TTCgttgaAC
101 CGTCCCGCGT ggcggtagcc gcAAAAGTGC ATcGCGGCTT GGATGGTGCT
151 GCCCGATTCTG ATGAGGGcga gcGCGTGTTC CAGCCGCAGG CGGCGCAGGC
201 GTCCGCGCAG GGTTCGCCG GTTTCGCGTT TGAAATAGCG TTTCAGGTAG
251 CATTTCGTTCA GCCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGGCG
301 GGCGAATTCG CTGTTCAAAA TATCGGCGGC TTCGTCTATG CGCCGGCGGC
351 GGTAGCCGTT GTCGTGGCGG CGGAAGGTGA AGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 176; ORF 043.ng>:

g043.pep

```

1 MVVSNQNIYA VGPSALFHIR RQKSVMPPER FVEPSRVAVA AKVHRGLDGA
51 ARFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQFDA AGDFGDGQRA
101 GEFAVQNIIG FVYAPAAVAV VVAEGEA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 177>:

m043.seq

```

1 ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCT CAGCACTTCT
51 TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT
151 GCCCGATTCTG ATGAGGGCGA GCGCGTGTTC CAGCCGCAGG CGGCGCAGGC
201 ATCCGCGCAG GGTTCGCCG GTTTCGCGTT TGAAATAGCG TTTCAGGTAG
251 CATTTCGTTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCG TGTTCAGGA TGTCGGCGGC TTCGTCTATG CGCCGACGGC
351 GGTAACCGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 178; ORF 043>:

m043.pep

```

1 MVVSNQNIYA AGPSALLHIR RQKSVMPSEF FVEPSRVAVA AKVHGGLDGA
51 AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFGDGQRT
101 GEFVLQDVGG FVYAPTAVTV VVAEGEAQ*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 043 shows 89.8% identity over a 128 aa overlap with a predicted ORF (ORF043.a) from *N. gonorrhoeae*:

m043/g043

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSEFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
	: : : : : :					
g043	MVVSNQNIYAVGPSALFHIRRQKSVMPPERFVEPSRVAVAAKVHRLDGAARFDEGERVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
	: : : : : :					
g043	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFAVQNIIGFVYAPAAVAV					
	70	80	90	100	110	120
	130					
m043.pep	VVAEGEAQX					
g043	VVAEGEAXX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 179>:

a043.seq

```

1 ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCT CAGCACTTCT
51 TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT

```

242

```

151 GCCGGATTCTG ATGAGGGCGA GCGCGTGTTT CAGCCGCAGG CGGCGCAGGC
201 ATCCGGCGAC GGTTCGCGG GTTTGCCTT TGAAATAGCG TTTCAGGTAG
251 CATTCGTTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCG TGTTCGAGGA TGTCGGCGGC TTCGTCTATG CGCCGACGGC
351 GGTAACCGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 180; ORF 043.a>:

```

a043.pep
1  MVVSNQNIYA AGPSALLHIR RQKSVMPSE FVEPSRVAVA AKVHGGLDGA
51  AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFGDGQRT
101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

```

m043/a043 100.0% identity in 129 aa overlap

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSEFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
a043	MVVSNQNIYAAGPSALLHIRRQKSVMPSEFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
	10	20	30	40	50	60
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
a043	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
a043	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
	70	80	90	100	110	120
m043.pep	VVAAEGEAQX					
a043	VVAAEGEAQX					
	130					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 181>:

```

g044.seq
1  ATGCTGCCCG ACCAGAGCGT CGAGTTCTTG CCACAAGTCG TCGTTTTTGA
51  CGGGCTGTTT GCGGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
101 CAGTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTTTCAGCC TCGATAACG GCGGTCAGCT
201 CCATGCGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTCG
251 CGGCTGCCGT AGCGCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 182; ORF 044.ng>:

```

g044.pep
1  MLPDQSVEFL PQVVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
51  GAAAFERFQP FDNGGQLHAV VGGLRFAAEK FFFAAVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 183>:

```

m044.seq
1  ATGCCGTCCG ACTAGAGCGT CGAGTTCTTT CCAGAAGTCG TCGTTTTTGA
51  CGGGCTGTTT GGAGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
101 CAGTTTTCCA TGCCATTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTTTCAGTCC TCGATGACG GCAGTCAGTT
201 CCATGCGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTCG
251 TGGTACCGT AGCGCAyTaa

```

This corresponds to the amino acid sequence <SEQ ID 184; ORF 044>:

```

m044.pep
1  MPDSDXSEFF PEVVVFDGLF GGGFPAVALP TVYPVFHAI F DVLRVGADDD
51  GAAAFERFQS FDDGSQFHAV VGGLRFAAEK FFFVATVAH*

```


244

501 GG TAGAACCT ACCTGCCCGT TGCCTAAAAT GAGGATTTTC ACGGTATGGG
551 TCGCCGGGTG A

This corresponds to the amino acid sequence <SEQ ID 188; ORF 046.ng>:

g046.pep

1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RYNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLVM AARFCATVEP TCPLPKMRIF TVWVAG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 189>:

m046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCAst CCGC.r.sGC gCGcCTGTAT
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTGTGT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TCGCGCGTTG CCGAAAACGG
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
501 GG TAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 190; ORF 046>:

m046.pep

1 MSAMLRPTSX PXRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLGM AARFCATVEP TCPLPKMRIF TVWVAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 191>:

a046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCAGT CCGCCGCGCC GCGCCTGTAT
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTGTGT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TCGCGCGTTG CCGAAAACGG
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
501 GG TAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 192; ORF 046.a>:

a046.pep

1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLGM AARFCATVEP TCPLPKMRIF TVWVAE*

m046/a046 98.4% identity over a 186 aa overlap

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXRACMMTIRTRSSAKRKT CNAPGQSIRP ASCSVTSCSG LMVSVMPNME					
a046	MSAMLRPTSSPPRRACMMTIRTRSSAKRKT CNAPGQSIRP ASCSVTSCSG LMVSVMPNME					

245

	10	20	30	40	50	60
m046.pep	70	80	90	100	110	120
	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
a046	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
m046.pep	130	140	150	160	170	180
	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
a046	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
a046	TVWVAEX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 046 shows 97.3% identity over a 185 aa overlap with a predicted ORF (ORF 046.ng) from *N. gonorrhoeae*:

m046/g046

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXXRACMMTIRTRSSAKRKTGNAPGQSIRPASCSTSCSGLMVSVMPNME					
g046	MSAMLRPTSPPPRACMMTIRTRSSAKRKTGNAPGQSIRPASCSTSCSGLMVSVMPNME					
	10	20	30	40	50	60
m046.pep	70	80	90	100	110	120
	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
g046	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
m046.pep	130	140	150	160	170	180
	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
g046	RYNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLVMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
g046	TVWVAGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 193>:

g047.seq

1	ATGGTCATCA	TACAGGCGcg	gcGCGGCGGG	CTGCTTGTCG	GACGCAGCAT
51	TGCCGACATC	GCCCAAGATT	TGCCCGACGG	GGCCGACTGC	CAAATCTGCG
101	CCGTTTACCG	CAACAACCGC	CTCATCGTCC	CCGCGCCGCA	AACCGTCATC
151	ATCGAAGGCG	ACGAAATCCT	GTTTGCCGCC	GCCGCGGAAA	ACATCGGGGC
201	GGTCATACCc	gaATTGCGCC	CCAAAGAAAC	CAGCACCCGC	CGCATCATGA
251	TTGCCGCGCG	CGGCAACATc	tgctACCGCC	TCGCCAAGCA	GCTCGAACAC

```

301 GCATAcacG TCAAAATCAT CGAATGCCGG CCGCGCcggtg ccgaATGGAT
351 AGCCGAAAAC ctcgAcaaCA CCCTCGTCCT GCAAGGTTTCG Gcaaccgacg
401 aAaccctgct cgAcaacgaa tacatcgacg aaatcgaCGT ATTCTGCGCC
451 CTGACCAACG ACGACGAAAG CAACATTAtg tCCGCCCTTT TGGCGAAAAA
501 CCTcggcgCG AAGCgcgtca tcggCATCGT CAACCGCTCA AGCTACGTCG
551 ATTTGCTCGA AGGCAACAAA ATCGACATCG TCGTCTCCCC CCACCTCATC
601 ACCATCGGCT CGATACTCGC CCACATCCGG CGCGGCGACA TCGTTGCCGT
651 CCACCCCATC CGGCGCGGCA CGGCGGAAGC CATCGAAGTC GTCGCGCACC
701 GCGACAAAAA AACTTCCGCC ATCATCGGCA GGCGCATCAG CGGCATCAAA
751 TGGCCCGAAG GCTGCCACAT TGCCGCCGTC GTCCGCGCCG GAACCGGCGA
801 AACCATTATG GGACACCATA CCGAAACCGT CATCCAAGAC GGTGACCACA
851 TCATCTTTTT CGTCTCGCGC CGGCGCATCC TGAACGAACT GGAGAAACTC
901 ATCCAAGTCA AAATGGGCTT TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 194; ORF 047.ng>:

g047.pep

```

1 MVIIQARRGG LLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETSTR RIMIAGGGNI CYRLAKQLEH
101 AYNVKIIECR PRRAEWIAEN LDNTLVLQGS ATDETLLDNE YIDEIDVFCA
151 LTNDDESNI M SALLAKNLGA KRVIGIVNRS SYVDLLEGNK IDIVVSPHLI
201 TIGSILAHIR RGDIVAVHPI RRGTAEAIEV VAHGDKKTS A IIGRRISGIK
251 WPEGCHIAAV VRAGTGETIM GHHTETVIQD GDHIIFFVSR RRILNELEKL
301 IQVKMGFFG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 195>:

m047.seq

```

1 ATGGTCATCA TACAGgCGcG C..syGCGGA sTGCTTGTCTG GACGCAGCAT
51 TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCCTCATC
151 ATCGAAGGCG ACGAAATCCT ATTTGCCGCC GCCGCCGAAA ACATCGGCGC
201 GGTCAATCCC GAATTGCGCC CCAAAGAAAC CCAAAGAAAC CAGCcCmgmm
251 GcATCATGAT TkCCGGCGGC GGCAACATCG GCTACCGTCT CGCCAAGCAG
301 CTCGAACACG CATACAACGT yAAATCATC GAATGCCGGC CGCGCCGTGC
351 CGAATGGATA GCCGAAAACC TCGACAACAC CCTCGTcyTG CAAGGTTTCG
401 CAACCGACGA AACCTTGCTC GACAACGAAT ACATCGACGA AATCGACGTA
451 TTCTGCGCCC TGACCAACGA CGACGAAAGC AACATTATGT CCGCCCTTTT
501 GCGGAaAAAC CTCGGCGCGA AGCGCGTCAT CGGCATCGTC AACCCTCAA
551 GCTACGTCGA TTTGCTCGAA GGCAACAAA TCGACATCGT CGTCTCCCCC
601 CACCTCATCA CCATCGGCTC GATACTCGCC CACATCCGGC GCGGCGACAT
651 CGTGCGCGTC CACCCATCC GCGCGGCAC GGCGGAAGCC ATCGAAGTCG
701 TCGCACACGG CGACAAAAA ACTTCCGCCA TCATCGGCAG GCGCATCAGC
751 GGCATCAAAT GGCCCGAAGG CTGCCACATT GCCGCGTCTG TCCGCGCCGG
801 AACC GGCGAA ACCATTATGG GACACCATAC CGAAACCGTC ATCCAAGACG
851 GCGACCACAT CATCTTTTTC GTCTCGCGCC GGCGCATCCT GAACGAACTG
901 GAAAACTCA TCCAGGTCAA AATGGGCTTT TTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 196; ORF 047>:

m047.pep

```

1 MVIIQARXXG XLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETQRN QPXXIMIXGG GNIGYRLAKQ
101 LEHAYNVKII ECRPRRAEWI AENLDNTLV L QGSATDETL DNEYIDEIDV
151 FCALTNDDES NIMSALLAKN LGAKRVIGIV NRSSYVDLLE GNKIDIVVSP
201 HLITIGSILA HIRRGDIVAV HPIRRGTAE A IEVVAHGDKK TSAIIGRRIS
251 GIKWPEGCHI AAVVRAGTGE TIMGHHTETV IQDGDHIIFF VSRRRIINEL
301 EKLIQVKMGF FG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 197>:

a047.seq

```

1 ATGGTCATCA TACAGGCGCG GCGCGGCGGA CTGCTTGTCTG GACGCAGCAT

```

```

51  TGCCGACATC  GCGCAAGATT  TGCCCGACGG  GGCCGACTGC  CAAATCTGCG
101 CCGTTTACCG  CAACAACCGC  CTCATCGTCC  CCGCGCCGCA  AACCGTCATC
151 ATCGAAGGCG  ACGAAATCCT  ATTTGCCGCG  GCGCGCGAAA  ACATCGGCGC
201 GGTCATACCC  GAATTGCGCC  CCAAAGAAAC  CAGCACCCGC  CGCATCATGA
251 TTGCCGGCGG  CGGCAACATC  GGCTACCGTC  TCGCCAAGCA  GCTCGAACAC
301 GCATACAACG  TCAAAATCAT  CGAATGCCGG  CCGCGCCGTG  CCGAATGGAT
351 AGCCGAAAAC  CTCGACAACA  CCCTCGTCCT  GCAAGGTTCT  GCAACCGACG
401 AAACCTGCT  CGACAACGAA  TACATCGACG  AAATCGACGT  ATTCTGCGCC
451 CTGACCAACG  ACGACGAAAG  CAACATTATG  TCCGCCCTTT  TGGCGAAAAA
501 CCTCGGCGCG  AAGCGCGTCA  TCGGCATCGT  CAACCGCTCA  AGCTACGTCG
551 ATTTGCTCGA  AGGCAACAAA  ATCGACATCG  TCGTCTCCCC  CCACCTCATC
601 ACCATCGGCT  CGATACTCGC  CCACATCCGG  CGCGGCGACA  TCGTTGCCGT
651 CCACCCATC  CGGCGCGGCA  CGGCGGAAGC  CATCGAAGTC  GTCGCACACG
701 GCGACAAAAA  AACTTCGGCC  ATCATCGGCA  GGCGCATCAG  CGGCATCAAA
751 TGGCCGAAG  GCTGCCACAT  TGCCGCCGTC  GTCCGCGCCG  GAACCGGCGA
801 AACCATTATG  GGACACCATA  CCGAAACCGT  CATCCAAGAC  GGCGACCACA
851 TCATCTTTTT  CGTCTCGCGC  CGGCGCATCC  TGAACGAACT  GGAAAAACTC
901 ATCCAAGTCA  AAATGGGCTT  TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 198; ORF 047.a>:

```

a047.pep
1  MVIIQARRGG  LLVGRSIADI  AQDLPDGADC  QICAVYRNNR  LIVPAPQTVI
51  IEGDEILFAA  AAENIGAVIP  ELRPKETSTR  RIMIAGGGNI  GYRLAKQLEH
101 AYNVKIIECR  PRRAEWIAEN  LDNTLVLQGS  ATDETLLDNE  YIDEIDVFAA
151 LTNDDESNIM  SALLAKNLGA  KRIVIGIVNR  SYVDLLEGNK  IDIVVSPHLI
201 TIGSILAHIR  RGDIVAVHPI  RRGTAEAEIV  VAHGDKKTS  IIGRRISGIK
251 WPEGCHIAAV  VRAGTGETIM  GHHTETVIQD  GDHIIFFVSR  RRILNELEKL
301 IQVKMGFFG*

```

m047/a047 96.5% identity over a 312 aa overlap

```

              10      20      30      40      50      60
m047.pep      MVIIQARXXGXLVGRSIADIAQDLPDGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA
              |||||  |  |||||||||||||||||||||||||||||||||||||||
a047           MVIIQARRGGLLVGRSIADIAQDLPDGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m047.pep      AAENIGAVIPELRPKETQRNPXXIMIXGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI
              |||||  |||||  :  ||  |||||||||||||||||||||||||||
a047           AAENIGAVIPELRPKETSTR---IMIAGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI
              70      80      90      100     110

              130     140     150     160     170     180
m047.pep      AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV
              |||||  |||||  |||||  |||||  |||||  |||||
a047           AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV
              120     130     140     150     160     170

              190     200     210     220     230     240
m047.pep      NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEIVVAHGDKK
              |||||  |||||  |||||  |||||  |||||  |||||
a047           NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEIVVAHGDKK
              180     190     200     210     220     230

              250     260     270     280     290     300
m047.pep      TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL
              |||||  |||||  |||||  |||||  |||||  |||||
a047           TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL
              240     250     260     270     280     290

              310
m047.pep      EKLIQVKMGFFGX
              |||||

```

a047 EKLIQVKMGFFGX
300 310

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 047 shows 96.2% identity over a 312 aa overlap with a predicted ORF (ORF 047.ng) from *N. gonorrhoeae*:

m047/g045

m047.pep	MVIIQARXXGXLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA	60
g047	MVIIQARRGGLLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA	60
m047.pep	AAENIGAVIPELRPKETQRNPXXIMIXGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI	120
g047	AAENIGAVIPELRPKETSTRR---IMIAGGGNICYRLAKQLEHAYNVKIIIECRPRRAEWI	117
m047.pep	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV	180
g047	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV	177
m047.pep	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEIVVAHGDKK	240
g047	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEIVVAHGDKK	237
m047.pep	TSIIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRRILNEL	300
g047	TSIIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRRILNEL	297
m047.pep	EKLIQVKMGFFGX	313
g047	EKLIQVKMGFFGX	310

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 199>:

g048.seq

1	ATGCTCGACA AAGGCGAGGA GTTGCCCGTC GATTTCACCA ACCGCCTGAT
51	TTACTACGTC ggcCCcgTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG
101	CAGGTCCGAC CACAGCCACC CGCATGGACA AATTACCCG CCAAATGCTC
151	AAACAAACCG GCCTCTTGGG CATGATCGGC AAATCCGagc gcgGcgcggc
201	cacctGCGAA GCcatCGCCG ACAACAAGGC CGTGTACCTC ATGGCAGTCG
251	GCGGCGCGGC ATACCTCGTG GCAAAAGCCA TCAAATCTTC CAAAGTCTTG
301	GCGTTCCCGG AATTGGGTAT GGAAGCCGTT TACGAATTG AAGTCAAAGA
351	TATGCCCGTA ACCGTCGCCG TGGACAGCAA AGGCGAATCC ATCCACGCCA
401	CCGCCCCGCG CAAATGGCAG GCGAAAATCG GCATCATCCC CGTCGAGTCT
451	TGA

This corresponds to the amino acid sequence <SEQ ID 200; ORF 048.ng>:

g048.pep

1	MLDKGEELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51	KQTGLGMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101	AFPELGMEAV YEFVKKMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151	*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 201>:

m048.seq

1	ATGCTCAACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCCTGAT
51	TTACTACGTC GGCCCCGTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG

м048. пер

```

1 MLNKGEELPV DFTNRLIIYV GPVDPVGVDEV VGPAGPTTAT RMDKFTRQML
51 EQTDLLGMIG KSERGVATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 APPELGMEAI YEFEVKDMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *

```

a048.seq

1	ATGCTCGACA	AAGGCGAAGA	ATTGCCCGTC	GATTTCACCA	ACCGCCTGAT
51	TTACTACGTC	GGCCCCGTCG	ATCCGGTCGG	CGACGAAATC	GTCCGCCCAG
101	CAGGTCGCCAG	CACCGCCACC	CGCATGCGACA	AATTCAACCCG	CCAAATGCTC
151	GAACAAACCG	ACCTCTTGGG	CATGATCGGC	AAATCCGAGC	GCGGCGCGGC
201	CACCTGCGAA	CGCATCGCCG	ACAAACAAAGC	CGGTGACTCT	ATGGCGAGTCG
251	GCGGCGCGGC	GTATCTCGTG	GCAAAGCCA	TCAATCTTTC	CAAAGTCTTG
301	GCGTTCCCG	AATTGGGCAT	GGAAGCCATT	TACGAATTTG	AAGTCAAAGA
351	CATGCCCCGTA	ACCGTCGCCG	TAGACAGCAA	AGGCGAATCC	ATCCAGCCCA
401	CCGCCCCGCC	CCAATGGCAG	GCGAAAATCG	GCATCATCCC	CGTCAAATCT
451	TGA				

a048.pep

```

1  MLDKGEELPV DFTNRLIIYV GPVDPVGDEI VGPAGPTTAT RMDKFTRQML
51  EQTDLLGMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAI YEFEVKDMFP TVAVDSKGES IHATAPPQWQ AKIGIIPVKS
151 *

```

```
m048.pep      10          20          30          40          50          60
MLNKGELPVDFTNRLIIYYVGPVDPVGDEVVGPAGPTTATRMDFKFTROMLEQTDLLGMIG
||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||
a048          MLDKGEELPVDFTNRLIIYYVGPVDPVGDEIVGPAGPTTATRMDFKFTROMLEQTDLLGMIG
              10          20          30          40          50          60

m048.pep      70          80          90          100         110         120
KSERGVATCEAIADNKAVIYLMVGGGAAYLVAKAIKSSKVLAFPELGMETIYEFVVKDMPV
|||||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
a048          KSERGAATCEAIADNKAVIYLMVGGGAAYLVAKAIKSSKVLAFPELGMETIYEFVVKDMPV
              70          80          90          100         110         120

m048.pep      130         140         150
TVAVDSKGESIHATAPRKWQAIGIIPVESX
|||||||:||:||:||:||:||:||:||:||:||:||||
a048          TVAVDSKGESIHATAPPQWQAIGIIPVKSX
              130         140         150
```

ORF 048 shows 96.4% identity over a 150 aa overlap with a predicted ORF (ORF 048.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m048.pep	MLNKGEELPVDFTNRLIYYVGPVDPVGDEVVGGPAGPTTATRMDKFTRQMLEQTDLGLMGIG					
	:					
g048	MLDKGEELPVDFTNRLIYYVGPVDPVGDEVVGGPAGPTTATRMDKFTRQMLKQTGLLGMIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m048.pep	KSERGVATCEAIAADNKAVYLMAVGGAAYLVAKAIKSSKVLAFPELGMEAIYEFEVKDMPV					
	:					
g048	KSEGAATCEAIAADNKAVYLMAVGGAAYLVAKAIKSSKVLAFPELGMEAIVYEFEVKDMPV					
	70	80	90	100	110	120
	130	140	150			
m048.pep	TVAVDSKGESIHATAPRKWQAKIGIIPVESX					
g048	TVAVDSKGESIHATAPRKWQAKIGIIPVESX					
	130	140	150			

q049.seq

1	ATGCGGGGCG	AGGCGTTTGA	TCAACCGTTC	GGTCAGCTCC	TGTTCCGGACA
51	GGCAGAACAC	TTCGCGCCGG	TTGACGGCTT	TCGGGTTCAG	GATATTGATT
101	TGGACGGGCA	TCAACGCCTC	TTCCGCACCG	CCTTCGCCGT	TTTCCGCAAC
151	CCCGTCTGCC	GCCGTACCGG	ATTCTGCCGC	ATCGGGGTTT	TCCCCGCCCT
201	CAATCTGTGC	GGTTTCAAAT	TCGGCACTGT	CTTTTTTGGC	ATCGAACCCG
251	ATTCTCCGCC	GCGATTTCGAT	GTGTTTTTCC	GAAAcgggca	tTTGCAGGGA
301	AGCCTgcgcg	TTGAGCCAGT	TTTCTTGAAG	GACGATCATC	GGGTCTGTTT
351	GCACTTCCTC	GCCGCAATCG	GCAACGGCgc	tGTTGTGTTC	TTCTGCCAT
401	TTCTTCGAT	ACGCCTTTAA			

g049.pcp

1 MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ DIDLDGHQRL FRTAFAVFRN
51 PVCRRGTGFCR IGVFPALNLC GFKFGTVVFG IEPDSPPRFD VFFRNRHLQG
101 SLRVEPVFLK DDHRVGDFDL AAIGNGAVVF FLFPFLQIRL*

m049.seq (partial)

100	ATGCGGGCGC	AGGCGTTTGA	TCAGCCGTTT	GGTCAGCTCC	TGTTCCGGACA
51	GGCAGAACAC	TTCGCGCCGG	TTGACGGCTT	TCGGGTTTCAG	GATATTGATT
101	TGGACGGGCA	TCAACGTTTC	TTCCGCATCG	TTTTCCCGGT	TTTCCGAAAC
151	CGCCGGCTCA	TTCTGTCCCG	ATTCTGCCTC	GTCGGCGTTT	TCCCGCCTTT
201	CAATCTGTCC	GGTTTCAAAT	TCGACACTGT	CTTTTTTGTT	ATCAAACCGG
251	ATTCTCCGCC	GCGATTTCAT	GTGTTTTTCC	GAAACCGACA	TTTGCAGGGA
301	AGACTGCGCC	TTCGACCCAGT	TTTCTGTGA	GACGATCATC	GGGTGCGTTT
351	CGCCTTCTCT	GTCGCAATCG	GCAACGGCGG	CATTGTGTTC	CTCCTGCCAT
401	TTTTTCAGAT	ACGCCTT...			

m049.pep (partial)

1 MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ DIDLDGHQRF FRIVFPVFRN
51 RRLRAGFCL VGVFPAFNLS GKFEDTVFFG IKPDSPPRFD VFFRNRLHQ
101 SLRVEPVFLK DDHRVGDFDL AAIGNGGIVF LLPFFQIRL...

a049.seq

```

1 ATGCGGGCGC AGGCGTTTGA TCAGCCGTTC GGTGAGCTCC TGTTCCGACA
51 GGCAGAACAC TTCGCGCCCG TTGACGGCTT TCGGGTTCAG AATATTGATT
101 TGGACGGGCA TCAACGCTTC TTCCGCACCG CCTTCGCCGT TTTCCGCAAC
151 CCCGTCTGCC GCCGTACCCG ATTCTGCCGC ATCGGCGTTT TCCCGCCTT
201 CAATCTGTCC GGTTCCTAAAT TCGGCACTGT CTTTTTTGGC ATCAAACCGG
251 ATTCTCCGCC GCGATTGAT GTGTTTTTCC GAAACCGACA TTTGCAGGGA
301 AGCCTGCGCG TTGAGCCAGT TTTCTGAAG GACGATCATC GGGTCGGTTT
351 CGACTTCCTC GCCGCAATCG GCAACGGCGG CATTGTGTTC CTCCTGCCAT
401 TTTTTCAGAT ACGCCTT

```

This corresponds to the amino acid sequence <SEQ ID 210; ORF 049.a>:

a049.pep

```

1 MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ NIDLDGHQRF FRTAFVFRN
51 PVCRRTRFCR IGVFPAFNLS GFKEGTVFFG IKPDSPPRFD VFFRNRLHQQ
101 SLRVEPVFLK DDHRVGDFEL AAIGNGGIVF LLPFFQIRL

```

m049/a049 90.6% identity over a 139 aa overlap

```

              10      20      30      40      50      60
m049.pep    MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLDGHQRFRRIVFPVFRNRRLIRAGFCL
              |||||
a049         MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLDGHQRFRRIVFPVFRNRRLIRAGFCL
              10      20      30      40      50      60

              70      80      90     100     110     120
m049.pep    VGVFPAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRLHQQSLRVEPVFLKDDHRVGDFDL
              :|||
a049         IGVFPAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRLHQQSLRVEPVFLKDDHRVGDFDL
              70      80      90     100     110     120

              130     139
m049.pep    AAIGNGGIVFLLPFFQIRL
              |||||
a049         AAIGNGGIVFLLPFFQIRL
              130

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 049 shows 86.3% identity over a 139 aa overlap with a predicted ORF (ORF 049.ng) from *N. gonorrhoeae*:

m049/g049

```

              10      20      30      40      50      60
m049.pep    MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLDGHQRFRRIVFPVFRNRRLIRAGFCL
              |||||
g049         MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLDGHQRFRRIVFPVFRNRRLIRAGFCL
              10      20      30      40      50      60

              70      80      90     100     110     120
m049.pep    VGVFPAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRLHQQSLRVEPVFLKDDHRVGDFDL
              :|||
g049         IGVFPALNLCGFKFDTVFFGIKPDSPPRFDVFFRNRLHQQSLRVEPVFLKDDHRVGDFDL
              70      80      90     100     110     120

              130     139
m049.pep    AAIGNGGIVFLLPFFQIRL
              |||||
g049         AAIGNGAVVFFLPFLQIRLX
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 211>:

g050.seq

```

1 atgggCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGg
51 cagccccGAA AAAGccgtgt TGATGGcaaA AGAATCCCTG ATGAGCCACA
101 TCGAcatCca aGaATTGCAG GAAAAAGCCG CGTccggggc ggaattgtcc
151 accaccgaAG ccCTGCGCCT cGAACTCTTT GAAAAGGTCA ACGCGCTGGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAT GCCGCCTCCA AACCGATTGC CATGATTCCC
301 AACTGTGCcg ccacCCGcca cgtcgAATTT GAATTGgACG GCTCAGGtcc
351 TGTCGAactc acgccCGcgc gtgtCGAAGA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 212; ORF 050.ng>:

g050.pep

```

1 MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVED*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 213>:

m050.seq

```

1 ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGTATCG GCATCGGCGG
51 C..agCCgAA AAAGCCGTGC TGATGGCAAA AGAGTCCCTG ATGAGCCACA
101 TCGACATTCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GgAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTGGG
201 CATCGGCGCA CAAGGCTTGG GCGGACTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA TCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAATC ACGCCGCCG GCGTCGAAGA TGGCCCATT TGA

```

This corresponds to the amino acid sequence <SEQ ID 214; ORF 050>:

m050.pep

```

1 MGAGWCPPGI LGIGIGGXAE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDGPI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 215>:

a050.seq

```

1 ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
51 TACGCCCGAA AAAGCCGTGT TGATGGCGAA AGAATCCCTG ATGAGCCACA
101 TCGACATCCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GGAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTAGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAATC ACGCCGCCG GCGTCGAAGA CTGGCCC

```

This corresponds to the amino acid sequence <SEQ ID 216; ORF 050.a>:

a050.pep

```

1 MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDWP

```

m050/a050 97.7% identity over a 129 aa overlap

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMAKESLS	MSHIDIQELQ	EKAASGAELST	TTEALRLELF		
a050	MGAGWCPPGILGIGIGGTPEKAVLMAKESLS	MSHIDIQELQ	EKAASGAELST	TTEALRLELF		

253

	10	20	30	40	50	60
m050.pep	70	80	90	100	110	120
	EKVNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGSGPVEL					
a050	EKVNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGSGPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
a050	TPPRVEDWP					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 050 shows 98.4% identity over a 127 aa overlap with a predicted ORF (ORF 050.ng) from *N. gonorrhoeae*:

m050/g050

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMAKESIMSHIDIQELQEKAASGAELSTTEALRLLELF					
g050	MGAGWCPPGILGIGIGGTPEKAVLMAKESIMSHIDIQELQEKAASGAELSTTEALRLLELF					
	10	20	30	40	50	60
	70					
m050.pep	EKVNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGSGPVEL					
g050	EKVNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGSGPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
g050	TPPRVEDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 217>:

g050-1.seq

```

1  ATGACCGTTA TCAAGCAAGA AGACTTTATT CAAAGTATCT GCGATGCCTT
51  CCAATTCATC AGCTACTACC ATCCAAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCCGCCG CCAGAGACGC GATGACGCG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCCGAA AACACCGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG GATGTGCAAT
251 GGGATGCCGA CATGAGCGTG GAAAAGATGG TTAACGAAG CGTACGCCGC
301 GCCTACACTT GGAAGGCCAA CACCCTGCGC GCTTCCGTCC TCGCCGATCC
351 GGCCGGCAAA CGCCAAAACA CCAGAGACAA CACCCCGCCG GTCATCCACA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GCGGCTCTG AAAACAAATC CAACTCGCT ATGCTCAACC CTTCGACAA
501 CATCGTCGAT TGGGTATTGA AAACATCCC GACGATGGGC GCGGGCTGTT
551 GTCTCCCGG CATCTTGGGC ATCGGCATCG GCGGCAGcgc CGAAAAGCC
601 GTGTGATGG cgaAAGAATC CCTGATGAG CACATCGACA TCCAAGAATT
651 GCAGGAAAAA GCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCGTCGAAC TTTGAAAAG GTCAACGCGC TGGGCATCGG CGGCAAGGC
751 TTGGCGGTC TGACCACCGT GTTGACGTG AAAATCCTCG ATTACCCGAC
801 CCATGCCGCC TCCAAACCGA TTGCCATGAT TCCCAACTGT GCGGCCACCC
851 GCCACGTGCA ATTTGAATTG GACGGCTCAG GTCCTGTGCA ACTCAGCCG
901 CCGCGCGTCG AAGACTGACC CGATCTGACT TACAGCCCCG ACAACGCCAA
951 ACGCGTCGAT GTCGATAAGC TGACCAAAGA AGAAGTGGA AGCTGGAAGA
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCGG CCGCGATGCC
1051 GCGCACAAAC GCCTCGTCAA TATGCTCGAC AAAGCGAGG AGTTGCCCGT
1101 CGATTTACAC AACCGCCTGA TTTACTACGT CGGCCCGTGC GATCCGGTCG
1151 GCGATGAAGT CGTCGGTCCC GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTTACCC GCCAATGCT CAAACAAACC GGCCTCTTGG GCATGATCGG

```

```

1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAACAAGG
1301 CCGTGTACCT CATGGCAGTC GCGGCGCGCG CATACCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGGTTCCCG GAATTGGGTA TGGGAAGCCGT
1401 TTACGAATTT GAAGTCAAAG ATATGCCCGT AACCGTCGCC GTGGACAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCGCG GCAAATGGCA GGCGAAAATC
1501 GGCATCATCC CCGTCGAGTC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 218; ORF 050-1.ng>:

g050-1.pep

```

1  MTFVIKQEDFI QSIDAFQFI SYHPKDYID ALYKAWQKEE NPAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVG M DVQWDADMSV EKMVNEGVRR
101 AYTWEGNTR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCRAKG
151 GGSENSKSLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMKESLMS HIDIQELOEK AASGAELST EALRLELF EK VNALGIGAQQ
251 LGGLTTVL DV KILDYPTHA A SKPIAMIPNC AATRHVEF EL DSGSPVELTP
301 PRVED*PDLT YSPDNGKRV DDKLTKEE VA SWKTGDVLL NGKILTGRDA
351 AHKRLVNMLD KGEELPVDF T NRIIYVGPV DPVGDEVV GP AGPTTATRMD
401 KFTROMLKQT GLLGMIGK SE RGAATCEA IA DNKAVYLM AV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAVY EF EVKDMPTV TA VDSKGESI HA TAPRKWQAKI
501 GIIPVES*

```

g050-1/p14407

```

sp|P14407|FUMB_ECOLI FUMARATE HYDRATASE CLASS I, ANAEROBIC (FUMARASE)
>gi|280063|pir|B44511 fumarate hydratase (EC 4.2.1.2) fumB, iron-dependent - Escherichia coli
>gi|146048 (M27058) anaerobic class I fumarase (EC 4.2.1.2) [Escherichia coli] Length = 548
Score = 172 bits (432), Expect = 4e-42
Identities = 138/488 (28%), Positives = 216/488 (43%), Gaps = 22/488 (4%)

```

```

Query: 11 QSIDAFQFISYHPKDYIDALYKAWQKEENPAKDAMTQILVNSRMCAENNRPICQDTG 70
Q+ DA + H K L+ E + K Q L NS + A+ P CQDTG
Sbjct: 53 QAFHDAFMLRPAHQQVAAILHDPEASEND---KYVALQFLRNSEIAAKGVLPCTCQDTG 109

```

```

Query: 71 IATVFLKVGMDVQWDADMSVEKMVNEGVRRAYTWEGNTRASVLADPAGKRQNTKDNTPA 130
A + K G V W E+ +++GV Y E N + A K NT N PA
Sbjct: 110 TAIIVGKKQQRV-WTGGGD-EETLSKGVNTYI-EDNLRYSQNAALDMYKEVNTGTNLPA 166

```

```

Query: 131 VIHMSIVPGGKVEVTCRAKGGGSENSKSL-----AMLNPSDNIVDWVLKTIPTMGAGWCP 185
I + V G + + C AKGGGS NK+ L A+L P + +++++ + T+G CP
Sbjct: 167 QIDLYAVDGDGEYKFLCVAKGGGSANKTYLYQETKALLTPG-KLKNFLVEKMRTLGTAAACP 225

```

```

Query: 186 PXXXXXXXXXXTEKAVLMKESLSHIDIQELOEKASGAELSTTEALRLELFKVNXXX 245
P T + L + +H EL + + L EL E+
Sbjct: 226 PYHIAFVIGGTS AETNLKTVKLASAHY-YDELPTGEGNEHQAFRDVQLEQELLEEAQKLG 284

```

```

Query: 246 XXXXXXXXXXXXTVDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGGG----PVELTPP 301
D++++ P H AS P+ M +C+A R+++ +++ G +E P
Sbjct: 285 LGAQFGGKYFAH-DIRVIRLPRHGASCPVGMGVSCSADRNIKAKINREGIWIIEKLEHNPG 343

```

```

Query: 302 RVEDXPDLTYSPDNGKRVVDVKLTKE---EVA SWKTGDVLLNGKILTGRDAAHKRLVNM 358
+ +VD+++ KE +++ + L L G I+ GRD AH +L +
Sbjct: 344 QYIPQELRQAGEGEAVKVDLNRPMKEILAQLSQYPVSTRSLTGTIIVGRDIAHAKLKL 403

```

```

Query: 359 LDKGEELPVDFNRIIYXXXXXXXXXXXXXXXXXXXXTTATRMDKFTROMLKQTGLLGMIGK 418
+D G+ELP + IYY TTA RMD + + G + M+ K
Sbjct: 404 IDAGKELPQYIKDHPYIYAGPAKTPAGYPSGLPPTAGRMDSYVDLLQSHGGSMIMLAK 463

```

```

Query: 419 SERGAATCEAIADNKAVYLMVAVGG-AAYLVAKAIKSSKVLAPFELGMEAVYEFVVKDMFV 477
R +A + YL ++GG AA L ++IK + +A+PELGMEA+++ EV+D P
Sbjct: 464 GNRSQQVTDACHKHGGFYLGSIGGPAAVLAQQSIKHLECVAYPELGMEAIWKIEVEDFPA 523

```

```

Query: 478 TVAVDSKG 485
+ VD KG
Sbjct: 524 FILVDDKG 531

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 219>:

m050-1.seq

```

1  ATGACCGTCA TCAAACAGGA AGACTTTATC CAAAGCATTT GCGATGCCTT
51  CCAATTCACT AGCTACTATC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCTGCCG CCAAAGACGC GATGACGCGA
151 ATTTTGGTCA ACAGCCGTAT GTGTGCGGAA AACACCGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG AACGTCCAAT
251 GGGATGCGGA CATGAGCGTG GAAGAGATGG TTAACGAAGG CGTACGCCCG

```

```
301 GCCTACACTT GGAAGGCAA TACGCTGCGC GCTTCCGTCC TCGCCGATCC
351 GGCCGGCAAA CGCCAAAACA CCAAGACAA CACCCCGGCC GTCATCCATA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GGCGGCTCTG AAAACAAATC CAACTCGCC ATGCTCAATC CTTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACCATGGGC GCGGGCTGGT
551 GTCTCTCCCG CATCTTGGGT ATCGGCATCG GCGGCACGCC CGAAAAAGCC
601 GTGTGATGG CAAAGAGTC CCTGATGAGC CACATCGACA TTCAAGAATT
651 GCAGGAAAG GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTGAAAAA GTCAACGCGC TGGGCATCGG CGCACAAGGC
751 TTGGGCGGAC TGACCACCGT GTTGGACGTG AAAATCCTCG ATTATCCGAC
801 CCACGCGGCC TCCAAACCGA TTGCCATGAT TCCGAAGTGC GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GCCCTGTCGA ACTCAGCCCG
901 CCGCGCGTCG AAGACTGGCC CGATTTGACT TACAGCCCGC ACAACGCCAA
951 ACGCGTCGAT GTCGACAAGC TGACCAAGA AGAAGTGCCA AGCTGGAAGA
1001 CCGCGGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCAG CCGCATGCCC
1051 GCACACAAAC GCCTCGTCGA TATGCTCAAC AAAGGCGAAG AATTGCCCGT
1101 CGATTTCACC AACCGCCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCC
1151 GCGATGAAGT CGTCGGTCCG GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTCACCC GCCAAATGCT CGAACAACC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGTGG CCACCTGCCA AGCCATCGCC GACAACAAAG
1301 CCGTGACCT CATGGCAGTC GCGGCGCGG CGTATCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GGCGTTCCCG GAATTGGGCA TGGGAAGCCAT
1401 TTACGAATTT GAAGTCAAAG ACATGCCCGT AACCGTCGCC GTAGATAGCA
1451 AAGGCGAATC CATCCAGGCC ACCGCCCGCG GCAATGGCA GCGGAAATC
1501 GGCATCATCC CCGTCGAATC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 220; ORF 050-1>:

m050-1.pep

```
1  MTVIKQEDFI QSIDAFQFI SYHHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVG M NVQWDADMSV EEMVNEGVRR
101 AYTWEQNTLR ASVLADPAG RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSENSKSLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELQEK AASGAELST EALRLELFEK VNALGIGAQG
251 LGGLTTVLVD KILDYPHTAA SKPIAMIPNC AATRHVEFEL DSGSPVELTP
301 PRVEDWPDLT YSPDNGKRV DKLTKEEVA SWKTGDVLLL NGKILTGRDA
351 AHKRLVMDLN KGEELPVDF NRIYYVGPV DPVGEVVG P AGPTTATRMD
401 KFTROMLEQT DLLGMIGKSE RGVATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAIYEF EVKMPVTV VDSKGESIHA TAPRKWQAKI
501 GIIPVES*
```

m050-1/g050-1 98.2% identity in 507 aa overlap

	10	20	30	40	50	60
m050-1.pep	MTVIKQEDFIQSIDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
g050-1	MTVIKQEDFIQSIDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
	10	20	30	40	50	60
m050-1.pep	NNRPICQDTGIATVFLKVG MNVQWDADMSVEEMVNEGVRRAYTWEQNTLRASVLADPAGK					
g050-1	NNRPICQDTGIATVFLKVG MDVQWDADMSVEKVMNEGVRRAYTWEQNTLRASVLADPAGK					
	70	80	90	100	110	120
m050-1.pep	RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGGSENKSLAMLNPSDNIVDWVLKTIPTMG					
g050-1	RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGGSENKSLAMLNPSDNIVDWVLKTIPTMG					
	130	140	150	160	170	180
m050-1.pep	AGWCPPGILGIGIGGTPEKAVLMAKESLM SHIDIQELQEK AASGAELSTTEALRLELFEK					
g050-1	AGWCPPGILGIGIGGTPEKAVLMAKESLM SHIDIQELQEK AASGAELSTTEALRLELFEK					
	190	200	210	220	230	240
m050-1.pep	VNALGIGAQGLGGLTTVLVDKILDYPHTAASKPIAMIPNCAATRHVEFELD GSGPVELTP					
g050-1	VNALGIGAQGLGGLTTVLVDKILDYPHTAASKPIAMIPNCAATRHVEFELD GSGPVELTP					
	250	260	270	280	290	300

```

      310      320      330      340      350      360
m050-1.pep PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLN
          |||||
g050-1      PRVEDXPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVNMLD
      310      320      330      340      350      360

      370      380      390      400      410      420
m050-1.pep KGEELPVDFNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTROMLEQTDLLGMIGKSE
          |||||
g050-1      KGEELPVDFNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTROMLKQTGLLGMIGKSE
      370      380      390      400      410      420

      430      440      450      460      470      480
m050-1.pep RGVATCEAIADNKAVYLMVGGAAYLVAKAIKSSKVLAFPELGMEAIYEFVKDMPVTVA
          |||||
g050-1      RGAATCEAIADNKAVYLMVGGAAYLVAKAIKSSKVLAFPELGMEAVYEFVKDMPVTVA
      430      440      450      460      470      480

      490      500
m050-1.pep VDSKGESIHATAPRKWQAKIGIIPVESX
          |||||
g050-1      VDSKGESIHATAPRKWQAKIGIIPVESX
      490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 221>:

```

a050-1.seq
1  ATGACCGTCA TCRAACAGGA AGACTTTATC CAAAGCATT GCGATGCCTT
51  CCAATTCATC AGCTACTACC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AACCCCGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGCAT GTGTGCCGAA AACAACCGCC CCATCTGCCA
201 AGATACCGGT ATCGCGACCG TGTTTTGAAG AGTCGGTATG GATGTGCAAT
251 GGGATGCAGA CATGAGCGTC GAAGAGATGG TTAACGAAGG CGTGCGCCGC
301 GCCTACACTT GGAAGGCCAA TACGCTGCGC GCTTCCGTTT TCGCCGACCC
351 CGCCGGCAAA CGCCAAAATA CCAAAGACAA CACGCCCGCC GTCATCCATA
401 TGAGCATCGT GCCGGCGGAC AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GCGGTTCTGT AAAACAAATC CAAACTCGCC ATGCTCAACC CTTCCGACAA
501 CATCGTTCGAT TGGGTATTGA AAACCATTCG GACCATGGGC GCGGGCTGGT
551 GTCCTCCCGG CATCTTGGGC ATCGGCATCG GCGGTACGCC CGAAAAGCC
601 GTGTTGATGG CGAAGAATC CCTGATGAGC CACATCGACA TCCAAGAATT
651 GCAGGAAAAA GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAAA GTCAACGCGC TAGGCATCGG CGCGCAAGGC
751 TTGGGCGGTC TGACCACCGT GTTGGACGTG AAAATCCTCG ATTACCCGAC
801 CCACGCCGCC TCCAAACCGA TTGCCATGAT TCCGAAGTGC GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GCCCTGTGCA ACTCACGCCG
901 CCGCGCGTCG AAGACTGGCC CGATTTGACT TACAGCCCGG ACAACGGCAA
951 ACGCGTCGAT GTCGACAAGC TGACCAAAGA AGAAGTGGCA AGCTGGAAAA
1001 CGGCGGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCAG CCGCGATGCC
1051 GCACACAAAC GCCTCGTCGA TATGCTCGAC AAAGGCGAAG AATTGCCCGT
1101 CGATTTTACC AACCGCCTGA TTACTACGT CGGCCCGGTC GATCCGGTCG
1151 GCGACGAAAT CGTCGGCCCA GCAGTCCGA CCACGCCAC CCGCATGGAC
1201 AAATTCACCC GCCAAATGCT CGAACAAACC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAAACAAAG
1301 CCGTGTACCT CATGGCAGTC GCGCGCGCGG CGTATCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GGCGTTCCCC GAATTGGGCA TGGAAGCCAT
1401 TTACGAATTT GAAGTCAAAG ACATGCCCGT AACCGTCGCC GTAGACAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCGCG CCCAATGGCA GGCGAAAATC
1501 GGCATCATCC CCGTCAAATC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 222; ORF 050-1.a>:

```

a050-1.pep
1  MTVIKQEDFI QSIDAFQFI SYHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVM DVQWDADMSV EEMVNEGVR
101 AYTWEQNTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGD KVEVTCAARG
151 GGSENKSLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELOEK AASGAELSTT EALRLELFEK VNALGIGAQQ
251 LGGLTTVLDV KILDYPTHAA SKPIAMIPNC AATRHVEFEL DSGSPVELTP
301 PRVEDWPDLT YSPDNGKRVD VDKLTKEEVA SWKTGDVLLL NGKILTGRDA
351 AHKRLVDMLD KGEELPVDFN NRIYYVGPV DPVGDEIVGP AGPTTATRMD
401 KFTROMLEQT DLLGMIGKSE RGAATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAIYEF EVKDMPVTVA VDSKGESIHA TAPPQWQAKI
501 GIIPVKS*

```


a050-1/m050-1 98.4% identity in 507 aa overlap

```

      10      20      30      40      50      60
a050-1.pep MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE
|||||
m050-1      MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE
      10      20      30      40      50      60

      70      80      90      100     110     120
a050-1.pep NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAITWEGNTLRASVLADPAGK
|||||
m050-1      NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAITWEGNTLRASVLADPAGK
      70      80      90      100     110     120

      130     140     150     160     170     180
a050-1.pep RQNTKDNTPAVIHMSIVPGDKVEVTCAAKGGGSENKSKLAMLNPSDNIVDWVLKTIPTMG
|||||
m050-1      RQNTKDNTPAVIHMSIVPGDKVEVTCAAKGGGSENKSKLAMLNPSDNIVDWVLKTIPTMG
      130     140     150     160     170     180

      190     200     210     220     230     240
a050-1.pep AGWCPPGILGIGIGGTPEKAVLMAKESLSHIDIQELQEKAASGAELSTTEALRLLEFKE
|||||
m050-1      AGWCPPGILGIGIGGTPEKAVLMAKESLSHIDIQELQEKAASGAELSTTEALRLLEFKE
      190     200     210     220     230     240

      250     260     270     280     290     300
a050-1.pep VNALGIGAQGLGGLTTVLDVKILDYPHAASKPIAMIPNCAATRHVEFELDGSGPVELTP
|||||
m050-1      VNALGIGAQGLGGLTTVLDVKILDYPHAASKPIAMIPNCAATRHVEFELDGSGPVELTP
      250     260     270     280     290     300

      310     320     330     340     350     360
a050-1.pep PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLD
|||||
m050-1      PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLN
      310     320     330     340     350     360

      370     380     390     400     410     420
a050-1.pep KGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDFTRQMLEQTDLLGMIGKSE
|||||
m050-1      KGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDFTRQMLEQTDLLGMIGKSE
      370     380     390     400     410     420

      430     440     450     460     470     480
a050-1.pep RGAATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAIYEFVVDMPVTVA
|||||
m050-1      RGVATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAIYEFVVDMPVTVA
      430     440     450     460     470     480

      490     500
a050-1.pep VDSKGESIHATAPPQWQAKIGIIPVKSX
|||||
m050-1      VDSKGESIHATAPRKWQAKIGIIPVESX
      490     500

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 223>:

g052.seq

```

1  ATGGCTTTGG TGGCGGAGGA AACGGAATA TCCGCGCCGT GTTTCAAAGG
51  CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGCGG CTCACTCCGA
251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
351 CGCCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 224; ORF 052.ng>:

g052.pep

1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
 101 RLRLETTWSP ACRKVKNA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 225>:

m052.seq

1 ATGGCTTTGG TGGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG
 51 CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
 151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
 201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGCGG CTCACTCCGA
 251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
 301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 226; ORF 052>:

m052.pep

1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
 101 RLRLETTWSP ACRKVKNA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 227>:

a052.seq

1 ATGGCTTTGG TCGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG
 51 CTGAGAGCCG ACAGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCTCCC
 151 AAGGGATTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
 201 GGCGGCTTTC CATTGCTTTA TATCAGTCGG CGACACGTGA CTCACTTCGA
 251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
 301 AGGCTGCGGC TGGAAATCAC ATGGTCGCCC GCCTGCAAAA AGGTGAAAAA
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 228; ORF 052.a>:

a052.pep

1 MALVAEETEI SAPCFKG*EP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGD* LTSMPLVTM LLIKPTVVPN
 101 RLRLEITWSP ACKKVKNA*

m052/a052 95.8% identity over a 119 aa overlap

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
a052	MALVAEETEI SAPCFKGXEP TGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
	10	20	30	40	50	60
m052.pep	SLVLALTAAFHSFISVGDTRLTPMPNLVTMLLIKPTVVPNRLRLETTWSPACRKVKNAAX					
a052	SLVLALTAAFHSFISVGDXTLTSMPLVTMLLIKPTVVPNRLRLEITWSPACKKVKNAAX					
	70	80	90	100	110	120

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 052 shows 95.8% identity over a 119 aa overlap with a predicted ORF (ORF 052.ng) from *N. gonorrhoeae*:

m052/g052

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					

```

g052      MALVAEETEISAPCFKGCEPTGDSRLSTTKSAPMPCANSASAKSKSATSPKGLDGVSKNS
           10      20      30      40      50      60
           70      80      90      100     110     120
m052.pep  SLVLALTAAFHSFISVGDWTLSMPNLATMLLIKPTVVPNRLRLLEITWSPACKKVKNAAAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g052      SLVLALTAAFHSFISVGDTRLTPMNLVTMLLIKPTVVPNRLRLLETTWSPACRKVKNAAX
           70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 229>:

```

g073.seq
1  ATGTGTATGC CATACGCAAT AAGGGTTTCA GACGGCATCT GCCGCATTTT
51 TCCGCCGATG CCGTCTGAAA CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AGTCCGGGGC GGatacCGGC GCGAGTTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT TGGTGATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GAAAAGAGT TCCACGACTT TCCACGCGC TGCTTGGTCG
301 GCGACTTCAA AACCGATGAC GATGCCGCCG CCGTTTTGCT GTTTGCGGAT
351 AAGCTCCGCC TCGGATGGT CGGCAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 230; ORF 073.ng>:

```

g073.pep
1  MCMPIAIRVS DGICRIFPPM PSETRNQRAS ACFKSSIKSP TYSKPTDRRT
51 SPGRIPAASF SSGCILPCVV VHGLVMVERT SPRLAVREKS STTFHAAAWS
101 ATSKPMTMPP PFCCLRISSA CGWSGNPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 231>:

```

m073.seq
1  ATGTGTATGC CATATAAGAT AAGGGTTTCA GACGGCATCT GCTGTCCAAT
51 GCGGTCTGAA ACACGCAATC AGCGTGCGAG TGCTGTTTTC AAATCGTCAA
101 TCAAATCGCC AACATATTCC AAACCGACCG ACAGGCGCAC CAATCCGGGG
151 CGGATGTTGG CCGCGAGTTT TTCTTCGGGC TGATCCTGCG CGTGCGTGGT
201 TGTCCACGGG TGGGTAATGG TCGAGCGCAC GTCACCGAGG TTGGCGGTGC
251 GGGAAAAGAG TTCCACGCCG TCCACAATT TCCACGCCG TTCTTGATCG
301 GCAACTTCAA AGCCGATGAC GATGCCGCCG CCGTTTTGCT GTTTGCGGAT
351 AAGCGCCGCC TGAGGATGGT CGGACAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 232; ORF 073>:

```

m073.pep
1  MCMPIKIRVS DGICCPMPSE TRNQRASACF KSSIKSPTYS KPTDRRTNPG
51 RMLAASFSSG CILPCVVVHG WVMVERTSPR LAVREKSSTP STTFHAASXS
101 ATSKPMTMPP PFCCLRISAA XGWSNDPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 233>:

```

a073.seq
1  ACGTGTATGT CATATAAGAT AAGGGTTTCA GACGGCATTT GCGGTGTTTT
51 TCCGCCGATG CCGTCTGAA. CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AATCCGGGGC GGATGTTGGC GCGAGTTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT GGGTAATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAGAAAAGT TCGACGCCGT CCACGACTTT CCACGCGGCT
301 GCTTGGTCGG CCACTTCAA GCGGATGACG ATGCCGCCG CTTTTGCTG
351 TTTGCGGATA AGCTCCGCCT GAGGATGGTC GGGTAATCCG GTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 234; ORF 073.a>:

```

a073.pep
1  TCMSYKIRVS DGICGVFPPM PSEXNRQRAS ACFKSSIKSP TYSKPTDRRT
51 NPGRMLAASF SSGCILPCVV VHGWVMVERT SPRLAVREKS STPSTTFHAA
101 AWSATSKPMT MPPPFCLRI SSA*GWSGNP V*

```

m073/a073 92.3% identity over a 130 aa overlap

260

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMMLAASF				
a073	TCMSYKIRVSDGICGVFPMPSEXRNQRASACFKSSIKSPTYSKPTDRRTNPGRMMLAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVMVERTSPRLAVREKSSTPTTFHAASXSATSCKPMTMPPPFCCCLRI				
a073	SSGCILPCVVVHGWVMVERTSPRLAVREKSSTPTTFHAAWSATSCKPMTMPPPFCCCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNDNPVX				
a073	SSAXGWSGNPVX				
		130			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 073 shows 87.0% identity over a 131 aa overlap with a predicted ORF (ORF 073.ng) from *N. gonorrhoeae*:

m073/g073

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMMLAASF				
g073	MCMPIAIRVSDGICRIFFPMPSETRNQRASACFKSSIKSPTYSKPTDRRTSPGRIPAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVMVERTSPRLAVREKSSTPTTFHAASXSATSCKPMTMPPPFCCCLRI				
g073	SSGCILPCVVVHGLVMVERTSPRLAVREKSST---TFHAAWSATSCKPMTMPPPFCCCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNDNPVX				
g073	SSACGWSGNPVX				
		120			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 235>:

g075.seq

```

1  ATGCCGCTT ACTTCATCAC CCTCTTAACG ATGGAAAATA CAAAAAGCGC
51  GGCGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTTTT GCGGTTTCGG GCAACGCTGC GTTTGCCTGT
151 GCCGCCAAG CCAGCGGGGC GGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTACGGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTT ACGAAATTTT
251 TAAAAAATG TGTTCGCGG CTTTGTGAAG GTTTAGAGA CCGCTGCCG
301 GGCCTCTTAA ACTTAATCTT CTTTTCGTA GAATCCGAAA ATTACAAATT
351 CCCCGCTAT CTCTCCAAT GCCGAGCTAA AAGCGTCTT ATAGCTGTCA
401 TATTACCG CTGA

```

This corresponds to the amino acid sequence <SEQ ID 236; ORF 075.ng>:

g075.pep

```

1  MPPYFITLLT MENTKSAKT PTTIQPASIP SAFAASKAFF AVSGNAAFAC
51  AAKASGAAVT TASFAPYLRQ VLINFMIFSF TKFLKKCVCV LCEGFRDRLP
101 GLNLNLIFFV ESENYKFPAY LFQCRKSVF IAVIFTG*

```

1	ATGCCGTCTT	ACTTCATCAC	TCTCTTAACG	ATGGAAAATA	CAAAAAGCGC
51	GGCGAAAATG	CCCACTACAA	TCCAACCGGC	TTCCATACCG	TCCGCTTTTG
101	CGGCTTCCAA	AGCGTTTTTT	GCCGTATCGG	GCAACGTTGC	ATTTGCATGT
151	GCGGCCAAAG	CCAGGGGAGC	AGCTGTTACA	ACAGCCAGTT	TTGCGCCGTA
201	TTTACGGCAG	GTGTTAATAA	ATTTTCATGAT	ATTTTCCTTC	AAAAAGTGTT
251	TGGCGGTAAT	GGATGGAGCG	TTTTTCAGAC	GACCGCGGAA	CATCCGAAAA
301	TCAGTCTTTT	AAAAATCCGA	ATACGACAAA	TTCGTATTGG	TTGCCGATTT
351	CTTCCAAACC	TGCGTTAATC	GCTTCTTCGA	AGTCGTAGAA	ATAATCGGCA
401	TTGGTGATTA	A			

m075 - pep

```

1  MPSYFITLLT MENTKSAAKM PTTIQPASIP SAFAASKAFF AVSGNVAFAC
51  AAKARGAAVT TASFAPYLQR VLINFMIFSF KKCLAVMDGA FFRPPNIRK
101 SVFOKSEYDK FVLVADFFQT CVNRFFEVE IIGIGD*

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 075 shows 65.7% identity over a 137 aa overlap with a predicted ORF (ORF 075.ng) from *N. gonorrhoeae*:

```

      10      20      30      40      50      60
m075 . pep  MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAGAAVT
             || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g075        MPPYFITLLTMENTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNAAFACAAGASGAVT
             10      20      30      40      50      60

      70      80      90      100     110
m075 . pep  TASFAPYLRQVLINFMIFSF----KKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVAD
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g075        TASFAPYLRQVLINFMIFSFTKFLKKVCVGLCEGFRDRLPGLLNLIFFVSESENYKFPAY
             70      80      90      100     110     120

      120     130
m075 . pep  FFQTCVNRFFEVEIIGIDX
             :||  ::  |:|  :|
g075        LFQCRAKSVFIAVIFTGX
             130

```

a075.seq

1	ATGCCGTCTT	ACTTCATCAC	TCTCTTAACG	ATGGAAGA	CAAAAAGCGC
51	GGCGAAACG	CCCATAACA	TCCAACCGG	TTCCATACCG	TCCGCTTTTG
101	CGGCTTCCAA	AGCGTTTTTT	GCTGTATTGG	GCAACGTTGC	ATTTGCATGT
151	CGGCCAAAG	CCAGGGGAGC	AGCTGTTCAC	ACAGCAGTT	TTGCGCGTA
201	TTTACGGCAG	GTGTTAATAA	ATTTTCATGAT	ATTTTCCTTC	AAAAAGTGTT
251	TGGCGGTAAT	GGATGGAGCG	TTTTTCAGAC	GACCGCCGAA	CATCCGAAAA
301	TCAGTCTTTT	AAAATCCGA	ATACGACAAA	TTCGTATTGG	TTGCCGATTT
351	CTTCCAAACC	TGCGTTAATC	GCTTCTTCGA	AGTCGTAGAA	ATAATCGGCA
401	TTGGTGATTA	A			

a075.pcp

1 MPSYFITLLT MEKTKSAAKT PTTIQPASIP SAFAASKAFF AVSGNVAFAC
51 AAKARGAAVT TASFAPYLQR VLFNFMIFSF KKCLAVMDGA FFRRPPNIRK
101 SVFOKSEYDK FVLVADFFQT CVNRFFEVEV IIGIGD*

m075/a075 98.5% identity over a 136 aa overlap

	10	20	30	40	50	60
m075.pep	MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
	:					
a075	MPSYFITLLTMEKTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m075.pep	TASFAPYLQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
a075	TASFAPYLQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
	70	80	90	100	110	120
	130					
m075.pep	CVNRFFEVEIIGIGDX					
a075	CVNRFFEVEIIGIGDX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 241>:

g080.seq

1	ATGTGGGATA	ATGCCGAAGC	GATGGAACGG	CTGACGCGCT	GGCTGCTTGT
51	CATGATGGCG	ATGCTGCTTG	CTGCGTCCGG	GCTGGTTTGG	TTTTACAATT
101	CGAATCATCT	GCCCGTCAAG	CAGGTGTCGC	TGAAGGGCAA	CCTGGTTTAT
151	TCCGATAAGA	AGGCATTGGG	CAGTTTGGCG	AAAGAATACA	TCCATGGGAA
201	TATTTTGAGG	ACGGACATCA	ATGGCGCACA	GGAAGCCTAC	CGCCGGTATC
251	CGTGGATTGC	GTCGGTCATG	GTGCGCCGCC	GTTTTCCCGA	TACGGTTGAG
301	GTCGTCCTGA	CCGAGCGCAA	GCCGGTTGCA	CGTTGGGGCG	ACCATGCCTT
351	GGTGGACGGC	GAAGGCAATG	TTTTTGAAGC	CCGCTTGGAC	AGACCCGGAA
401	TGCCGGTATT	CAGAGGCGCG	GAAGGAACGT	CTGCCGAAAT	GCTCCGCCGT
451	TATGACGAAT	TTTCGACTGT	TTTGGCAAAA	CAGGGTTTGG	GCATCAAAGA
501	GATGACCTAT	ACGGCACGTT	CGGCGTGGAA	TGTCGTTTTG	GACAACGGCA
551	TCACCGTCAG	GCTCGGACGG	GAAAACgAGA	TGAAACGCCT	CCgGCTTTTT
601	ACcgAAGCGT	GGCAGCATCT	gttgcGTAAG	AATAAAATC	GGTTATCCTA
651	TGTGGATATG	Aggtataagg	acggatttTC	agtcccccat	gctCCCGACG
701	GTTTACCCGA	AAAAGAAATcc	gAAGAAATatt	gggaacaggt	ttgggacata
751	ttacggcctg	gcgtcggaaa	cggttcgacg	caaatttcaa	tcagttatAA
801	GGGCAGacga	acaatggaac	AGcagtaa		

This corresponds to the amino acid sequence <SEQ ID 242; ORF 080.ng>:

g080.pep

1	MWDNAEAMER	LTRWLLVMMMA	MLLAASGLVW	FYNSNHLPVK	QVSLKGNLVY
51	SDKKALGSLA	KEYIHGNILR	TDINGAQEAY	RRYPWIASVM	VRRRFPDIVE
101	VVLTERKPVA	RWGDHALVDG	EGNVFEARLD	RPGMPVFRGA	EGTSAEMLRR
151	YDEFSTVLAK	QGLGIKEMTY	TARSAWNVVL	DNGITVRLGR	ENEMKRLRLF
201	TEAWQHLLRK	NKNRLSYVDM	RYKDGFSVPH	APDGLPEKES	EEYWEQVWDI
251	LRPGVGNST	QISISYKGRR	TMEQQ*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 243>:

m080.seq

1	ATGTGGGATA	ATGCCGAAGC	GATGGAACGG	CTGACGCGCT	GGCTGCTTGT
51	CATGATGGCG	ATGCTGCTTG	CTGCGTCCGG	GCTGGTTTGG	TTTTACAATT
101	CGAATCATCT	GCCCGTCAAG	CAGGTGTCGC	TGAAGGGCAA	CCTGGTTTAT
151	TCCGATAAGA	AGACATTGGG	CAGTTTGGCG	AAAGAATACA	TCCATGGGAA
201	TATTTTGAGG	ACGGACATCA	ATGGCGCACA	GGAGGCCTAC	CGCCGGTATC
251	CGTGGATTGC	GTCGGTCATG	GTGCGCCGCC	GTTTTCCCGA	CACGGTTGAG
301	GTCGTCCTGA	CCGAGCGCAA	GCCGGTCGCG	CGTTGGGGCG	ACCATGCCTT
351	GGTGGACGGC	GAAGGCAATG	TTTTTGAAGC	CCGCTTGGAC	AGACCCGGAA
401	TGCCGGTATT	CAGAGGCGCG	GAAGGAACGT	CTGCCGAAAT	GCTCCGCCGT
451	TATGACGAAT	TTTCGACTGT	TTTGGCAAAA	CAGGGTTTGG	GCATCAAAGA
501	GATGACCTAT	ACGGCACGTT	CGGCGTGGAT	TGTCGTTTTG	GACAACGGCA
551	TCACCGTCAG	GCTCGGACGG	GAAAACGAGA	TGAAACGCCT	CCGGCTTTTT

601 ACCGAAGCGT GGCAGCATCT GTTGCCTAAA AATAAAATC GGTTATCCTA
 651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTTCCGACG
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 2441; ORF 080>:

m080.pep
 1 MWDNAEAMER LTRWLLVMM MLLAASGLVW FYNSNHLPVK QVSLKGNLVY
 51 SDKKTGLGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDTVE
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR
 151 YDEFSTVLAK OGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRL
 201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY ASDGLPEKES EE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 080 shows 97.9% identity over a 242 aa overlap with a predicted ORF (ORF 080.ng) from *N. gonorrhoeae*:

m080/g080

m080.pep	10	20	30	40	50	60
	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLPVKQVSLKGNLVYSDKKTGLGSLA					
080	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLPVKQVSLKGNLVYSDKKTGLGSLA					
	10	20	30	40	50	60
m080.pep	70	80	90	100	110	120
	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTVEVVLTERKPVARWGDHALVDG					
080	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTVEVVLTERKPVARWGDHALVDG					
	70	80	90	100	110	120
m080.pep	130	140	150	160	170	180
	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKOGLGIKEMTYTARSAWIVVL					
080	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKOGLGIKEMTYTARSAWIVVL					
	130	140	150	160	170	180
m080.pep	190	200	210	220	230	240
	DNGITVRLGRENEMKRLRLFTEAWQHLLRKKNKRLSYVDMRYKDGFSVRYASDGLPEKES					
080	DNGITVRLGRENEMKRLRLFTEAWQHLLRKKNKRLSYVDMRYKDGFSVRYASDGLPEKES					
	190	200	210	220	230	240
m080.pep	EE*					
080	EEYWEQVWDILRPGVNGSTQISISYKGRRTMEQQX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 245>:

a080.seq

1 ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
 51 CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
 101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTAGTTTAT
 151 TCCGATAAGA AAGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
 201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGGTATC
 251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA CACGGTTGAG
 301 GTCGTCCTGA CCGAGCGCAA GCCGGTCGCG CGTTGGGGCG ACCATGCCTT
 351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGTTTGGAC AGACCCGGAA
 401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
 451 TATGACGAAT TTTGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
 501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTCGTTTGT GACAACGGCA

264

551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT
 601 ACCGAAGCGT GGCAACATCT GTTGCCTAAA AATAAAAATC GGTTATCCTA
 651 TGTGGATATG AGGTATAAGG ACGGATTTC AGTCCGCTAT GCTCCCGACG
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 246; ORF 080.a>:

a080.pep
 1 MWDNAEAMER LTRWLLVMM MLLAASGLVW FYNNSHLPVK QVSLKGNLVY
 51 SDKKALGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDVE
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR
 151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF
 201 TEAWQHLLRK KNKRLSYVDM RYKDGFSVRY APDGLPEKES EE*

m080/a080 99.2% identity over a 242 aa overlap

	10	20	30	40	50	60
m080.pep	MWDNAEAMER	LTRWLLVMM	MLLAASGLVW	FYNNSHLPVK	QVSLKGNLVY	SDKKTLGSLA
a080	MWDNAEAMER	LTRWLLVMM	MLLAASGLVW	FYNNSHLPVK	QVSLKGNLVY	SDKKALGSLA
	70	80	90	100	110	120
m080.pep	KEYIHGNILR	TDINGAQEAY	RRYPWIASVM	VRRRFPDVE	VVLTERKPVA	RWGDHALVDG
a080	KEYIHGNILR	TDINGAQEAY	RRYPWIASVM	VRRRFPDVE	VVLTERKPVA	RWGDHALVDG
	130	140	150	160	170	180
m080.pep	EGNVFEARLD	RPGMPVFRGA	EGTSAEMLRRY	DEFSTVLAK	QGLGIKEMTY	TARSAWIVVL
a080	EGNVFEARLD	RPGMPVFRGA	EGTSAEMLRRY	DEFSTVLAK	QGLGIKEMTY	TARSAWIVVL
	190	200	210	220	230	240
m080.pep	DNGITVRLGR	ENEMKRLRLF	TEAWQHLLRK	KNKRLSYVDM	RYKDGFSVRY	ASDGLPEKES
a080	DNGITVRLGR	ENEMKRLRLF	TEAWQHLLRK	KNKRLSYVDM	RYKDGFSVRY	APDGLPEKES
m080.pep	EEX					
a080	EEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 247>:

g081.seq
 1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTCCGAT
 51 GCCGTCTGAA AACAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGATA
 101 TTCGGAAGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGACGCG
 151 CATGATTTTG TTGGAGGCGT ATTGTCTGCG GGCGCGGCGG CGGTTGTGGT
 201 TTCGCGCGAA GATTGCGCGG CTTGGGCGG CGCGTTGAAA GTCGATGACA
 251 CGCTTGCCGC GTTGCAAACG TTGGCGAAGG CGTGGCGCGA TAATGTGAAC
 301 CCGTTTGTGT TCGGCATTAC CGGTTGCGGC GGCAAGACGA CGGTGAAGGA
 351 GATGCTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATGAT GCCGTTTCGG
 401 CGACGCGCAG CAACTTCAAC AACCACatcg gaTTGCCGCT GACTTTATTG
 451 AAATtaacAcg aAAACACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
 501 TTTTGGcgaa ctggcggtTt taacgcaaaT CGCCAAACCC GATGCCGCTT
 551 TGGtcaACAA CGCCCTGCGC GCCATGTGCG GATGCGGTTt cgacggagtg
 601 GCGGATATTG CCAAAGcgaa aagcGAGATT TatgcagGct tATGTTcAGA
 651 CGGCATGGCA CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
 701 CGGCAACGTT TAATTTGAAT ACGTGCACTT TCGGCGTCGA TAGCGGCGAT
 751 GTCCGCGCGG AAAATATCGT GCTGAAACCT TTGTCGTGCG AATTTGATT


```

801 GGTGTGCGGC GACGAGCGCA CTGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG CAAGGCTTCA GCAACATCAA
951 AGGCCGTCTG AACGTCAAAG CCGGCATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAATCCC GACAGTATGA AAGCCGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG CATTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAGGAc gaAGCCGCCG CCATGCACGC CGAagtcgGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGcggaAA AATTTGGCGC GGACGGTTTG TGGTTCGCCG CCAAAGACCC
1251 GTTGATTCAA GTGTTGAGCC ACGATTGGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTG GCGCTTTATG CAGatggaAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTga

```

This corresponds to the amino acid sequence <SEQ ID 248; ORF 081.ng>:

```

g081.pep
1 MKPLDLNFIC QALKLPMPSE NKPVSRIVTD SRDIREGDVF FALAGGRFDA
51 HDFVGGVLSA GAAAVVVSRE DCAALGGALK VDDTLAALQT LAKAWRDNVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFDD AVSATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTQIAKP DAALVNNALR AHVCGGFDGV
201 GDIKAKSEI YAGLCSDGMA LIPQEDANMA VFKTATFNLN TCTFGVDSGD
251 VRAENIVLKP LSCEFDLVCG DERTAVVLPV PGRHNHVNAA AAAALALAG
301 LSLNDVAEGL QGFSNIKGRL NVKAGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMMGELGED EAAAMHAEVG AYARDQGIEA AYFVGDNVSE
401 AAEKFGADGL WFAAKDPLIQ VLSHDLPERA TVLVKGSRPM QMEEVVEALE
451 DK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 249>:

```

m081.seq
1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 CCCGTCTGAA AGCAAACCCG TGTGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGAGCG GTTTGACGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCT GGTGCGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATTGTGCTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTGCCGC ATTGCAAACG CTGCAAAAGG CGTGGCGTGA AAATGTGAAT
301 CCGTTTGTGT TCGGCATTAC CGGTTCCGGC GGCAAGACGA CGGTGAAGGA
351 AATGCTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATGAT GCCGTGTTGG
401 CGACGCGAGG CAACCTCAAC AACCATATCG GATTGCCGCT GACTTTGTTG
451 AAGTTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTCGCGGAA CTGGCGGTTT TAACGCAMAT CGCCAAACCA AATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GGCGATATTG CCAAAGCGAA AAGCGAGATT TACCAAGGTT TATGTTCAAG
651 CGGCATTGCA CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTGGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTTCACGCGG AAAATATTGT GCTGAAACCG TTGTCGTGCG AATTGTGATT
801 GGTGTGCGGC GATGAGCGCG CCGCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCTT GACAGCATGA AAGCTGCGAT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAACTG GCGGAGGACG AAGCCGCCGC TATGCACGCC GAAGTCGGCG
1151 CGTATGCCCG CGACCAAGGC ATCGAAGCGG CTTATTTTGT CGGCGACAAC
1201 AGCGTCGAAG CGGCGGAAAA ATTTGCGCGG GACGGTTTGT GGTCGCCCGC
1251 CAAAGACCCG TTGATTCAAG TGTTGCGCCA CGATTTGCCC GAACGCGCCA
1301 CCGTGTGGT GAAAGGTTTCG CGCTTTATGC AGATGGAAGA AGTGGTCGAG
1351 GCATTGGAGG ATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 250; ORF 081>:

```

m081.pep
1 MKPLDLNFIC QALKLPMPSE SKPVSRIVTD SRDIRAGDVF FALAGERFDA
51 HDFVEDVLAAGAAVVVSRE DCAAMDGALK VDDTLAALQT LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFDD AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTXIAKP NAALVNNAMR AHVCGGFDGV

```

201 GDIKAKSEI YQGLCSDGIA LIPQEDANMA VFKTATLNLN TRTFGIDSGD
 251 VHAENIVLKP LSCEFDLVCG DERAADVLPV PGRHNVHNA AAAALALAAG
 301 LSLNDVAEGL KGFSNIKGR LNVKSGIKGAT LIDDTYNANP DSMKAAIDVL
 351 ARMPAPRIFV MGD MGELGEL GEDEAAAMHA EVGAYARDQG IEAAYFVGDN
 401 SVEAAEKFGA DGLWFAAKDP LIQVLRHDL PERATVLVKGS RFMQMEEVVE
 451 ALEDK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 081 shows 94.1% identity over a 455 aa overlap with a predicted ORF (ORF 081.ng) from *N. gonorrhoeae*:

m081/g081

m081.pep	10	20	30	40	50	60
	MKPLDLNFICQALKLPMPSESKPVSRIVTDSRDIRAGDVFFALAGERFDAHDFVEDVLAA					
g081	MKPLDLNFICQALKLPMPSENKPVSRIVTDSRDIREGDVFFALAGGRFDAHDFVGGVLSA					
	10	20	30	40	50	60
m081.pep	70	80	90	100	110	120
	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
g081	GAAAVVVSREDCAALGGALKVDDTLAALQTLAKAWRDNVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	130	140	150	160	170	180
	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGE LAVLTXIAKP					
g081	AVLRRRFGDDAVSATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGE LAVLTQIAKP					
	130	140	150	160	170	180
m081.pep	190	200	210	220	230	240
	NAALVNNAMRAHVGCGFDGVDIAKAKSEIYQGLCSDGIALIPQEDANMAVFKTATLNLN					
g081	DAALVNNALRAHVGCGFDGVDIAKAKSEIYAGLCSDGMALIPQEDANMAVFKTATFNLN					
	190	200	210	220	230	240
m081.pep	250	260	270	280	290	300
	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGDERAAVLPVPGRHNVHNA AAAALALAAG					
g081	TCTFGVDSGDVRAENIVLKPLSCEFDLVCGDERTAVVLPVPGRHNVHNA AAAALALAAG					
	250	260	270	280	290	300
m081.pep	310	320	330	340	350	360
	LSLNDVAEGLKGFSNIKGR LNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
g081	LSLNDVAEGLQGFSNIKGR LNVKAGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	310	320	330	340	350	360
m081.pep	370	380	390	400	410	420
	MGDMGELGELGEDEAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
g081	MGDMGELGE---DEAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
	370	380	390	400	410	
m081.pep	430	440	450			
	LIQVLRHDLPERATVLVKGS RFMQMEEVVEALEDKX					
g081	LIQVLSHDLPERATVLVKGS RFMQMEEVVEALEDKX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 251>:

a081.seq

```

1  ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51  GCCGTCTGAA AGCAAACCCG TGTGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGATGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCG GGTGCGGGCG CGGTTGTGGT
201 TTCGCGCGAA GATTGCGTTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTACCGC GTTGCAAATG TTGGCGAAGG CGTGGCGCGA GAATGTGAAC
301 CCGTTTGTGT TCGGTATTAC CGGCTCGGGC GGCAAGACGA CGGTGAAGGA
351 AATGTTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATAAT GCCGTTTGG
401 CGACGGCAGG CAACTTCAAC AACCACATCG GATTGCCGTT GACTTTGTTG
451 AAATTAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GTATGAACCA
501 TTTTGGCGAA CTGGCGGTTT TGACACAAAT CGCCAAACCC GATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GCGGATATTG CCAAAGCGAA AAGCGAGATT TATCAAGGCT TATGTTTCAGA
651 CGGCATGGCG CTGATTCTCT AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTCCACGCGG AAAATATCGT GCTGAAACCG TTGTCGTGCG AATTTGATTT
801 GGTGTGCGGC AACGAGTGGC CAGCCGTGGT TCTGCCCGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCCGCCGCCG CGCTGTCTTT GGCTGCAGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCTT GACAGCATGA AAGCTGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGTGAGGAC GAAGCCGCGC CCATGCACGC CGAAGTCGGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGCGGAAA AATTTGGCGC GGACGGTTTG TGGTTCGCCG CCAAAGACCC
1251 GTTGATTCAA GTGTTGCGCC ACGATTGACC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTT GCGCTTTATG CAGATGGAAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 252; ORF 081.a>:

a081.pep

```

1  MKPLDLNFIC QALKLPMPSE SKPVSRIVTD SRDIRAGDVF FALAGGRFDA
51  HDFVEDVLAA GAAVVVSRE DCVAMDGALK VDDTLTALQM LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDN AVLATAGNEN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFG E LAVLTQIAKP DAALVNNAMR AHVCGFDGV
201 GDIKAKSEI YQGLCSGMA LIPQEDANMA VFKTATLNLN TRTFGIDSGD
251 VHAENIVLKP LSCEFVLVCG NECAAVVLPV PGRHNVHNA A A A A L S L A A G
301 LSLNDVAEGL KGFSNIKGR L NVKSGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRI F MGDMLGED E A A M H A E V G AYARDQGIEA AYFVGDN SVE
401 AAEKFGADGL WFAAKDPLIQ VLRHDLPERA TVLVKGSREM QMEEVVEALE
451 DK*

```

m081/a081 96.7% identity over a 455 aa overlap

	10	20	30	40	50	60
m081.pep	MKPLDLNFICQALKLPMPSESKPVSRIVTDSDIRAGDVFFALAGERFDAHDFVEDVLAA					
a081	MKPLDLNFICQALKLPMPSESKPVSRIVTDSDIRAGDVFFALAGGRFDAHDFVEDVLAA					
	10	20	30	40	50	60
m081.pep	GAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAVVVSREDCVAMDGALKVDDTLTALQMLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	GAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAVVVSREDCVAMDGALKVDDTLTALQMLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	130	140	150	160	170	180
m081.pep	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGELAVLTQIAKP					
a081	AVLRRRFGDNAVLATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGELAVLTQIAKP					

268

	130	140	150	160	170	180
	190	200	210	220	230	240
m081.pep	NAALVNNAMRAHVGCDFGVGDIKAKSEIYQGLCSGIALIPQEDANMAVFKTATLNLN					
a081	DAALVNNAMRAHVGCDFGVGDIKAKSEIYQGLCSGDMALIPQEDANMAVFKTATLNLN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m081.pep	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGDERAAVLPVPGRHNHVNAAAAAALALAAG					
a081	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGNECAAVLPVPGRHNHVNAAAAAALSALAAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m081.pep	LSLNDVAEGLKGFNSNIKGRNLNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
a081	LSLNDVAEGLKGFNSNIKGRNLNVKSGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m081.pep	MGDMGELGELGEDEAAAMHAEVGAAYARDQGIEAAYFVGDNVVEAAEKFGADGLWFAAKDP					
a081	MGDMGELGE---DEAAAMHAEVGAAYARDQGIEAAYFVGDNVVEAAEKFGADGLWFAAKDP					
	370	380	390	400	410	
	430	440	450			
m081.pep	LIQVLRHDLPERATVLVKGSRFMQEVEVALEDKX					
a081	LIQVLRHDLPERATVLVKGSRFMQEVEVALEDKX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 253>:

```

g082.seq
1  atGTGGTTGT TGAAGTTGCC TGCCGTCGCC GAAACGGCAT CATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAGCATCTC CTTACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAACGGGT TCACATTATC GCGCCACGCC
151 TCGCCAACG TTTGCAACGC GGCAAGCGTG TCATCGACTT TCAACGCGCC
201 GCCCAAAGCC GCGCAATCTT CGCGCGAAAC CACAACGCC GCGCGCCCG
251 CAGACAATAC GCCTCCAACA AAATCATGCG CGTCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC TTCCCGAATA TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTGTGTTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTCATAT TTGCTTTCGT TAATATTCCG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTA AACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTT TAGACGTATT TTAGCCGAT TTGCCTTTTC CCGCATACCA
601 CCGCGCGGGG TCGTCGGAAT GTCTGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCGGCAC ATCGGGGACA TTCCCCCAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 254; ORF 082.ng>:

```

g082.pep
1  MWLLKLPVA ETASSPKRRR NTAASISFTV VLPPEVMPN TNGFTLSRHA
51  FANVCNAASV SSTFNAPPKA AQSSRETTA AAPADNTPPT KSCASNRPPA
101 NAKNTSPSRI SRLSVTMRDT GLPSDGIGSL RAWQMKFRSS GFIFAFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSAF FLYVSFFRRI FSRFAFSRIP
201 RRGVVGLSVD KGKVIAPARH IGDIPPKIIA VIGQLVGFDT RPTAESAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 255>:

```

m082.seq
1  ATGnnGTTGT TGAAGTTGCC TGCCGTCGCC AACACGGCAT CATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAGCATTTT CTTACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAACGGAT TCACATTTTC ACGCCACGCC
151 TTTGCCAGCG TTTGCAATGC GGCAAGCGTG TCATCGACTT TCAACGCGCC

```

```

201 ATCCATTGCA GCACAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCAG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CGTCAAACCG CTCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTCGCTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTACTTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAACAC AGATTATTTT CCCATTCTCA TTCGGAATTT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGTCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGGCA GTCCGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCAAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTCGATACC CGTCCAAC TG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 256; ORF 082>:

```

m082.pep
  1 MXLLKLPAVA NTASSPKRRR NTAASISFTV VLPPEPVMPN TNGFTFSRHA
 51 FASVCNAASV SSTFNAPSIA AQSSRETTA AAPAANTSST KSCASNRSFA
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSXF FLYVSFFRRI PSRFASFRI
201 RRGVVQSVD KGKVIAFALH IGNIPPKIIA VIGQLVGFD TPTAESAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 082 shows 92.7% identity over a 247 aa overlap with a predicted ORF (ORF 082.ng) from *N. gonorrhoeae*:

m082/g082

	10	20	30	40	50	60
m082.pep	MXLLKLPAVANTASSPKRRRNTAASISFTVLPPEPVMPNTNGFTFSRHAFASVCNAASV					
	:					
g082	MWLLKLPAVAETASSPKRRRNTAASISFTVLPPEPVMPNTNGFTLSRHAFANVCNAASV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m082.pep	SSTFNAPSIAAQSSRETTAAAPAANTSSTKSCASNRSFANAKNTSPARMSRLSVTMRDT					
g082	SSTFNAPPKAAQSSRETTAAAPADNTPTKSCASNRPANAKNTSPSRISRLSVTMRDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m082.pep	GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSXF					
	:					
g082	GLFSDGIGSLRAWQMKFRSSGFIFAFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSAF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m082.pep	FLYVSFFRRIFSRFASRI PRRGVVQSVDKGKVIAFALHIGNIPPKIIA VIGQLVGFD T					
g082	FLYVSFFRRIFSRFASRI PRRGVVGLSVDKGKVIAFARHIGDIPPKIIA VIGQLVGFD T					
	190	200	210	220	230	240
m082.pep	RPTAESAX					
g082	RPTAESAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 257>:

a082.seq

```

  1 ATGTGTTGT TGAAGTTGCC TGCCGTCGCC AAAACGGCAT TATCGCCGAA
 51 ACGGCGGCGC AATACCGCAG CCAACATTTC CTTCACCGTC GTCTTGCCGC

```

270

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101 CCGAGCCGGT AATACCGAAC ACAAACGGGT TCACATTCTC GCGCCACGCC
151 TTCGCCAACA TTTGCAACGC GGTAAGCGTG TCATCGACTT TCAACGCGCC
201 ATCCATTGCA ACGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCCG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CATCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTTGCTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTAATTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGTCGAT TTGCCTTTT CCGCATACCA
601 CGGCGCGGGG TCGTCGGGCA GTCCGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCCAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTCGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 258; ORF 082.a>:

```

a082.pep
1 MWLLKLPAVA KTALSPKRRR NTAANISFTV VLPPEPVIPN TNGFTFSRHA
51 FANICNAVSV SSTFNAPSIA TQSSRETTA AAPAANTSST KSCASNRPPA
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSAF FLYVSFFRRI FSRFAFSRIP
201 RRGVVGQSV DKGKVI AFALH IGNIPPKIIA VIGQLVGFD TPTAES*

```

m082/a082 95.5% identity over a 247 aa overlap

```

              10      20      30      40      50      60
m082.pep      MXLLKLPAVANTASSPKRRRNTAASISFTVVLPPEPVMPTNGFTFSRHAFASVCNAASV
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a082           MWLLKLPAVAKTALSPKRRRNTAANISFTVVLPPEPVIPTNGFTFSRHAFANICNAVSV
              10      20      30      40      50      60

              70      80      90      100     110     120
m082.pep      SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRSPANAKNTSPARMSRLSVTMRDT
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a082           SSTFNAPSIATQSSRETTTAAAPAANTSSTKSCASNRPPANAKNTSPARMSRLSVTMRDT
              70      80      90      100     110     120

              130     140     150     160     170     180
m082.pep      GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSXF
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a082           GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSAF
              130     140     150     160     170     180

              190     200     210     220     230     240
m082.pep      FLYVSFFRRIFSRFAFSRIPRRGVVGQSV DKGKVI AFALHIGNIPPKIIA VIGQLVGFD
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a082           FLYVSFFRRIFSRFAFSRIPRRGVVGQSV DKGKVI AFALHIGNIPPKIIA VIGQLVGFD
              190     200     210     220     230     240

m082.pep      RPTAESAX
              | | | | | |
a082           RPTAESAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 259>:

```

g084.seq
1 ATGAAacaAT CCGcccgaat aAAAAATATG GATCAGACAT TAAAAAATAC
51 attgggcatt tGCGCGcttt tagcctTTTG TTTTggcgcg gccatCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGC
151 GCTTTGGCTT CGGTGTGATT TTTATTATTA TTGGCACGCG GCTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCCG CTGGCTGTAT GGTGCGCCTT CTTATCAGAT AGTCGGTTTCG
301 ATATTGGAAG GCAATCCTGC CGAGGCGCGT GAATTTGTCG GCAATCTTCC
351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTTT GGCTTGACAG

```

401 TTTGGAAATA TTGTGTATCT GTGGGGGTAT TTGCTGACGT AAAAACTAT
 451 AAACGTCGCA GCAAAATATG GCTGACCATA TTATTGACTT TGATTTTGTG
 501 CTGCGCGGTG ATGGAGAAAA TCGccggcgca taaAGATTGG CGAGaacctg
 551 atgcccgcct gttgttgaat ATTTTCgacc tgtattaCga cttggctttc
 601 cgcgcgggca CAATATGCCG CCAAGCGCGC CCacattttg gaagCagcaa
 651 aaaaagcgtC AACATGGCAt atccgccaac ttgcgccccaa gTataa

This corresponds to the amino acid sequence <SEQ ID 260; ORF 084.ng>:

g084.pep

1 MKQSARIKNM DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
 51 ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVGWLY GAPSYQIVGS
 101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS VGVFADVKNY
 151 KRRSKIWLTI LLTLILSCAV MEKIAQDKDW REPDAGLLLN IFDLYYDLAF
 201 RAGTICRQAR PHFGSSKKS SV NMAYPPTCAQ V*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 261>:

m084.seq

1 ATGAAACAAT CCGCCC GAAT AAAa .ATATG AATCAGACAT TACTTTATAC
 51 ATTGGGCATT TCGCGCTTT TAACCTTTnn nnnnnnnnnnn nnnnnnnnnnn
 101 nnnnnTATCA CCCnGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGT
 151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCAGCG GTTCCCGCG
 201 CGTTTCTTCA GTTGTTTTAC TGATTACGT CGGCACAACC GCCCTATATT
 251 TGCCGGTCGG CTGGCTGTAT GGTGCGCCGT CTTATCAGAT AGTCGGTTTCG
 301 ATATTGGAAA GCAATCCTGC CGAGGCGCGT GAATTTGTG GCAATCTTC
 351 CGGGTCGCTT TATTTGTGC AGGCATTATT TTTCAATTTT GGCTTGACAG
 401 TTTGGAAATA TTGTGTATCG GGGGGGTAT TTGCTGACGT AAAAACTAT
 451 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTG
 501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG
 551 ATGCCGGCCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTTGGCT.TC
 601 CGCGCCGGCA CAATATGCCG CCAAGCGCGC CCACATTTG GAAGCAGCAA
 651 AAAAAAGCTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

This corresponds to the amino acid sequence <SEQ ID 262; ORF 084>:

m084.pep

1 MKQSARIKXM NOTLLYTLGI CALLTFXXXX XXXXXYHPEY EYGYRYSAVG
 51 ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVGWLY GAPSYQIVGS
 101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS GGVFADVKNY
 151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLLN IFDLYYDLAX
 201 RAGTICRQAR PHFGSSKKS SV NMAYPSCCAQ V*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 084 shows 90.5% identity over a 231 aa overlap with a predicted ORF (ORF 084.ng) from *N. gonorrhoeae*:

m084/g084

	10	20	30	40	50
m084.pep	MKQSARIKXMNQTLTYTLGICALLTF-----YHPEY EYGYRYSAVGALASVVFLLL				
	: :				
g084	MKQSARIKNMDQTLKNTLGLICALLAFCFGA AIASGYHLEY EYGYRYSAVGALASVVFLLL				
	10	20	30	40	50
	60	70	80	90	100
m084.pep	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGS ILESNPAEAREFVGNLPGSL				
g084	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGS ILESNPAEAREFVGNLPGSL				
	70	80	90	100	110
	120	130	140	150	160
m084.pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL				
g084	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMEKIAQDKDW				
	130	140	150	160	170
	130	140	150	160	180

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	180	190	200	210	220
m084 . pep	REPDAGLLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX				
g084	REPDAGLLLNIFDLYYDLAFRAGTICRQARPHFGSSKKSVMAYPPTCAQVX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 263>:

a084 . seq

```

1  ATGAAACAAT CCGCCGAAT AAAAAATATG GATCAGACAT TAAAAAATAC
51  ATTGGGCATT TGC GCGCTTT TAGCCTTTTG TTTTGGCGCG GCCATCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTATTTC TGCCGTGGGT
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCCG CTGGCTGTAT GGTGCGCCGT CTTATCAGAT AGTCGGTTCG
301 ATATTGAAA GCAATCCTGC CGAGGCGCGT GAATTGTGCG GCAATCTTCC
351 CGGGTCGCTT TATTTGTGC AGGCATTATT TTTCATTTT GCCTTGACAG
401 TTTGGAGATA TTGTGTATCG GGGGGGGTAT TTGCTGACGT AAAAACTAT
451 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTG
501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTTC CGAGAACCTG
551 ATGCCGGCCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTTGGCTTCC
601 .GCGCCGGCA CAATATGCCG CCAAGCGCGC CCACATTTG GAAGCAGCAA
651 AAAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 264; ORF 084.a>:

a084 . pep

```

1  MKQSARIKMN DQTLKNTLGI CALLAFCFGA AIASGYHLEY EGYRYSAVG
51  ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVGWLY GAPSYQIVGS
101 ILESNPAEAR EFGVNLPGSL YFVQALFFIF GLTVWRYCVS GGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLN IFDLYYDLAS
201 XAGTICRQAR PHFGSSKKSVMAYPSCCAQ V*

```

m084/a084 92.2% identity over a 231 aa overlap

	10	20	30	40	50	60
m084 . pep	MKQSARIKXMNQTLTYLGICALLTFXXXXXXXHYPEYEGYRYSAVGALASVVFLLL					
	: :					
a084	MKQSARIKNMDQTLKNTLGICALLAFCFGAAIASGYHLEYEGYRYSAVGALASVVFLLL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m084 . pep	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILES NPAEAREFVGNLPGSL					
a084	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILES NPAEAREFVGNLPGSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m084 . pep	YFVQALFFIFGLTVWKYCVS GGVFADVKNYKRRSKIWL TILLTLILSCAVMDKIASDKDL					
a084	YFVQALFFIFGLTVWRYCVS GGVFADVKNYKRRSKIWL TILLTLILSCAVMDKIASDKDL					
	130	140	150	160	170	180
	190	200	210	220	230	
m084 . pep	REPDAGLLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
a084	REPDAGLLLNIFDLYYDLASXAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 265>:

g085 . seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGCGACCGT TGAAAGATAA

```



```

51  GGCAAAAGGC GTGTTCTGA TCGGCGTCGA TCGCGCCGCA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AACCTGACCG ACTGCGTCAC TTTGGAAGAG
151 GCGGTTTCAGA CGGCATACGC CCAAGCCGAA GCGGGCGATA TTGTCTTGCT
201 CAGCCCCGCC TCGCGGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT tatCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 266; ORF 085.ng>:

g085.pep

```

1  MGKGQDFTPL RDALKDKAKG VFLIGVDAPO IRRDLGCGL NLTDCVTL EE
51  AVQTAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 267>:

m085.seq

```

1  ATGGGTAAAG GGCAGGACTT CACGCCCTG CGCGATGCAC TGGTAGGCAA
51  GGCAAAAGGC GTGTTCTGA TTGGTGTGCA TCGCGCCGCA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AATATGACCG ACTGCGCCAC TTTGGGAGAA
151 GCCGTTTCAGA CGGCATATGC CCAAGCCGAA GCAGGCGATA TTGTGTTGCT
201 CAGCCCCGCC TCGCGGAGCT TTGATATGTT CAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT TATCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 268; ORF 085>:

m085.pep

```

1  MGKGQDFTPL RDALVGKAKG VFLIGVDAPO IRRDLGCGL NMTDCATL GE
51  AVQTAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 085 shows 94.7% identity over a 94 aa overlap with a predicted ORF (ORF 085.ng) from *N. gonorrhoeae*:

m085/g085

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGLNMTDCATLGEAVQTAYAQA E					
g085	MGKGQDFTPLRDALKDKAKGVFLIGVDAPOIRRDLGCGLNLTDCTVLEEAVQTAYAQA E					
	10	20	30	40	50	60
	70	80	90			
m085.pep	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
g085	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 269>:

a085.seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGGACGCGC TTGCCGCGCA
51  GGCAAAAGGC GTGTTCTGA TCGGTGTGCA TCGCGCCGCA ATCCGCCGCG
101 ATTTGGACGG CTGCGATCTG AATATGACCG ACTGCGCCAC TTTGGAAGAA
151 GCGGTTTCAGA AGGCATATGC CCAAGCCGAA GCGGGCGATA TCGTGCTGCT
201 CAGCCCCGCC TCGCGGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT TATCGGGGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 270; ORF 085.a>:

a085.pep

```

1  MGKGQDFTPL RDALAGKAKG VFLIGVDAPO IRRDLGCDL NMTDCATL EE
51  AVQKAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

m085/a085 94.7% identity over a 94 aa overlap

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGLNMTDCATLGEAVQTAYAQA E					

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```

|||||
a085  MGKGQDFTPLRDALAGKAKGVFLIGVDAPQIRRDLDGCDLNMTCATLEEAQKAYAAQAE
      10      20      30      40      50      60
      70      80      90
m085.pep  AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX
|||||
a085  AGDIVLLSPACASFDMFKGYAHRSEVFIGAFKALX
      70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 271>:

```

g086.seq
1   ATGGTGGTGC TGATGACGGC GTTCGGCCTG CTGATGATTT ATTCGGCTTC
51  TGTGTATTTG GCATCGAAGG AAGGCGGCGA TCAGTTTTTC TATTTGACCA
101 GGCAGGCGGG GTTCGTCGTT GCCGGCCTTA TAGCGAGCGG TTTTATATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTGC
201 CTTATCCGGC CTGTTGCTGG TAGCCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTCA AGCTGGCAGT CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTTGCGCA GCATGGAAAG TTTGGGTTGG CAGTCGATTT
401 GCGGGGGGAC GGCCAACCTG ATTATGTCCG CCACCAATCC GCAGGCACGT
451 CGTGAAACAT TAGAAATGTA CGGCGGTTTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTTCC
551 GTTCGTTTGT CGTCATTACC GTCATTACCG TTGGAATGCT GTTCTGCGCA
601 GGATTGCCGT GGAAATATTT TTTTGTCTCG GTAGGCAGCG TCTTGGGTGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTTGGA CCCGTGAAA GACCCGAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGTTTCGGTA TGGGTTTGGG
801 TCGGAGTTTG AGCAAACGCG GCTTCTGCCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCTGAA GAATTCGGCT TCTTCGGGAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTTCCA TCGGCAAGCA
951 GLPCGCGCAT TTGGGtttgA CTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CGGTATCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA CCAAAGGTCT GACGctgCcg tTGATGTCCT ATGGcggTTC
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTTG CGTATCGATT
1151 ATGAAAACCG CCAGAAAATG CGCGGTTACC GGGTGGAGTA AA

```

This corresponds to the amino acid sequence <SEQ ID 272; ORF 086.ng>:

```

g086.pep
1   MVVILMTAFGL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGFLW
51  FLCRMRTWRR LVPWIFALSG LLLVAVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTREE VLRSMESLGW QSIWRGTANL IMSATNPQAR
151 RETLEMYGRF RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VITVGMFLFA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDLPWK DPQGAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGWLVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGIQ SFFNIGVNIG
351 ALPTKGLTLP LMSYGGSSVF FMLISMMLLL RIDYENRQKM RGYRVE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 273>:

```

m086.seq
1   ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATTT ATTCGGCTTC
51  TGTGTATTTG GCATCAAAAG AAGGCGGCGA TCAGTTTTTC TATTTGACCA
101 GACAGGCGGG GTTCGTCGTT GCCGGCTTGA TAGCGAGCGG TTTGTTATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTGC
201 CCTATCCGGC CTGTTGCTGG TAGTCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTCA AGCTGGCGGT CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTTGcGCA GCATGGAAAG TTTGGGTTGG CAGTCGATTT
401 GCGGGGGGAC GGCCAATCTG ATCATGTCCG CCACCAATCC GCAGrCACGT
451 CGTGAAaACAT TAGAAATGTA CGGCGGTWTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTTCC

```

```

551 GTTCGTTTGT CGTCATTACC GTCATTGCCG TTGAATGCT GTTTTGGCA
601 GGATTGCCGT GGAAATATTT TTTCGTCTCG GTAGGCAGCG TCTTGGGCGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTGGGA CCCGTGAAA GACCCGCAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTTGGG
801 TCGGAGTTTG AGCAAACGCG GCTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCCGAA GAATTCGGTT TCTTCGGTAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGTTTGA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CGGkrTCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA mCAAAGyCT GACGCyGCCG Tg.AtGTCCw ATGGCGGTTC
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTkG CGTATAGATT
1151 ATGAAAACCG CCGGAAAATG CGCGGTATC GGGTGGAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 274; ORF 086>:

```

m086.pep
1  MVVLMTAFSL LMIYSASVYL ASKEGGDOFF YLTRQAGFVV AGLIASGLLW
51  FLCRMRTWRR LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTREE VLRSMESLGW QSIWRGTANL IMSATNPQXR
151 RETLEMYGRX RAIILPIMLV AFGLVLIMVQ PDFGSFVVIT VIAVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK DPQAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGLVVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGXQ SFFNIGVNIG
351 ALPKKGLTXP XMSXGSSVF FMLISMMLLX RIDYENRRKM RGYRVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 086 shows 96.7% identity over a 396 aa overlap with a predicted ORF (ORF 086.ng) from *N. gonorrhoeae*:

m086/g086

	10	20	30	40	50	60
m086.pep	MVVLMTAFSLLMIYSASVYLASKEGGDOFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
g086	MVVLMTAFGLLMIYSASVYLASKEGGDOFFYLTRQAGFVVAGLIASGLWFLCRMRTWRR					
	10	20	30	40	50	60
m086.pep	70	80	90	100	110	120
	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLFLKAVILYLASLFTREE					
g086	LVPWIFALSGLLLVAVLIAGREINGATRWIPLGPLNFQPTLFLKAVILYLASLFTREE					
	70	80	90	100	110	120
m086.pep	130	140	150	160	170	180
	VLRSMESLGWQSIWRGTANLIMSATNPQXRRETLEMYGRXRRAIILPIMLVAFGLVLIMVQ					
g086	VLRSMESLGWQSIWRGTANLIMSATNPQARRETLEMYGRFRAIILPIMLVAFGLVLIMVQ					
	130	140	150	160	170	180
m086.pep	190	200	210	220	230	240
	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFDPWK					
g086	PDFGSFVVITVITVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFDPWK					
	190	200	210	220	230	240
m086.pep	250	260	270	280	290	300
	DPQAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIEEFGFFGMCVL					
g086	DPQAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIEEFGFFGMCVL					
	250	260	270	280	290	300
	310	320	330	340	350	360

```

a086.seq
1      ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATTT ATTCGGCTTC
51     TGTGTATTTG GCATCAAAAG AAGGCGGCGA TCAGTTTTTC TATTTGACCA
101    GACAGGCGGG GTTCGTCGTT GCCGCGTTGA TAGCGAGCGG TTTGTTATGG
151    TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTCG
201    CCTATCCGGC CTGTTGCTGG TAGTCGTATT GATTGCCGGG CGCGAAATCA
251    ATGGCGCGTA CCGTTGGATA CCTTTGGGTC GTTGAATTTT CCAGCCGACC
301    GAGCTGTCCA AGCTGGCGGT CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351    CCGTGAAGAA GTGTTGCGCA GCATGGAAG TTTGGGTTGG CAGTCGATTT
401    GGCGGGGGAC GGCCAATCTG ATCATGTCCG CCACCAATCC GCAGGCACGT
451    CGTGAACAT TAGAAATGTA CGGCCGTTTC CCGCCGATAT TCCTGCCGAT
501    TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTTTC
551    GTTCGTTTGT CGTCATTACC GTCAATTGCC TTGGAATGCT GTTTTTGGCA
601    GGATTGCCGT GGAATATATT TTTTCGTCCT GTAGGCAGCG TCTTGGGCGG
651    GATGGTCCGT ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701    CATTTTGGGA CCGGTGGAAG GACCCGAGG GTGCCGGCTA CCAGCTTACC
751    CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTTGGG
801    TGCAGATTTG AGCAAACGCG GCTTTCTGCC GGAAGCGCAT ACCGATTTTA
851    TTTTGGCTAT CATCGCCGAA GAATTCCGGT TCTTCGGTAT GTGCGTGCTG
901    ATATTCTGTT ACGGTGGCTT GGTGGTGCGG GCGTTTTCCT TCGGCAAGCA
951    GTCCGCGCAT TTGGGTTTGA CTTTC AACGCG CTATATCGCT TCGGGTATCG
1001   GCATTTGGAT CGGTATCCAA AGTTTCTTCA ATATCCGTGT GAACATCGGT
1051   GCTTTGCCGA CCAAGGTCTA GACGCTGCCG TTGATGTCTT ATGGCGGTTT
1101   GTCAGTCTTT TTCATGCTGT TACAGCATGAT GCTGTGTGTG CGTATAGATT
1151   ATGAAAACCG CCGGAAAATG CGCGGTTACC GGGTGGAGTA A

```

a086.pap

1	MVVLMTAFSL	LMIYSASVYL	ASKEGGDQFF	YLTRQAGFVV	AGLIASGLLW
51	FLCRMRTWR	LVPWIFALSG	<u>LLLVVVLIAG</u>	REINGATRWI	PLGPLNFQPT
101	ELFKLAVLY	LASLFTTRREE	VLRSMESLGW	QSIWRGTANL	IMSATNPQAR
151	RETLEMYGRF	<u>RAILPIMLV</u>	<u>AFGLVLIMVQ</u>	PDFGSFVVIT	<u>VIAVGMFLA</u>
201	<u>GLPWKYFFVL</u>	<u>VGSVLGGMVL</u>	MITAAPYRVQ	RVVAFLDPPK	DPQAGGYQLT
251	HSLMAIGRGE	WFGMGLGASL	SKRGFLPEAH	TDIFIAIIE	EFGFGMGNVL
301	<u>IFCYGILVVR</u>	AFSGTKQSRD	LGLTFNAYIA	SGDIGWIGI	FFFNIGVNI
351	<u>ALPTKGTLTP</u>	LMSYGGSSVF	FMLISMMLLL	RIDYENRRKM	RGYRVE*

	10	20	30	40	50	60
m086.pep	MVVLMTAFSLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
a086	MVVLMTAFSLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m086.pep	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLEFKLAVILYLASFTRREE					
a086	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLEFKLAVILYLASFTRREE					

277

	70	80	90	100	110	120
m086.pep	130	140	150	160	170	180
	VLRSMESL	GWQSIWRGTANLIMS	SATNPQXRRETLEMY	GRXRAILPIML	VAFGLVLIMVQ	
a086	VLRSMESL	GWQSIWRGTANLIMS	SATNPQARRETLEMY	GRFRAILPIML	VAFGLVLIMVQ	
	130	140	150	160	170	180
m086.pep	190	200	210	220	230	240
	PDFGSFVVIT	VIAVGMLFLAGL	PWKYFFVLVGS	SVLGGMVL	MITAAPYRVQ	RVVAF
a086	PDFGSFVVIT	VIAVGMLFLAGL	PWKYFFVLVGS	SVLGGMVL	MITAAPYRVQ	RVVAF
	190	200	210	220	230	240
m086.pep	250	260	270	280	290	300
	DPQGAGYQL	THSLMAIGRGEW	FGMGLGASLS	KRGFLPEA	HTDFIFAI	IAEEFGFF
a086	DPQGAGYQL	THSLMAIGRGEW	FGMGLGASLS	KRGFLPEA	HTDFIFAI	IAEEFGFF
	250	260	270	280	290	300
m086.pep	310	320	330	340	350	360
	IFCYGWL	VVRAFSIGKQSR	DLGLTFNAY	IASGIGIW	IGXQSFFN	IGVNIGAL
a086	IFCYGWL	VVRAFSIGKQSR	DLGLTFNAY	IASGIGIW	IGXQSFFN	IGVNIGAL
	310	320	330	340	350	360
m086.pep	370	380	390			
	XMSXGGSS	VFEMLISM	LLXRIDYEN	RRKMRG	RYRVEX	
a086	LMSYGGSS	VFEMLISM	LLLRIDYEN	RRKMRG	RYRVEX	
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 277>:

g087.seq

```

1  ATGGGCGGTA AAACCTTTAT GCTGATGGCG GCGGGAACGG GCGGACACAT
51  TTCCAGCT CTGGCTGTGG CGGATTCATT GCGCGTGC GCATCATG
101 TAATTTGGCT GGGCAGCAAG GATTTCGATG AAGAGCGCAT CGTGCCGCAA
151 TACGGCATA GCTTGGAAC GCTGGCGATT AAAGGAATAC GCGGCAACGG
201 CATCAAACGC AAGCTGATGC TTCCGTTTAC TCTGTACAAA ACCGTCCGCG
251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGCCT CATCGGCTTC
301 GCGGTTTTTG TTACCTTTCC CGGCGGTCTG GCGGCGAAAC TCTTGGCGGT
351 GCCGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGCTTG TCCAACGCC
401 AccTGTCGCG ctGGGCGAAA CGGGTGTTGT ACGCTTTTCC GAAAGCGTTC
451 AGCCACGAAG GCGGTTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
501 CCGCCCGTG CCTGCCGAAC GCTTCCAAGG GCGCGAAGGC CGTCTGAAAA
551 TTTTGGTGGT CGGCGGCAGT TTGGGTGCGG ACGTTTGA CAAAACCGTA
601 CCGCAGGCGT TGGCACTGCT GCCTGAAGAG GTGCGCCCGC AGATGTACCA
651 CCAGTCGGGG CGTAACAAGC TGGGCAATCT TCAGGCGGAT TATGACGCGT
701 TGGGCGTGAA AGCGGAATGC GTGGAATTTA TTACCGACAT GGTGTCCGCC
751 TACCGTGATG CCGATTGGT GATTTGCCGT GCCGCGCGC TGACGATTGC
801 CGAGTTGACG GCGGCGGGC TGGGCGCGTT GTTAGTGCCG TATCCTCAGC
851 CCGTTGATGA CCATCAAACC GCCAACGCGC GTTTCATGGT GCAGGCAGAA
901 GCGGGGCTGC TGTGCGGCA AACCCAGTTG ACGGCGGAAA AACTCGCCGA
951 AATCCTCGGC AGCCTCAACC GCGAAAAATG CCTCAAATGG GCGGAAAAACG
1001 CCCGTACGTT GGCATTGCCG CACAGCGCGG ATGACGTTGC CGAAGCCGCG
1051 ATTGCGTGTG CGGCGTAAA

```

This corresponds to the amino acid sequence <SEQ ID 278; ORF 087.ng>:

g087.pep

```

1  MGGKTFMLMA GGTGGHIFPA LAVADSLRVR GHVIVLGSK DSMEERIVPO
51  YGIRLETLAI KGIRNGIKR KLMLPFTLYK TVREAQRIIR KHRVECIVIGF
101 GGFVTFPGLL AAKLLGVPIV IHEQNAVAGL SNRHLSRWAK RVLVAFPKAF
151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKTV

```

201 PQALALLPEE VRPQMYHQSG RNKLGNLQAD YDALGVKAEC VEFITDMVSA
 251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE
 301 AGLLLPQTQL TAEKLAEILG SLNREKCLKW AENARTLALP HSADDVAEAA
 351 IACAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 279>:

m087.seq
 1 ATGGGCGGTA AAACCTTTAT GCTGawkkCG GCGGGAACGG GCGGACATAT
 51 TTTCCCCGCG CTGGCGGTGG CCGATTTCATT GCGCGCGCGC GGCCATCATG
 101 TGATTTGGCT GGGCAGCAAG GATTCGATGG AAGAGCGTAT CGTGCCGCAA
 151 TACGGCATAC GCTTGGAAC GCTGGCGATT AAAGGCGTGC GCGGCAACGG
 201 CATCAAACGC AAACCTGATGC TGCCGGTTAC TTTGTATCAA ACCGTCCGCG
 251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGGCT CATCGGCTTC
 301 GCGGCTTCG TTACCTTCCC GGGCGGTTTG GCGGCGAAGC TATTATGCGT
 351 GCCGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGTTTG TCCAACCGCC
 401 ACCTGTCCGCG CTGGGCGAAG CGGGTGTTGT ACGCTTTTCC GAAAGCGTTC
 451 AGCCACGAAG GCGGCTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
 501 CCTGCCCGTG CCTGCCGAAC GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA
 551 TTTTGGTGGT CCGCGGCAGT TTGGGCGCGG ACGTTTTGAA CAAAACCGTA
 601 CCGCATGCAT TGGCTTTGCT GCGCGACAAT GCGCGTCCGC ATATGTACCA
 651 CCAATCGGGA CCGGGCAAGC TGGGCATCTT GCAGGCGnnn nnnnnnnnnn
 701 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 751 nnnGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCACG CGGTTGACGA
 801 TCACCAAACC GCCAACGCGC GTTTTATGGT GCAGGCGGAG GCGGATTGCG
 851 TGTGCGCGCA AACCAGTTG ACGGCGGAAA AACTCGCCGA GATTCTCGGC
 901 GGCTTAAACC GCGAAAAATG CCTCAAATGG GCAGAAAACG CCCGTACGTT
 951 GGCAGTGGC CACAGTGGC ACGACGTGGC GGAAGCCGCG ATTGCGTGTG
 1001 CGGCGTAA

This corresponds to the amino acid sequence <SEQ ID 280; ORF 087>:

m087.pep
 1 MGGKTFMLXX GGTGGHIFPA LAVADSLRAR GHVWLGSK DSMEERIVPO
 51 YGIRLETIAI KGVRGNGIKR KLMLPVTLYQ TVREAQRIIR KHRVECVIGF
 101 GGFVTFPGL AAKLLXVPIV IHEQNAVAGL SNRHLRWAK RVLVAFPKAF
 151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKTV
 201 PHALALLPDN ARPHMYHQSG RGKLGILQAX XXXXXXXXXX XXXXXXXXXX
 251 XAGLGALLVP YPHAVDDHQT ANARFMVQAE AGLLLPQTQL TAEKLAEILG
 301 GLNREKCLKW AENARTLALP HSADDVAEAA IACAA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 087 shows 83.9% identity over a 355 aa overlap with a predicted ORF (ORF 087.ng) from *N. gonorrhoeae*:

m087/g087

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVWLGSKDSMEERIVPQYGIRLETIAI					
g087	MGGKTFMLMAGGTGGHIFPALAVADSLRVRGHHVWLGSKDSMEERIVPQYGIRLETIAI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m087.pep	KGVRGNGIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGLAALKLVPIV					
g087	KGIRGNGIKRKLMLPFTLYKTVEAQRIIRKHRVECVIGFGGFVTFPGLAALKLVPIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLRWAKRVLVAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
g087	IHEQNAVAGLSNRHLRWAKRVLVAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
	130	140	150	160	170	180

279

	190	200	210	220	229
m087 . pep	RLKILVVGGSLGADVLNKTVPHALALLPDNARPHMYHQSGRGKLGILQA-----				
	: :: : :				
g087	RLKILVVGGSLGADVLNKTVPQALALLPEEVRPQMYHQSGRNKLGNLQADYDALGVKAEC				
	190	200	210	220	230
			230	240	250
m087 . pep	-----AGLGALLVPYPHAVDDHQTANARFMVQAE				
	: : :				
g087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHQTANARFMVQAE				
	250	260	270	280	290
	260	270	280	290	300
m087 . pep	AGLLLPQTQLTAEKLAEILGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX				
	: : :				
g087	AGLLLPQTQLTAEKLAEILGSLNREKCLKWAENARTLALPHSADDVAEAAIACAAX				
	310	320	330	340	350

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 281>:

a087 . seq

```

1  ATGGGCGGTA  AAACCTTTAT  GCTGATGGCG  GCGGGAACGG  GCGGACATAT
51  TTTCCCCGCG  CTGGCGGTGG  CGGATTCATT  GCGCGCGCGC  GGCCATCATG
101 TAATTTGGCT  GGGCAGCAAG  GATTTCGATG  AAGAGCGCAT  CGTGCCGCAA
151 TACGACATCC  TGCTCGAAAC  GCTGGCGATT  AAAGCGGTGC  GCGGCAACGG
201 CATCAAACGC  AAGCTGATGC  TGCCGTTTAC  TTTGTATCAA  ACTGTCCGCG
251 AAGCGCAGCA  GATTATCCGC  AAACACCGTG  TCGAGTGGCT  CATCGGCTTC
301 GCGGCTTCG  TTACCTTTCC  CGGCGGTTG  GCGGCGAAGT  TATTAGCGCT
351 GCCGATTGTG  ATTCACGAGC  AAAACGCCGT  GGCAGGTTTG  TCCAACCGCC
401 ACCTGTCGCG  CTGGGCGAAG  CGGGTGTTGT  ACGCTTTTCC  GAAAGCGTTC
451 AGCCACGAAG  GCGGCTTGGT  CGGCAACCCC  GTCCGCGCCG  ATATTAGCAA
501 CCTGCCCGTG  CCTGCCGAAC  GCTTCCAAGG  GCGTGAAGGC  CGTCTGAAAA
551 TTTTGGTGGT  CGGCGGCAGT  TTGGGCGCGG  ACGTTTGTAA  CAAAACCGTA
601 CCGCAGGCAT  TGGCTTTGCT  GCCCGACAAT  GCGCGTCCGC  AGATGTACCA
651 CCAATCGGGA  CGGGGCAAGC  TGGGCAGCTT  GCAGGCGGAT  TACGACGCGC
701 TGGGCGTGCA  AGCGGAATGC  GTGGAATTTA  TTACCGATAT  GGTGTCCGCC
751 TACGCGGATG  CCGATTGGT  GATTTGCCGT  GCCGCGCGCG  TGACGATTGC
801 CGAGTTGACG  GCGGCGGGAT  TGGGTGCGTT  GTTAGTGCCG  TATCCTCAGC
851 CCGTTGATGA  CCATCAAACC  GCCAACGCGC  GTTTATGGT  GCAGGCGGAG
901 CGGGATTGTC  TGTGCGGCA  AACCCAGTTG  ACGGCGGAAA  AACTCGCGGA
951 GATTCTCGGC  GGCTTAAACC  GCGAAAAATG  CCTCAAATGG  GCAGAAAACG
1001 CCCGTACGTT  GGCAGTCCG  CACAGTGCGG  ACGACGTTGC  CGAAGCCGCG
1051 ATTGCGTGTG  CGGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 282; ORF 087.a>:

a087 . pep

```

1  MGGKTFMLMA  GGTGGHIFPA  LAVADSLRAR  GHVIVLWLSK  DSMEERIVPQ
51  YDILLETLAI  KGVNRNGIKR  KLMLPFTLYQ  TVREAQQIIR  KHRVECVIGF
101 GGFVTFPGGL  AAKLLGVPIV  IHEQNAVAGL  SNRHLSRWAK  RVLVYAFPKAF
151 SHEGGLVGNP  VRADISNLPV  PAERFQREG  RLKILVVGGS  LGADVLNKTVP
201 QALALLPDN  ARPQMYHQSG  RGKLGSLQAD  YDALGVQAE  VEFITDMVSA
251 YRDADLVICR  AGALTIAELT  AAGLGALLVP  YPHAVDDHOT  ANARFMVQAE
301 AGLLLPQTQL  TAEKLAEILG  GLNREKCLKW  AENARTLALP  HSADDVAEAA
351 IACAA*

```

m087/a087 85.4% identity over a 355 aa overlap

	10	20	30	40	50	60
m087 . pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVIVLWLSKDSMEERIVPQYGIRLETIAI					
	: : :					
a087	MGGKTFMLMAGGTGGHIFPALAVADSLRARGHHVIVLWLSKDSMEERIVPQYDILLETIAI					
	10	20	30	40	50	60

280

	70	80	90	100	110	120
m087.pep	KGVRRNGIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVPIV					
a087	KGVRRNGIKRKLMLPFTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLGVPIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQGREG					
a087	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQGREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m087.pep	RLKILVVGSLGADVLNKTVPHALALLPDNARPHMYHQSGRGKLGILQAXXXXXXXXXXX					
a087	RLKILVVGSLGADVLNKTVPQALALLPDNARPMYHQSGRGKLGSLQADYDALGVQAE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m087.pep	XX-----XXXXXXXXXAGLGALLVPYPHAVDDHQTANARFMVQAE					
a087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHQTANARFMVQAE					
	250	260	270	280	290	300
	290	300	310	320	330	
m087.pep	AGLLLPQTQLTAEKLAIEILGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
a087	AGLLLPQTQLTAEKLAIEILGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 283>:

```

g088.seq
1  ATGTTTATAT  GGCTCGCACA  TTTTCAGCAAC  TGGTTAACCG  GTCTGAATAT
51  TTTTCAATAC  ACCACATTCC  GCGCCGTTAT  GCGCGCGTTG  ACCGCCTTGG
101 CGTTTTCCTT  GATGTTTCGG  CCGTGGACGA  TACGCAGGCT  GACCGCGCTC
151 AAATGCCGGC  AGGCAGTGCG  TACCGACGGC  CCGCAAACCC  ACCTCGTCAA
201 AAACGGCAGC  CCGACGATGG  GCGGTTTCGG  GATTCTGACC  GCCATTACCG
251 TGTCCACCCT  GTTGTGGGGC  AACTGGGCGA  ACCGATATAT  CTGGATTCTC
301 TTGGGCGTAC  TGCTTGCCAC  CGGTGCGCTC  GGTTTTACG  ACGACTGGCG
351 CAAAGTCGTT  TATAAAGACC  CCAACGGCGT  GTCCGCCAAA  TTCAAATGG
401 TGTGGCAGTC  AAGCGTTGCC  GTTatcgCG  GTttggcATT  GTTTTACctt
451 gCcgCcaATT  CCGCAACAA  TATTTTGATT  GTCCCGtttT  TCAAACAAAT
501 CGCCCTGCGG  CTGGGCGTGG  TCGGCTtttt  gGtggtgtCT  TACCTGACCA
551 TCGTCGGCAC  ATCCAACGCC  GTCAACCTCA  CcgaCGGCTT  GGACGCGCTT
601 GCCGCcttcc  cgttcgtcct  cgttgccgcC  GGGCTCGCCA  ttttcgcctA
651 CGTCAGCGGA  CACTACCAAT  TTTCCCAATA  CCTCCAGCTT  CCCTATGTCG
701 CCGGCGCGAA  CGAAGTCGCT  ATATTCTGCA  CCGCCATGTG  CGGCGCGTGC
751 CTCGGATTTT  TGTGGTTCAA  CGCCTATCCC  GCGCAAGTCT  TTATGGGCGA
801 TGTCGGCGCG  CTGGCATTGG  GTGCCGCGCT  CGGTaccGtt  gCCGTcaTcg
851 tCCGCCAAGA  ATTTGTcctc  gtcattatGG  GCGGTCTGTT  cgtcgtagaa
901 gccgtgTCCG  TTATGCTTca  tgtcggCTGG  TACAAGAAAA  Ccaaaaaacg
951 CATCTTcCTg  acgGcaccga  ttcataacca  ttaCCaactt  cgatgCTGga
1001 aagaaaacgca  agtcgtcgtc  CGTTtCTGGA  TTAtTaccat  cgtcgtgggt
1051 tTgatagggt  tGagtaccct  caAAattcgc  ggaaactatg  ccgTCCGAAC
1101 ACCTTTCAGA  CGGCATTGA  ACGCGCAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 284; ORF 088.ng>:

```

g088.pep
1  MFLWLAHFSN  WLTGLNIFQY  TTFRAVMAAL  TALAFSLMFG  PWTIRRLTAL
51  KCGQAVRTDG  PQTHLVKNGT  PTMGGSLILT  AITVSTLLWG  NWANPYIWL
101 LGVLLATGAL  GFYDWRKV  YKDPNGVSAK  FKMVWQSSVA  VIAGLALFYL
151 AANSANNILI  VPFFKQIALP  LGVVGLVL  YLTIVGTSNA  VNLTGDLGL

```


m088.seq

1	ATGTTTTTAT	GGCTCGCACA	TTTCAGCAnC	TGGTTAACCG	GTCTGAATnn
51	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn
101	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn
151	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn
201	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn
251	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn
301	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn
351	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn
401	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn
451	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn
501	nnnnnnnnnnnn	nnnGGCGTGG	TCGGCTTTT	GGTGTGTCT	TACCTGACCA
551	TCGTGCGCAC	ATCCAATGCC	GTCAACCTCA	CCGACGGCTT	GGACGGCCTT
601	GCGACCTTCC	CCGTCGTCCT	CGTTGCCGCC	GGCCTCGCCA	TCTTCGCCTA
651	TGCCAGCGGC	CACTCACAA	TTGCCCAATA	CCTGCAATTA	CCTTACGTTG
701	CCGGCGCAAA	CGAAGTGGTG	ATTTTCTGTA	CCGCCATTGT	CGGCGCGTGC
751	CTCGGTTTCT	TGTGGTTTAA	CGCTATCCC	CGCGAAGTCT	TTATGGGCGA
801	TGTCGGTGCA	TGTGCATTGG	TGCGCGGCT	CGGTACCGTC	GCGGTTATCG
851	TCCGCCAAGA	GTTTGTCTCT	GTCATTATGG	GCGGATTATT	TGTCGTAGAA
901	GCCGTATCCG	TTATGCTTCA	GGTTGGCTGG	TATAAGAAAA	CCAAAAAACG
951	CATCTTCCTG	ATGGCGCCCA	TCCATACCA	CTACGAACAA	AAAGGCTGGA
1001	AAGAAACCCA	AGTCGTCGTC	CGCTTTTGGa	TTATTACCAT	CGTCTTGGTG
1051	TTGATCGGTT	TGAGTACCTT	CAAAATCCGC	TGAACCTATG	CCGCTCTGAAC
1101	ATCTTTCAGA	CGGCATTGTA	ACGCGCAATA	A	

```

1  MFLWLAHFSN WLTGLNIFOY TTFRVMAAL TALAFSLMFG PWTIRRLTAL
51  KCGQAVRTDG PQTHLVKNGT PTMGGSLLLT AITVSTLLWG NWANPYIWL
101 LGVLATGAL GFYDDWRKVV YKDPNGVSAK FKMVQSSVA VIAGLALFYL
151 AANSANNILI VPFFKQIALP LGVVGFVLVS YLTIVGTSNA VNLTDGLDGL
201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQ PYVAGANEVA IFCTAMCGAC
251 LGLFVFNAPY AQVFMDGVS LALGAALGTV AVIVRQEFVL VIMGGLFVVE
301 AVSVLNLHVWG YKTKTKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV
351 LIGLSTLKIR GNYAVRTPFR RHLNAQ*

```

m088.pgp

1	MFLWLAHFSX	WLTGLNXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX
51	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX
101	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX
151	XXXXXXXXXX	XXXXXXXXXX	<u>XGVVGFVLVS</u>	<u>YLTIVGTSNA</u>	<u>VNLTDLGLDGL</u>
201	<u>ATFPVVLVAA</u>	<u>GLAIFAYASG</u>	<u>HSQAQYLQL</u>	<u>PYVAGANEVV</u>	<u>IFCTAMCGAC</u>
251	<u>LGFLWFNAP</u>	<u>AQVFMGDVGA</u>	<u>LALGAALGTV</u>	<u>AVIVRQEFVL</u>	<u>VIMGGLFVVE</u>
301	<u>AVSVMLQGVW</u>	<u>YKKTKRIFL</u>	<u>MAPIHHYEQ</u>	<u>KGWKETQVVV</u>	<u>RFWIITIVLV</u>
351	<u>LIGLSTLKIR</u>	<u>XTYAVXTSFR</u>	<u>RHLNAQ*</u>		

Homology with a predicted ORF from *N.gonorrhoeae*

m088/g088

m088.pep
 GVVGFLVLSYLTIVGTSNAVNLTGDLGDLA
 |||||
 g088 IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFLVLSYLTIVGTSNAVNLTGDLGDLA
 150 160 170 180 190 200

	40	50	60	70	80	90
m088.pep	TFPVVLVAAGLAI FAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGFLWFNAYPA : : : :					
g088	AFPFFVLVAAGLAI FAYVSGHYQFSQYLQLPYVAGANEVAIFCTAMCGACLGFLWFNAYPA 210 220 230 240 250 260					
	100	110	120	130	140	150
m088.pep	QVFMGDVGALALGAALGTVAIVIRQEFVLVIMGGLFVVEAVSVM LQVGWYKTKKRIFLM :					
g088	QVFMGDVGALALGAALGTVAIVIRQEFVLVIMGGLFVVEAVSVM LHVGVWYKTKKRIFLT 270 280 290 300 310 320					
	160	170	180	190	200	
m088.pep	APIHHH YEQKGWKETQVVVRFWIITIVLV LIGLSTLKIRXTYAVXTSFRRHLNAQX : :					
g088	APIHHHYQLRCWKETQVVVRFWIITIVVVLIGLSTLKIRGN YAVRTPFRRHLNAQX 330 340 350 360 370					

```
a088.seq
1 ATGTTTTTTAT GGCTCGCAC A TTT CAGCAAC TGGTTAACCG GTCTGAATAT
51 TTTTCAATAC ACCACATTCC CGGCCGTCAT GGC CGCGCTTG ACCGCGCTTG
101 CGTTTTTCCCT GATGTTTCGGC CCGTGGACGA TACG CAGCGCT GACCGCGCTG
151 AAATCGCGGC AGGCAGTGCG TACCGACGGT CCGCAAACCC ACCTCGTCAA
201 AAACGGCAGC CCGACGATGG GCGGTTGCT GATTCTGACC GCCATTACCG
251 TGTCCACCCT GTTGTGGGGC AACTGGGCAA ACCCGTATAT CTG GATTCTC
301 TTGGCGGTAT TGCTCGCCAC GGGCGCACT GGTTTTTACG ACAGCTGGCG
351 CAAAGTCGTC TATAAAGACC CCAACGGCGT GTCCGCCAAA TTCAAATGG
401 TGTGGCAGTC AAGCGTTGCC ATTATCGCCG GTTTGGCATT GTTTTACCTT
451 GCCGCCAATT CCGCCAACAA TATTTTGATT GTCCCGTTCT TCAAACAAAT
501 CGCCCTGCGC CTGGGCGTGG TCGGCTTTTT GGTGTTGTCT TACCTGACCA
551 TCGTCGGCAC ATCCAACTGC GTCAACCTCA CCGACGGCTT GGACGGCCTT
601 CGGACCTTCC CCGTCGTCT CTGTGCCGCC GGCCTTGCCA TCTTCGCTTA
651 TGCCAGCGGC CACTCACAAT TTGCCAATA CCTGCAATTA CCTTACGTTG
701 CCGGCGCAAA CGAAGTGGTG ATTTTCTGTA CCGCATGTG CGGCGCGTGC
751 CTCGGTTTCT TGTGGTTTAA CGCCTATCCC GCGCAAGCTT TTATGGGCGA
801 TGTCCGTGCA TTGGCATTGG GTGCCGCGCT CGGTACCGCT CGCGTCACTG
851 TCCGCCAAGA GTTTGTCTTC GTCAATTATG GCGGATTATT TGTCGTAGAA
901 GCGGTATCCG TTATGCTTCA GGTGCGCTGG TATAAGAAAA CCAAAAAACG
951 CATCTTCCCTG ATGGCGCCCA TCCATCACCA CTACGAACAA AAAGGCTGGA
1001 AAGAAACCCA AGTCGTCGTC CGCTTTTGGA TTATTACCAT CGTCTTGGTG
1051 TTGATCGGTT TGAGTACCCT CAAATCCGC TGAACCTATG CCGTCTGAAC
1101 ACCTTTCAGA CGGCATTTGA ACGCGCAATA A
```

```
a088.pap
  1  MFLWLAHFSN  WLTGLNIFQY  TTFRAVMAAL  TALAFLMFG  PWTIRRLTA
51  KCGQAVRTDG  PQTHLVKNGT  PTMGGSLLT  AITVSTLLWG  NWANPYYIWL
101 LGVLLATGAL  GFYDLWRKVV  YKDPNGVSAK  FKMVQSSVA  ILAGLALFYL
151 AANSANNILI  VPFQKIALP  LGVVGFVLVS  YLTIVGTSNA  VNLTGDLGL
201 ATFPVVLVAA  GLAIFAYASG  HSQFAQYLQL  PYVAGANEV  IFCTAMCGAC
251 LGFLWFNAYP  AQVEMGDVGA  LALGAALGT  AVIVRQEFVL  VIMGGFLFVE
301 AVSVMLQVGW  YKKTKKRIFL  MAPIHHHYEQ  KGWKETQVVV  RFWIITIVLV
351 LIGLSTLKR  *TYAV*TPFR  RHLNAQ*
```

```

                150      160      170      180      190      200
m088.pep  XXXXXXXXXXXXXXXXXXXXXXXXXXXXGVVGFLVLSYLTIVGTSNAVNLTGDLGLA
                |||
a088      IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFLVLSYLTIVGTSNAVNLTGDLGLA

```

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	150	160	170	180	190	200
	210	220	230	240	250	260
m088.pep	TFPVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVFCTAMCGACLGFLWFNAYPA					
a088	TFPVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVFCTAMCGACLGFLWFNAYPA					
	210	220	230	240	250	260
	270	280	290	300	310	320
m088.pep	QVFMGDVGALALGAALGTVAIVRQEFVLVIMGGFVVEAVSVMLOVGWYKTKKRIFLM					
a088	QVFMGDVGALALGAALGTVAIVRQEFVLVIMGGFVVEAVSVMLOVGWYKTKKRIFLM					
	270	280	290	300	310	320
	330	340	350	360	370	
m088.pep	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLHNAQX					
a088	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLHNAQX					
	330	340	350	360	370	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 289>:

g089.seq

```

1  ATGCCGCCCA AAATCACGAA GAGCGGGTTT TGCAAACCGG CAATCGCGGC
51  GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATG AATACCACGC
101 CGTTTTTCTC GCCGATTTT TCCACACGGT GCGGCAAGCC TTGAAGGTT
151 TTGACGTGTT CCAGCAATGC TTCGCGCGGC AAACCGACGG CCTCGCACAA
201 AGCCACGGCA GCCATAACGT TGGCGGCGTT GTGCAAACCT TGCAGCGGGA
251 TGTCTTGCGT AGAAATCAAA TCTTCATTGC CTTGTTTAA ACAGCCCGTC
301 CCGCGTTCCA ACCAAAAATC GGCTTCGTGT TCCAAGGAAA ACCGTTTCAC
351 TTCACGCCCT GCCCGTTTCA TGGCGCGGCA GAACACGTCG TCCGCATTCA
401 AAACCTGCAC TCCATCGCCA CGGAAATCT CGGCTTTGGT ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 290; ORF 089.ng>:

g089.pep

```

1  MPPKITKSGF CKPAIAAAVA PTFVPLLSSM NTTPFFSPIF STRCGKPWKV
51  LTCSSNASRG KPTASHKATA AITLAALCKP CSGMSCVEIK SSLPCFKQPV
101 PRSNQKSASC SKENRFTSRP ARFMARQNTS SAFKCTPSP RKISALVCA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 291>:

m089.seq

```

1  ATGCCGCCCA AAATCACKAw GAGCGGATTT TGCAAACCGG CAATCGCGGC
51  GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATA AACACCACGC
101 CGTTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC TTGAAGGTT
151 TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG CCTCACACAA
201 AGCCACKGCA GCCATGACGT TAGCGGCGTT GTGCAKACCT TGCAACGGwA
251 TGTCTTGCGT GACAATCAAA TCTTCATTGC CTTGTTTCAG GCGGCCTGTC
301 TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA ACCATTTTAC
351 CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG TCCGCATTCA
401 AAACCTGCAC GCCGTCGCCA CGGAAATCT TGGCTTTGGT ATGCGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 292; ORF 089>:

m089.pep

```

1  MPPKITXSGF CKPAIAAAVA PTFVPLLSSI NTTPFFSPIF STRCGRPWKV
51  LTCSSNASRD KPMASHKATA AMTLAALCXP CNGMSCVTIK SSLPCFRRPV
101 SRSNQKSASC SNENHFTSRP ARFIARQNAS SAFKCTPSP RKILALVCA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 089 shows 88.6% identity over a 149 aa overlap with a predicted ORF (ORF 089.ng)

from *N. gonorrhoeae*:

m089/g089

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	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTT PFFSPIFSTRCGRPWKVLTCSSNASRD					
	: : : : :					
g089	MPPKITXSGFCKPAIAAAVAPT FVPLLSSMNTT PFFSPIFSTRCGRPWKVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRSNQKSASCSNENHFTSRP					
	: : : : : : : : :					
g089	KPTASHKATAAITLAALCKPCSGMSCVEIKSSLPCFKQFVPRSNQKSASCSKENRFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	: : : : :					
g089	ARFMARQNTSSAFKTCTPSPRKISALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 293>:

a089.seq

```

1  ATGCCGCTA AAATCACGAA GAGCGGATTT TGCAAACCGG CAATCGCGGC
51  GGCGGTGCGA CCGACGTTTC TGCCTTTGCT GTCGTCGATG AACACCACGC
101 CATTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC TTGAAAGGTT
151 TTGACGTGTT CGAGCAATGC TTCGCGCGGC AAACCGACGG CTTGCGACAA
201 GGCAACGGCA GCCATCACGT TAGTGCGGTT GTGCAAGCCT TGCAGCGGAA
251 TATCTTGCGT GGCAATCAAA TCTTCATTGC CTTGTTTCAG GCGACCTGTC
301 TCACGTTCCA ACCAAAAATC GGCTTCGTAT TCCAACGAAA ACCATTTCAC
351 CTCGCGCCCG GCGCGCTTCA TCGCACGACA GAACGCATCG TCCGCATTCA
401 AAACCTGCAC ACCGTCGCCA CGGAAAATCT TGGCTTTGGT ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 294; ORF 089.a>:

a089.pep

```

1  MPPKITXSGF CKPAIAAAVA PTFVPLLSSM NTTPFFSPIF STRCGRP*KV
51  LTCSSNASRG KPTASHKATA AITLVALCKP CSGISCVAIK SSLPCFRRPV
101 SRSNQKSASY SNENHFTSRP ARFIARQNAS SAFKTCTPSP RKILALVCA*

```

m089/a089 91.9% identity over a 149 aa overlap

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTT PFFSPIFSTRCGRPWKVLTCSSNASRD					
	: : : : :					
a089	MPPKITXSGFCKPAIAAAVAPT FVPLLSSMNTT PFFSPIFSTRCGRPWKVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRSNQKSASCSNENHFTSRP					
	: : : : : : : : :					
a089	KPTASHKATAAITLVALCKPCSGISCVAIKSSLPCFRRPVSRSNQKSASYSNENHFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	: : : : :					
a089	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 295>:

g090.seq

```

1  ATGCGCGTAG TCGAGCAAAT CGTCGTAGCG GTCGAGATGG TCTTCGAA

```

q090.pcp

1 MRVVEQIVVA VEMVFGNVHH RRRSRAQAFG VFQLEAGKLP HPHVRLFAFA
51 LQFCLQDGR TDIARNDGIQP ALDAEIADQA GYRGFAVAAG NRNHLVAAAV
101 HNVROQLDVA XHAXRRFA*

m090.seq

seq	1	ATGCGCATAG	TCGAGCAAGT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGA
	51	TGTTTCAGCAC	CGTCGCGCGA	GTCGGACGCA	GGCTTTCGGT	GTTTTCCAGT
	101	TGGAAGCTGG	AAAGCTCCAA	CACCCACACG	TCGCGCTTTT	TGCCTTCGCG
	151	CTGCCATTCC	GCCTCAAAA	CCGGCGTGCC	GATATTGCC	GCGATAACGG
	201	TATCCAGCCC	GCACTTGATA	CAGAGATAGC	CGACCAGGCT	CGTTACCGTG
	251	GTTTTGCCGT	TGCTGCCGGT	AATCGCAATT	ACCTTGTCGT	CCCGCGGGT
	301	CACAATTGCC	GCCAGCAATT	CGATGTCGCC	CAACACGCGT	.CCGCGGTTT
	351	TGCTTGA				

м090. пер

1 MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA
51 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NRRNYLVVPAV
101 HNVROOFDVA OHAXRFFA*

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 090 shows 83.9% identity over a 118 aa overlap with a predicted ORF (ORF 090.ng) from *N. gonorrhoeae*:

m090/g090

	10	20	30	40	50	60
m090.pep	MRIVEQVVAVEMVFGNVQHRRRSRTQA	FGVFQLEAGKLQHPHVRLFAFALP	FRLQNRA			
	: :	:	:	:	:	: :
g090	MRVVEQIVVAVEMVFGNVHRRRSRAQ	AFGVFQLEAGKLPHPHVRLFAFALO	FCLQDGR			
	10	20	30	40	50	60
	70	80	90	100	110	119
m090.pep	DIARDNGIQPALDTETADQARYRGFAVAAGNRN	YLVVPVAVHNVRQQFDVAQHAXRRFX				
	: :	:	:	:	:	:
g090	DIARNDGIQPALDAEITADQAGYRGFAVAAGNRNHLVAAAHNV	RQLDVAXHAXRRFX				
	70	80	90	100	110	

a090.seq

seq	1	51	101	151	201	251	301	351
	ATGCGCGTAG	TCGAGCAAGT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGA	AA		
	TGTTTCAGCAC	TGTCGCCGCA	GTCGGGCGCA	GGCTTTCCGT	GTTTTCAGT			
	TGGAAACTGG	AAAGCTCCAA	CACCCACACG	TCCGCCTTTT	TGCCCTCGCG			
	CTGCAATTCC	GCCTCCAAAA	CCGGCGCGCC	GATATTGCC	GCGATAACGG			
	TATCCAGCCC	ACACTTGATG	CAGAGATAGC	CGACCAGGCT	CGTTACCGTG			
	GTTTTCGGCT	TGCTGCCGGT	AATCGCAATC	ACCTTGTCGC	CGCGGCGGTT			
	CACAATGTCC	GCCAGCAATT	CGATGTCGCC	CAACACGCGT	C. CGCCGTTT			
	CGCTTAA							

This corresponds to the amino acid sequence <SEQ ID 300; ORF 090.a>:

a090.pep

1 MRVVEQVVVA VEMVFGNVQH CRRSRAQAFG VFQLETGKLQ HPHVRLFAFA
 51 LQFRLQNRRA DIARDNGIQP TLDAEIADQA RYRGFAVAAG NRNHLVAAA
 101 HNVRRQFDVA QHAXRRFA*

m09/a090 91.5% identity over a 117 aa overlap

	10	20	30	40	50	60
m090.pep	MRIVEQVVVA	VEMVFGNVQH	RRRSRTQAF	GVFQLEAGKLQ	HPHVRLFAF	ALPFRQLQNRRA
a090	MRVVEQVVVA	VEMVFGNVQH	CRRSRAQAF	GVFQLETGKLQ	HPHVRLFAF	ALQFRLQNRRA
	10	20	30	40	50	60

	70	80	90	100	110	119
m090.pep	DIARDNGIQP	ALDTEIADQA	RYRGFAVAAG	NRNHLVVP	PAVHNVRRQ	QFDVAQHAXRRFAX
a090	DIARDNGIQP	TLDAEIADQA	RYRGFAVAAG	NRNHLVAAA	VHNVRRQ	QFDVAQHAXRRFAX
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae*

g090-1.seq This sequence contains multiple stop codons (not shown)

This corresponds to the amino acid sequence < ORF 090-1.ng>:

g090-1.pep (not shown)

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2>:

m090-1.seq

1 ATGACGGCGT TTGCATTCA GACGGCATCA CAAAGCCTTA AACGCTTCGA
 51 TAAACACTTC CGAACGGTGC GCGTAGCCTT TGAACATATC AAAGCTCGCG
 101 CAGGCGGGGC TGAGCAACAC AATATCGCCT GCTTCGGCTT GGGCATATGC
 151 CGTCTGAACG GCTTCTCCCA AAGTGGCGCA GTCGGTCATA TTCAAGCCGC
 201 AGCCGTCCTA ATCGCGGCGG ATTTGCGGCG CATCGACACC AATCAAGAAC
 251 ACGCCTTTTG CCTTGCCTAC CAGTGCAATCG CGCAGGGGCG TGAAGTCCCTG
 301 CCCTTTACCC ATGCCGCCCA AAATCACGAA GAGCGGATTT TGCAAACCGG
 351 CAATCGCGGC GGCAGTCGCG CCGACATTCTG TGCCTTTGCT GTCGTCGATA
 401 AACACCAACG CGTTTTTCTC GCCGATTTTT TCCACGCGGT GCGGCAGGCC
 451 TTGGAAGGTT TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG
 501 CCTCACACAA AGCCACGGCA GCCATGACGT TAGCGCGGTT GTGCAGACCT
 551 TGCAACGGAA TGTCTTGCCT GACAATCAAA TCTTCATTGC CTTGTTTTCAG
 601 CGGCGCTGTC TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA
 651 ACCATTTTAC CTGCGCGCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG
 701 TCCGCATTCA AAACCTGCAC GCCGTCGCCA CGGAAAATCT TGGCTTTGGT
 751 ATGCGCATAG TCGAGCAAGT CGTCGTAGCG GTCGAGATGG TCTTCGGAAA
 801 TGTTCAGCAC CGTCGCCGCA GTCGGACGCA GGCTTTCGGT GTTTTCCAGT
 851 TGGAGGCTGG AAAGTCCCAA CACCACACG TCCGCTTTT TGCCTTCGCG
 901 CTGCCATTCC GCCTCCAAA CCGCGGTGCC GATATTGCC GCGATAACGG
 951 TATCCAGCCC GCACTTGATA CAGAGATAGC CGACCAGGCT CGTTACCGTG
 1001 GTTTTGCCGT TGCTGCCGGT AATCGCAATT ACCTTGTCGT CCCGGCGGTT
 1051 CACAATGTCC GCCAGCAATT CGATGTCGCC CAACACGCGT CCGCCGTTTT
 1101 GCTTGAACGC CTCAATATCC GGCTGCCGCT CGCTGATGCC GGGACTGAGA
 1151 GCCAGAATAT CGAAACCGTT GTCCAGCGCA TCTTTCAGAC GGCCCGTGTA
 1201 AAACACCAAC CCGTCAAACA TCTTACCGAT TTGCGACACG CGTTCCGGCT
 1251 TCAGCTCCGC ATCATACGCA GCAACCTCCG CGCCGTTTT GCGCAGGTAG
 1301 GCAATCATGG AAATACCGT ACCGCCGAGT CCGCGACGA GGATTTTTTT
 1351 GTTTTGAAAA GTCATTTTGG TTTGTCCTAA

This corresponds to the amino acid sequence <SEQ ID 3; ORF 090-1>:

m090-1.pep

1 MTAFAFQTAS QSLKRFDKHF RTVRVAFEH KARAGGAEQH NIACFGLGIC
 51 RLNGFSQSGA VGHIAAAVQ IAADLRRI DT NOEHAFCLAY QCIAQGREVL
 101 PFTTHAAQNH ERILOTGNRG GSRADIRAF VVDKHHAVFL ADFPHAVRQA
 151 LEGFDVFEQC FARQTDGLTQ SHGSHDVSGV VQTLQNVLR DNQIFIALFQ
 201 AACLAFOPEI SPVFQRKPFY LAPGTLHRAA ERIVRIQNLH AVATENLGFQ
 251 MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA
 301 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NRNHLVVP
 351 HNVRRQFDVA QHASAVLLER LNIRLPLADA GTESQNIETV VQRIQVTPARV
 401 KHQPVKHLR LRHAFRLQLR IIRSNLRAVF AQVGNHGNTR TAESGDEDFD
 451 VLKSHFGLS*

This corresponds to the amino acid sequence <SEQ ID 304; ORF 091.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 305>:

This corresponds to the amino acid sequence <SEQ ID 306; ORF 091>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 091 shows 84.2% identity over a 101 aa overlap with a predicted ORF (ORF 091.ng) from *N. gonorrhoeae*:

m091/g091

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 307>:

```
a091.seq
1  ATGGAATAC  CCGTGCCGCC  AAGTCCGCGC  ACGAGGATT  TTTTGTTTG
51  GAAATCATT  TGGTTTGTC  TAAACAATAT  CATATTGAG  AGGGGATGC
101 TGATCCTGT  CAAGCCGCT  TCAGACGCA  TCGCGAGCT  TTCAATAAC
151 CGCTTTCAG  CGTTGGTCA  TGTGCGAGCT  GTCTTGGTA  CCGTTTTGAC
201 AAGCCTTGC  AAGCCATTCT  TGTGCAAGGG  CGCGGTCTT  GCGCACGCC
251 CGTCCTTCG  CATACTAC  GCCCAATTG  TTTTGGGC
```

This corresponds to the amino acid sequence <SEQ ID 308; ORF 091.a>:

a091.pep

```

1  MEIPVPPSPA TRIFLEWKSF WFLVKQIILS RGCLILLKPL SDGIASCSIT
51  RFQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLG

```

m091/a091 93.8% identity over a 96 aa overlap

```

              10      20      30      40      50      60
m091.pep    MEIPVPPSPATRIFLEKSFWFVLKQIILSRRCPLPKPLSDGIASCSITRLQALVIVAA
              |||||
a091         MEIPVPPSPATRIFLEKSFWFVLKQIILSRGCLILLKPLSDGIASCSITRFQALVIVAA
              10      20      30      40      50      60

              70      80      90      100
m091.pep    VLVSVLTSLAKPFLCKGAVLAHAASFGIHHQAIVLGLGYPLR
              |||||
a091         VLVSVLTSLAKPFLCKGAVLAHAASFGIHHQAIVLG
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 309>:

g092.seq

```

1  ATGTTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGTCCGC
51  AAACGGTCAG ACCTTTAAAA TAACGCCTTT ACGCACTAAA AACCAACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTAA GCAACATCCA TTTTGTCCGT
151 ATCGGCGGCG TCGGCATGAG CGGTATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGTTCCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGAGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC AGAACACGTT
301 AACGGTgcgg ATGTCGTCGT TGCCTCTACC GCCGTCAAGA AAGAAaatcc
351 CGAAGTtgtc gcTGCgTTGG AGCGGCAAAT TCCCGTTATT CCGCGCGCCT
401 TGATGCTGGC AGAGCTGATG CGCTTCCGTG ACgGcatcgc cattgccggT
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTC GACCCCACTT TCGTTATCGG CGGCAAACTC AACGCCGCAG
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAATCCGATG CCTCTTTCCT ACATCTGACC CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTGTTGACAG CGAACACGTC CGCGCGATTT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GGC CGC GCAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGc gtggcGCTgg
1001 aagtcGgCGC ATcggttgAA GCGAtcCAA AaggCTTGCT CGGCTTTGAA
1051 GCGGTCGGCC GCCGCTTCCA AAAATAcggc gacatCAagt tgccaaacgg
1101 cggGaccgCT TTgctGGTGG ACGATTAcgg ACACCACCCC GTCGAAATGG
1151 CGGcaaccct tgccgcTGCA CGCGGCGCGT ATCCGGAAAA acgtTTGGTG
1201 CtgcCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTACTCAATA CCGTTGatGc GCTGGTACTG ACCGAAGTTT
1301 AtgccgcccG CGAAGAGCCG GTTGCCGCCG CCGactcCCG CGCCTTGGCG
1351 CGTGCTATCC GCGTATTGGG CAAACTTGAG CCGATTACT GCGAAAatgt
1401 cgccgACCTG CCGCAAATGC TGATGAATGT TTTACAGGAT Gcggatgttg
1451 tgttgAATAT GggTgcggga agcatcaacc gcgttccttc cgcgctgttg
1501 gaattgtcga AACAGAttg A

```

This corresponds to the amino acid sequence <SEQ ID 310; ORF 092.ng>:

g092.pep

```

1  MFFISIRYIF VRKLWCANGQ TFKITPLRTK NQPERNIMMK NRVSNIHFVG
51  IGGVGMGSGIA EVLHNLGFKV SGSDQARNAA TEHLSSLGIQ VYPGHTAEHV
101 NGADV VVAST AVKENPEVV AALERQIPVI PRALMLAELM RFRDGIALAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK

```



```

251 AFLCVDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP VAAADSRALA
451 RAIRVLGKLE PIYCENVADL PQMLMNVLQD GDVVLNMGAG SINRVPSALL
501 ELSKQI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 311>:

```

m092.seq
1 ATGTTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGCGCGC
51 AAACGGTCAG CCCTTTAAAA TAACGCCTTT ACGCATCGAA AATCCACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTTA CCAACATCCA TTTTGTGGT
151 ATCGGCGGCG TCGGCATGAG CGGCATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGTTTCGG ATCagGCGCG AAATGCCGCT ACCGAGCATT
251 TGGGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC CGAACACGTT
301 AACGGTGC GG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCTGT ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAACTC AACGCCGCGC
551 GCACTAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCGCAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTTGG AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CCGCTTTGAA
1051 GCGGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 CGGGACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CCGCGACCTT TCCCGCCGCA CGCGGCGCGT ATCTGAAAAA ACGTTTGGTA
1201 CTCGCTTCC AGCGGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTCCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCGCCG CCGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTTGAACGT TTTGCAGGAC GGCGACATCG
1451 TGTTGAATAT GGGCGCGGGA AGCATCAACC GCGTCCCGC CGCGTGCTG
1501 GCATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 312; ORF 092>:

```

m092.pep
1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFGV
51 IGGVGMGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGLAIAAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYLEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNVLQD GDIVLNMGAG SINRVPAALL
501 ALSKQI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 092 shows 96.6% identity over a 506 aa overlap with a predicted ORF (ORF 092.ng) from *N. gonorrhoeae*:

m092/g092

```

10 20 30 40 50 60
m092.pep MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFGVIGGVGMGIA

```

a092.seq

1	ATGTTTTTTA	TTTCAATCCG	CTATATATTT	GTCAGAAAAC	TATGGCGCGC
51	AAACGGTCAG	CCCTTTAAAA	TAACGCCTTT	ACGCATCGAA	AATCCACCGG
101	AACGCAACAT	TATGATGAAA	AATCGAGTGA	CCAACATCCA	TTTTGTGGT
151	ATCGGCGGGC	TCGGCATGAG	CGGTATCGCC	GAAGTCTTGC	ACAATTGTGG
201	TTTTAAAGTT	TCCGTTTCGG	ATCAGGCGCG	AAATCCCGCT	ACCGAGTACG
251	TGGCGACGCT	GGGCATTCAA	GTTTATCCCG	GCCATACCGA	AGAACACGTT

```

301 AACGGTGCGG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCCTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGCG
451 ACGCAGGCA AAACACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAATC AACGCCGAG
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGT GTTGAGAAGC
701 TGCATCAGG GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTATTGACAG CGAACACGTC CGCGCGATTT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGG CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GGC GCGCAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GGTGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 TGAACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGGCGACCCT TTCCGCCGCA CGCGCGCGT ATCCGGAAAA ACGTTTGGTA
1201 CTCGCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTGGAAGA
1251 CTTTACCAA GTCTCAATA CCGTTGACGC GCTGGTGTG ACCGAAGTTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCGCCG CTGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTGGG CAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGAACGT TTTGCAGGAC GGCGACATCG
1451 TGTGAATAT GGGTCCGGA AGCATCAACC GCGTCCCCG CGCGCTGCTG
1501 GAATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 314; ORF 092.a>:

a092.pep

```

1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFGV
51 IGGVMSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGIAGIAG
151 THGKTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 VVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLSAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLNLVQD GDIVLNMGAG SINRVPAALL
501 ELSKQI*

```

m092/a092 99.4% identity over a 506 aa overlap

	10	20	30	40	50	60
m092.pep	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFGVIGGVMSGIA					
a092	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFGVIGGVMSGIA					
	10	20	30	40	50	60
m092.pep	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
a092	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
	70	80	90	100	110	120
m092.pep	AALQQIPVIPRALMLAELMRFRDGIAGTHGKTTTTLTASILGAAGLDPTFVIGGKL					
a092	AALQQIPVIPRALMLAELMRFRDGIAGTHGKTTTTLTASILGAAGLDPTFVIGGKL					
	130	140	150	160	170	180
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
a092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
	190	200	210	220	230	240
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
a092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					

292

	190	200	210	220	230	240
	250	260	270	280	290	300
m092.pep	FIHRMPFYGKAFLCIDSEHVRILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV					
a092	FIHRMPFYGKAFLCIDSEHVRILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m092.pep	QMKGHEQGSFEVVLNMPGRHNVNLALAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG					
a092	QMKGHEQGSFEVVLNMPGRHNVNLALAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m092.pep	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYLEKRLVLA FQPHRYTRTRDLFEDFTK					
a092	DIKLPNGGTALLVDDYGHHPVEMAATLSAARGAYPEKRLVLA FQPHRYTRTRDLFEDFTK					
	370	380	390	400	410	420
	430	440	450	460	470	480
m092.pep	VLNTVDALVLTEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
a092	VLNTVDALVLTEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
	430	440	450	460	470	480
	490	500				
m092.pep	GDIVLNMGAGSINRVPAALLALSQIX					
a092	GDIVLNMGAGSINRVPAALLELSQIX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 315>:

g093.seq

```

1  atGCAGAAAtt ttgGCAAAGT ggccgtATTG ATGGGtggtT TTTCCAGCGA
51  ACGAGAAatc tcgctGGACA GCgGTACCGC CATTTTGAAC GCCTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGACC CTAAGGAAAC GCCGTATATCC
151 GAACTGAAGG AGCGGGGCTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGCGCAA GACGGGGCTG TTCAGGTGC ATTGGAATG TTGGGCATTC
251 CCTATACCGG CAGCGGTGTC GCCGCCTCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGA GGCATTGGGA TTACCCGTTT CCGAGTTTCGC
351 CGTACTGTAC GATGATACCG ATTTGATGC CGTCGAAGAA AAATTGGGTC
401 TGCCGATGTT TGTGAAGCCG GCGGCCGAAG GCAGCAGCgt cggcgtggta
451 aaAGTCAAAG AAAaaggccg TCTGAAAAGC GTTtacgaag aatTGAAaCA
501 CCTTcagggg cgaAatcatt gccgAacgTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATA ACATCATCCC
601 CGCAACCGAG TTTTACGAct acgaagccaa GtacaacCGA GACGAcacca
651 tttatCAATG TCCTTCGGAA GATTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTCGCGG CGCACAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 316; ORF 093.ng>:

g093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDsGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKERGFQTA FNILHGTYGE DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLY DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV
151 KVKEKGRLKS VYEELKHLQG RNHCRTFYRR RRIFLRPPER QRAARHTHP
201 RNRVLRLSQ VQPRRHLSM SFGRFDRSRR KPDARTGGS RGTGNRCGLR
251 ARRFQRYRR QTLsvGNQHP ARYDRP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 317>:

m093.seq

```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CTAAAGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCtAA GACGGGGCGG TTCAGGGTGC ATTGGAAC TGGGGCATTG
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTTGGCA GGCATTGGGA TTGCCCCTTC CCGAGTTTCG
351 CGTCCTGCAC GACGACACTG ATTTTCGATG CGTCGAAGAA AAATTGGGGC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CCTTCAGGG. CGAAATCATT GCCGAACGTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACCG CAAAGGGCTG CCCGGCATA ACATCATTCC
601 CGCAACCGAG TTTTACGACT ACGAAGCCAA GTACAACCGC GACGACACCA
651 TTTATCAATG TCCTTCGGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTTCGGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACCG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACGAGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 318; ORF 093>:

```

m093 . pep
1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGX DGA VQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AEGSSVGVV
151 KVKGKGR LKS VYEELKHLQX RNHCRTFYRR RRI FLPRPER QRAARHTHHS
201 RNRVLR LRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGS RAGNRCGR LR
251 ARRFQRYRR QTL SVGNQHP ARYDEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 093 shows 96.7% identity over a 276 aa overlap with a predicted ORF (ORF 093.ng) from *N. gonorrhoeae*:

m093/g093

m093 . pep	10	20	30	40	50	60
	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS ELKAQGFQTA					
g093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS ELKERGFQTA					
m093 . pep	70	80	90	100	110	120
	FNILHGTYGX DGA VQGALELL LGIPYTGSGV AASAIGMDKY RCKLIWQAL GLPVPEFAVLH					
g093	FNILHGTYGEDGA VQGALELL LGIPYTGSGV AASAIGMDKY RCKLIWQAL GLPVPEFAVLY					
m093 . pep	130	140	150	160	170	180
	DDTDFDAVEE KLGLPMFVKP AEGSSVGVV KVKGKGR LKS VYEELKHLQX RNHCRTFYRR					
g093	DDTDFDAVEE KLGLPMFVKP AEGSSVGVV KVKEKGR LKS VYEELKHLQGRNHCRTFYRR					
m093 . pep	190	200	210	220	230	240
	RRI FLPRPERQRAARHTHHS RNRVLR LRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGS R					
g093	RRI FLPRPERQRAARHTHHS RNRVLR LRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGS R					
m093 . pep	250	260	270			
	RAGNRCGR LRARRFPQRYRR QTL SVGNQHP ARYDEPX					
g093	RTGNRCGR LRARRFPQRYRR QTL SVGNQHP ARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 319>:

a093.seq

```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CCAAGGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAAGT TTGGGCATTG
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGTGCAAAC TGATTTGGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CGTCCTGCAC GACGACACTG ATTTGATGCG CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CTTTCAGGG. CGAAATCATT GCCGAACGGT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCTG TGTGAAACCG CAAAGGCCCTG CCCGGCATAC ACATCATCCC
601 CGCGACCGAG TTTTATGACT ACGAAGCCAA GTACAACCGC AACGACACCA
651 TTTATCAATG TCCTTCGGAA GATCTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTTCGCG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACCG CAAACTCTAT CTGTTGAAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 320; ORF 093.a>:

a093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGE DGA VQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAEGSSVGTV
151 KVKGKGRILK VYEELKHFXQ RNHCRTVYRR RRIFLPCVER QPARHTHHP
201 RDRV L*LR SQ VQQRHHLMS SFGSRSDRSR KPDARTGGS RAGNRCGR LR
251 ARRFQRYRR QTL SVGNQHP ARYDRP*

```

m093/a093 95.7% identity over a 276 aa overlap

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLSELKAQGFQTA					
a093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLSELKAQGFQTA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m093.pep	FNILHGTYGX DGA VQGALELLG IPYTGSGVA ASAIGMDKYRCKLIWQALGLPVPEFAVLH					
a093	FNILHGTYGEDGA VQGALELLG IPYTGSGVA ASAIGMDKYRCKLIWQALGLPVPEFAVLH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m093.pep	DDTDFDAVEEKLGLPMFVKPAAEGSSVGTVKVKGKGRILKSVYEELKHLQXRNHCRTFYRR					
a093	DDTDFDAVEEKLGLPMFVKPAAEGSSVGTVKVKGKGRILKSVYEELKHFXQXRNHCRTFYRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m093.pep	RRIFLPRPERQRAARHTHHSRNRVLRSLRSQVQPRRHLSMSFGRFDRSRKPDARTGGS					
a093	RRIFLPCVERQPARHTHHPRDRVLRSLRSQVQPRRHLSMSFGRSDRSRKPARTGGS					
	190	200	210	220	230	240
	250	260	270			
m093.pep	RAGNRCGR LRARRFPQRYRRQTL SVGNQHPARYDEPX					
a093	RAGNRCGR LRARRFPQRYRRQTL SVGNQHPARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 321>:

```
g094.seq
  1 ATGTATTTCG CTTTGCCCAA GCGGGCGTTG GTGCCTGCGG CGTTGAGTTT
 51 GCCGCCGATA ACGAAAGTGG GGTTCGAGTCC TGCCGCGCCG AGGATGGAGG
101 CCGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTAcggc aatggcgatg
151 cCGTCACGGA AGCGCATCAG CTCTGCCAGC ATCAAGGCGC GCGGAATAAC
201 GGGAAATTGC CGTCCAACG CAgcgacaAC TTCGGgattT TCTTTCTTGA
251 CGGCGGTAGA GGCAACGACG ACATccgcAC CGTTAACGTG TTCTGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 322; ORF 094.ng>:

```
g094.pep
  1 MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
 51 PSRKRISSAS IKARGITGIC RSNAATTSGF SFLTAVEATT TSAPLTCSAV
101 WPG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 323>:

```
m094.seq
  1 ATGTATTTCG CTTTGCCCAA GCGGGCGTTA GTGCCTGCGG CGTTGAGTTT
 51 GCCGCCGATA ACGAAAGTCG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CCGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTGCCGGC AATGGCGATG
151 CCGTCACGGA AGCGCATCAA CTCCGCCAAC ATCAGGGCGC GCGGAATAAC
201 GGGAAATTGC TGCTCCAACG CAGCGACAAC TTCGGGATT TCTTTTTTGA
251 CGGCGGTAGA GGTAACGACG ACATCCGCAC CGTTAACGTG TTCGGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 324; ORF 094>:

```
m094.pep
  1 MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
 51 PSRKINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
101 WPG*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 094 shows 95.1% identity over a 103 aa overlap with a predicted ORF (ORF 094.ng) from *N. gonorrhoeae*:

```
m094/g094

      10      20      30      40      50      60
m094.pep MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRISSAN
          |||
g094     MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRISSAS
          |||

      10      20      30      40      50      60

      70      80      90     100
m094.pep IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
          :|
g094     IKARGITGICRSNAATTSGFSFLTAVEATTTTSAPLTCSAVWPGX
          :|

      70      80      90     100
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 325>:

```
a094.seq
  1 ATGTATTTCG CTTTGCCCAA GCGGGCGTTG GTGCCTGCGG CGTTGAGTTT
 51 GCCGCCGATA ACGAAAGTCG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CCGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTGCCGGC AATGGCGATG
151 CCGTCACGGA AGCGCATCAA CTCCGCCAAC ATCAGGGCGC GCGGAATAAC
201 GGGAAATTGC TGCTCCAACG CAGCGACAAC TTCGGGATT TCTTTTTTGA
251 CGGCGGTAGA GGTAACGACG ACATCCGCAC CGTTAACGTG TTCTGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 326; ORF 094.a>:

296

a094.pep
 1 MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
 51 PSRKRINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
 101 WPG*

m094/a094 100.0% identity over a 103 aa overlap

	10	20	30	40	50	60
m094.pep	MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVV VLPCVPAMAMPSRKRINSAN					
a094	MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVV VLPCVPAMAMPSRKRINSAN					
	10	20	30	40	50	60
	70	80	90	100		
m094.pep	IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX					
a094	IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 327>:

g095.seq
 1 ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT
 51 TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
 101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
 151 AACACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
 201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG
 251 TCCTCGTCGA TATTGGTAAC GACGGACATA ATCGGGGTCA GTGTAGGAAA
 301 GAGGCATCGG ATCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG
 351 CGGGCGTTGG TGCCTGCGGC GTTGA

This corresponds to the amino acid sequence <SEQ ID 328; ORF 095.ng>:

g095.pep
 1 MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
 51 NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCQRK
 101 EASDRRLRQR CIRLCPSGRW CLRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 329>:

m095.seq
 1 ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT
 51 TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
 101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
 151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
 201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG
 251 TCCTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
 301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG
 351 CGGGCGTTAG TGCCTGCGGC GTTGA

This corresponds to the amino acid sequence <SEQ ID 330; ORF 095>:

m095.pep
 1 MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
 51 NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCQRK
 101 DASDRRLRQR CIRLCPSGRX CLRR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 095 shows 97.6% identity over a 124 aa overlap with a predicted ORF (ORF 095.ng) from *N. gonorrhoeae*:

m095/g095

	10	20	30	40	50	60
m095.pep	MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG					


```

g095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60
           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMVFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||
g095      HTVDEIDKRLMQFFDAVPVGIHMVFVDIGNDGHNRCQCRKEASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
g095      CLRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 331>:

```

a095.seq
1  ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTCG GCGCCGACGT
51  TTTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAATC GCGCGGACGT GTTCGCTGTC
151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGCTTC TCAACACTGT GCCCGTAGGT ATCCATATGG
251 TCTTCGTCTGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTGCC TTTGCCCAAG
351 CGGGCGTTGG TGCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 332; ORF 095.a>:

```

a095.pep
1  MSFHLNMDGE FHLRADVFDV GGVVDVGGIVQ TVSSIRFAHF GQNRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQLLNTVPVG IHMVFDIGN DGHNRCQCRK
101 DASDRRLRQR CIRLCPSGRW CLRR*

```

m095/a095 96.0% identity in 124 aa overlap

```

           10      20      30      40      50      60
m095.pep  MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           |||||
a095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60
           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMVFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||
a095      HTVDEIDKRLMQLLNTVPVGIHMVFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
a095      CLRRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 333>:

```

g096.seq
1  ATGGCCGGTC ATACCGGGCA GGGTGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCGATT
101 GCCTGTGCGC CGCGAACCGC CAGTTCGCGC ATCAGGCTTT CTTGCGCTTC
151 GGTCAAATCT TCCGAAGGAC ATTGataaat ggtgTCGTCT CGGttgtaCt

```

g096.pap

1 MAGHTGQGVDFQIEFAVGI FEEIDAHAAF RTDCLCAANR QFAHQAFFGF
51 GQIFRRTLIN GVVSVVLGEF VVKLGCGDDV YAGQPFVQD GAGIFAAADK
101 TEGNDEAPEG VSILRKRFSD GLFL*

m096. seq

1	ATGGCTCGTC	ATACCGGGCA	GGGTGTTGAT	TTCCAACAGA	TAGAGTTTGC
51	CGTCGGTATC	TTTGAGGAAA	TCGACCGCGA	CGCAGCGCTT	CGCACCGATT
101	GCCTCGCGCG	CGCGAACCAG	CAGTTCGCGC	ATCAGGCTTT	CTTCCGGCTT
151	GGTCAAATCT	TCCGAAGGAC	ATTGATAAAT	GGTGTGCTCG	CGGTCTTACT
201	TGGCTTCGTA	GTCGTAATAA	TCGGTTGCGG	GAATGATGTG	TATGCCGGGC
251	AGCCCTTTGC	CGTTCAGGAC	GGGGCAGGAA	TATTCCGCGC	CGCCGATAAA
301	ACGTTTCGGCA	ATGATTTTCG	CC. TGAAGT	GTTTCAATTC	TTCTGTAACG
351	CTTTTCAGAC	GGCCTTTTCC	TTTGA		

m096.pwp

1 MARHTGQGVDFQIQIEFAVGI FEEIDAAHAF RTDCLRAANR QFAHQAFFGF
51 GQIFRRTLIN GVVAVVLGFV VVKLGCGNDV YAGQPPFVQD GAGIFAAADK
101 TFGNDEAXEG VSILRKRFSD GLFL*

m096/g096 96.0% identity in 124 aa overlap

		10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGIFEEIDAHAAERTDCLRAANRQFAHQAFFGFGQIFRRTLIN						
g096	MAGHTGQGVDFQQIEFAVGIFEEIDAHAAERTDCLCAANRQFAHQAFFGFGQIFRRTLIN						
		10	20	30	40	50	60
m096.pep	GVVAVVLGFVVKLGCGNDVYAGQPFVAVDGAGIFAAADKTFGNDFAXEGVSILRKRFSD						
	: :						
g096	GVSIVLGFVVKLGCGDDVYAGQPFVAVDGAGIFAAADKTFGNDFAPFEGVSILRKRFSD						
		70	80	90	100	110	120
m096.pep	GLFLX						
g096	GLFLX						

a096.seq

1	ATGGCCGGTC	ATACCGGGCA	GGGTGTTGAT	TTCCAACAGA	TAGAGTTTGC
51	CGTCGGTATC	TTTGAGGAAA	TCGACGCGCA	CGCAGCGCTT	CGCACCGATT
101	GCCTCGCGCG	CGCGAACCAC	CAGTTTCGCG	ATCAGGCTTT	CGTTCGGCTT
151	GGTCAGATCT	TCCGAAGGAT	ATTGATAAAT	GGTGTGTTG	CGTTGCTACT
201	TGGCTTCGTA	GTCATAAAAC	TCGGTCGCGG	GGATGATGTG	TATGCCGGGC
251	AGGCCTTTGC	CGTTCAACAC	AGGGCAGGAA	TATTCGCGCG	CGCCGATAAA
301	CCGTTTCGGCA	ATGATTTTCG	CCT . GAAAGT	GTTTCAATT	TTCTGTAACG
351	CTTTTCAGAC	GAGCCTTTTC	TTTGA		

a096.pep

1 MAGHTGOGVD FQQIEFAVGI FEEIDAHAAF RTDCLRAANR QFAHQAFFGF

51 GQIFRRTLIN GVVAVVLGFV VIKLGRGDDV YAGQAFVQH RAGIFAAADK
101 PFGNDFAXES VSILRKRFSD GLFL*

m096/a096 92.7% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGIFEEIDAHAAERTDCLRAANRQFAHQAFFGFGQIFRRTLIN					
a096	MAGHTGQGVDFQQIEFAVGIFEEIDAHAAERTDCLRAANRQFAHQAFFGFGQIFRRTLIN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVVKLGCGNDVYAGQPFQVQDGAGIFAAADKTFGNDFAFEGVSILRKRFSD					
a096	GVVAVVLGFVVIKLGCGNDVYAGQAFVQHRAGIFAAADKPFNGDFAXESVSILRKRFSD					
	70	80	90	100	110	120
m096.pep	GLFLX					
a096	GLFLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 339>:

g097.seq

1	ATGGATATTT	CAAAACAAAC	ATTGCTGGAT	AGGGTTTTTA	ACCTGAAGGC
51	AAACGGTACG	ACGGTACGTA	CCGAGTTGAT	GGCGGGTTTG	ACGACCTTTT
101	TGACGATGTG	CTACATCGTT	ATCGTCAATC	CCCTGATTTT	GGGCGAGACC
151	GGAATGGATA	TGGGGGCGGT	ATTCTGCGCT	ACCTGTATCG	CATCCGCCAT
201	CGGCTGTTTT	GTCATGGGTT	TTATCGGCAA	CTATCCGATT	GCGCTTGCCC
251	CGGGGATGGG	GCTGAATGCC	TATTTACCTT	TTGCCGTCGT	TAAGGGTATG
301	GGCGTGCCTT	GGCAGGTGGC	GTTGGGTGCG	GTGTTCAATT	CCGGTCTGAT
351	TTTCATCCTG	TTCAGCTTTT	TTAAAGTCAG	GGAAATGCTG	GTCAACGCAC
401	TGCCTATGGG	TTTGAAATG	TCGATTGCCG	CCGGTATCGG	TTTGTTTTTG
451	GCACTGATTT	CCCTGAAAGG	CGCAGGCATT	ATCGTTGCCA	ATCCGGCAAC
501	CTTGGTCGGC	TTGGGCGATA	TTCATCAGCC	CAGCGCACTG	TTGGCATTGT
551	TCGGTTTTGT	CATGGTGGTC	GTATTGGGGT	ATTTCCGCGT	TCAAGGCGCA
601	ATCATCATCA	CCATTCTGAC	GATTACCGTC	ATTGCCAGCC	TGATGGGTTT
651	GAACGAGTTT	CACGGCGTGG	TCGGCGAAGT	ACCGGGCATT	GCGCCGACCT
701	TTATGCAGAT	GGATTTTAAA	GGTCTGTTTA	CCGTCAGCAT	GGTCAGCGTG
751	ATTTTCGTCT	TCTTCTTGGT	CGATTGTTC	GACAGTACCG	GAACGCTGGT
801	CGGCGTATCC	CACCGTGCCG	GACTGCTGGT	GGACGGTAAG	CTGCCCCGCC
851	TGAAACGCGC	ACTGCTTGCA	GACTCTACCG	CCATTGTGGC	AGGTGCGGCT
901	TTGGGTACTT	CTTCAACCAC	GCCTTATGTG	GAAAGCGCGG	CGGGCGTATC
951	GGCAGGCGGA	CGGACCGGCC	TGACGGCGGT	TACCGTCGGC	GTATTGATGC
1001	TGGCGTGTCT	GATGTTCTCC	CCATTGGCGA	AAAGTGTTC	GGTATTTGCC
1051	ACCGCGCCCG	CACTGCTTTA	TGTCGGCACG	CAGATGCTCC	GCAGTGCGAG
1101	GGACATTGAT	TGGGACGATA	TGACTGAAGC	CGCGCCCGCG	TTCTTGACCA
1151	TGTCTTCAT	GCCGTTTACC	TATTGCGATT	CAGACGGCAT	CGCCTTCGGC
1201	TTCATCAGCT	ATGCCGTGGT	CAAACTTTTG	TGTCGCCCGA	CTGGGGACGT
1251	GCCGCCTATG	GTATGGGTTG	TTGCCGTATT	GTGGGCATTG	AAATTCTGGT
1301	ATTTGGGCTG	A			

This corresponds to the amino acid sequence <SEQ ID 340; ORF 097.ng>:

g097.pep

1	MDISKQTLDD	RVFNLKANGT	TVRTELMAGL	TTFLTMCIYV	IVNPLILGET
51	GMDMGAVFVA	TCIASAIGCF	VMGFIGNYP	ALAPGMGLNA	YFTFAVVKGM
101	GVPWQVALGA	VFISGLIFIL	FSFFKVREML	VNALPMGLKM	SIAAGIGLFL
151	ALISLKGAGI	IVANPATLVG	LGDHQPASL	LALFGFVMV	VLGYFRVQGA
201	IIITILTITV	IASLMGLNEF	HGVVGEVPGI	APTFMQMDFK	GLFTVSMVSV
251	IFVFFLVDLF	DSTGTLVGVS	HRAGLLVDGK	LPRLKRALLA	DSTAIVAGAA
301	LGTSSSTPYV	ESAAGVSAGG	RTGLTAVTVG	VLMLACLMPF	PLAKSVPVFA
351	TAPALLYVGT	QMLRSARDID	WDDMTEAAPA	FLTIVFMPFT	YSIADGIAFG

1	ATGGACACTT	CAAAACAAAC	ACTGTTGGAC	GGGATTTTTA	AGCTGAAGGC
51	AAACGGTACK	ACGGTGC GTA	CCGAGTTGAT	GGCGGGTTTG	ACAAC TTTTT
101	TGACGATGTG	CTACATCGTT	ATCGTCAACC	CTCyGATTTT	GGGCGAGACC
151	GGCATGGATA	TGGGGGCGGT	ATTCTGTCGT	ACCTGTATCG	CGTCTGCCAT
201	CGGCTGTTTT	GTTATGGGTT	TTGTCCGCAA	CTATCCGATT	GCATCTCGCAC
251	CGGGATGGG	GCTGAATGCC	TATTTACCTT	TTGCGTCGT	TAAGGGTATG
301	GGCGTGCCTT	GGCAGTTTGC	GTTGGGTGCG	GTTGTCATCT	CCGGTCTGAT
351	TTTTATCCTG	TTCAGCTTTT	TTAAAGTCAG	GGAAATGCTG	GTCAACGCAC
401	TGCCTATGGG	TTTGAAAATG	TCGATTGCTG	CCGGTATCGG	TTTGTTTTTG
451	GCAC TGATTT	CCCTGAAAGG	CGCAGGCATT	ATCGTTGCCA	ATCCGGCAAC
501	CTTGGTCGGT	TTGGGCGATA	TTCATCAGCC	GTCCGCGTTG	TTGGCATTTGT
551	TCGGTTTTGC	TATGGTGGTC	GTATTGGGAC	ATTTCCGCGT	TCAAGGCGCA
601	ATCATCATCA	CCATCTTGAC	CATTACCGTC	ATTCCGACCC	TGATGGGTTT
651	GAATGAATTT	CACGGCATCA	TCGGCGAAGT	ATCCGAGCAT	CGCCGCACTT
701	TTATGCAGAT	GGATTTTGAA	GGCCTGTTTA	CCGTCAGCAT	GGTCAGTGTG
751	ATTTTCGTCT	TCTTCTTGGT	CGATCTATTT	GACAGTACCG	GAACGCTGGT
801	CGGCATATCC	CACCGTGCCG	GGCTGCTGGT	GGACGGTAAG	CTGCCCCGCC
851	TGAAACGCGC	ACTGCTTGCA	GACTCTACCG	CCATTGTGGC	AGGTGCGGCT
901	TTGGGTA CTT	CTTCCACCAC	GCCTTATGTG	GAAAGCGCGG	CGGGCGTATC
951	GGCAGGCGGA	CGGACCGGCC	TGACGGCGGT	TACCGTCGGC	GTATTGATGC
1001	TCGCCTGCCT	GATGTTTTCA	CTTTTGCGGA	AAAGTGTTC	CGCTTTTGCC
1051	ACCGCGCCCG	CCCTGCTTTA	TGTCGGCACG	CAGATGCTCC	GCAGTGCGAG
1101	GGATATTGAT	TGGGACGATA	TGACGGAAGC	CGCACCTGCG	TTCTTGACCA
1151	TTGTTTTTCAT	GCCGTTTACT	TATTCGATTG	CAGACGGCAT	CGCTTTCGGC
1201	TTCATCATGT	ATGCCGTGGT	TAAACTTTTA	TGCCGCGCGA	CCAAAGACGT
1251	TCGCCCTATT	GATATGATTG	TTGCCGTATT	GTGGGCAC TG	AAAT TCTGGT
1301	ATTGGGCTG	A			

m097.pcp

1	MDTSKQTLLE	GIFLKLKANGT	TVRTELMAGL	TTFLTMCIYV	IVNPXILGET
51	GMDMGAVFVA	TCIASAIGCF	VMGFVGNYP	ALAPGMGLNA	YFTFAVVKGM
101	GVFQWQALGA	VFISGLIFIL	FSFFKVREML	VNALPMGLKM	SIAAGIGLFL
151	ALISLKGAGI	IVANPATLVG	LGDIHQPSAL	LALFGFAMVV	VLGHFRVQGA
201	IIITILITIV	IASLMGLNEF	HGIIGEVPSI	APTFMQMDFE	GLFTVSMVSV
251	IFVFFLVLDL	DSTGTLVGIS	HRAGLLVDGK	LPRLKRALLA	DSTAIVAGAA
301	LGTSSSTTYP	ESAGVVSAGD	RTDLTAVTVG	FLMLACMFES	PLAKSVPAFA
351	TAPALLVYGT	QMLRSARDID	WDDMTEAAPA	VLTIVFMPFT	YSIADGIAFG
401	FISYAVVKLL	CRRTKDVPPM	VWIVAVLWAL	KFWYLG*	

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 097 shows 96.3% identity over a 436 aa overlap with a predicted ORF (ORF 097.ng) from *N. gonorrhoeae*:

m097/g097

[illegible]

m097 . pep	FSFFKVR	EMLVN	ALP	MLK	MSIA	AAGIGL	FLALIS	SLKG	AGII	VANPAT	LVGL	GD	IHQ	PSAL
g097	FSFFKVR	EMLVN	ALP	MLK	MSIA	AAGIGL	FLALIS	SLKG	AGII	VANPAT	LVGL	GD	IHQ	PSAL
		130		140		150		160		170		180		
m097 . pep	LALFGF	FAMVV	VLGH	FRVQ	GAII	ITILT	ITV	IASL	MGLN	EFHGI	IGEV	PSI	APT	FMQ
g097	LALFGF	FAMVV	VLGH	FRVQ	GAII	ITILT	ITV	IASL	MGLN	EFHGI	IGEV	PSI	APT	FMQ
		190		200		210		220		230		240		
m097 . pep	GLFTV	SMVSV	IFVFF	LV	DLFD	STGT	LVG	IS	HRAG	LLVD	GKLP	R	LLAD	STA
g097	GLFTV	SMVSV	IFVFF	LV	DLFD	STGT	LVG	IS	HRAG	LLVD	GKLP	R	LLAD	STA
		250		260		270		280		290		300		
m097 . pep	LGTSS	STTPY	VESA	AAGV	SAGGR	TGLT	AVT	VG	VLML	ACLM	FSPL	AKSV	PAF	ATAP
g097	LGTSS	STTPY	VESA	AAGV	SAGGR	TGLT	AVT	VG	VLML	ACLM	FSPL	AKSV	PAF	ATAP
		310		320		330		340		350		360		
m097 . pep	QMLRS	ARDID	WDDM	TEA	APAF	L	TIV	FMP	FTYS	IADG	IAFG	FIS	YAV	VKLL
g097	QMLRS	ARDID	WDDM	TEA	APAF	L	TIV	FMP	FTYS	IADG	IAFG	FIS	YAV	VKLL
		370		380		390		400		410		420		
m097 . pep	VWIV	AVLW	ALKF	WYL	LGX									
g097	VWIV	AVLW	ALKF	WYL	LGX									
		430												

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 343>

a097 . seq

```

1  ATGGACACTT CAAAACAAAC ACTGTTGGAC GGGATTTTTA AGCTGAAGGC
51  AAACGGTACG ACGGTGCGTA CCGAGTTGAT GGCGGGTTTG ACAACTTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAACC CTCTGATTTT GGGCGAGACC
151 GGCATGGATA TGGGGGCGGT ATTCGTCGCT ACCTGTATCG CGTCTGCCAT
201 CGGCTGTTTT GTTATGGGTT TTGTCGGCAA CTATCCGATT GCACTCGCAC
251 CGGGGATGGG GCTGAATGCC TATTTACCTT TTGCCGTCGT TAAGGGTATG
301 GGCCTGCCTT GGCAGGTTGC GTTGGGTGCG GTGTTTCATCT CCGGTCTGAT
351 TTTTCATCTG TTCAGCTTTT TTAAAGTCAG GGAAATGCTG GTCAACGCAC
401 TGCCTATGGG TTGAAAATG TCGATTGCTG CCGGTATCGG TTTGTTTTTG
451 GCACTGATTT CCCTGAAAGG CGCAGGCATT ATCGTTGCCA ATCCGGCAAC
501 CTTGGTCGGC TTGGGCGATA TTCATCAGCC GTCCGCGTTG TTGGCACTGT
551 TCGGTTTTGC CATGGTGGTC GTATTGGGAC ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATTTTGAC GATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAACGAATTT CACGGCATCA TCGGCGAAGT GCCGAGCATT GCGCCGACTT
701 TTATGCAGAT GGATTTTAAA GGGTTGTTTA CCGTCAGCAT GGTGAGCGTG
751 ATTTTCGTCT TTTTCCTAGT CGATCTGTTC GACAGTACCG GAACACTGGT
801 CCGTGTATCG CATCGTGCCG GACTGCTGGT GGACGGTAAG CTGCCCCGCC
851 TGAAACGCGC ACTGCTTGCA GACTCTACCG CTATTGTGGC AGGTGCGGCT
901 TTGGGTACTT CTTCAACCAC GCCTTATGTG GAAAGTGCGG CGGGCGTATC
951 GGCAGGCGGG CGGACAGGTC TGACGGCGGT TACCGTCGGC GTATTGATGC
1001 TCGCCTGCCT GATGTTTTCA CCTTTGGCGA AAAGTGTTCC CGCTTTTGCC
1051 ACCGCGCCCG CCCTGCTTTA TGTGCGCACG CAGATGCTCC GCAGTGCGAG
1101 GGACATCGAT TGGGACGATA TGACGGAAGC CGCACCAGCA TTCCTGACCA
1151 TTGTCTTCAT GCCGTTTACC TATTCGATTG CAGACGGCAT CGCTTTCGGC
1201 TTCATCAGTT ATGCCGTGGT TAAACTTTTA TGCCGCGGCA CCAAAGACGT
1251 TCCGCCTATG GTATGGATTG TTGCCGTATT GTGGGCACTG AAATTCTGGT

```

1301 ATTTGGGCTG A

This corresponds to the amino acid sequence <SEQ ID 344; ORF 097.a>:

a097.pep

```
1  MDTSKQTLDD GIFKLGKANGT TVRTELMAGL TTFLTMCYIV IVNPLILGET
51  GMDMGAVFVA TCIASAIGCF VMGFVGNYP I ALAPGMGLNA YFTFAVV KGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIG LFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IIITILTITV IASLMGLNEF HGIIGEVPSI APTFMQDFK GLFTVSMVSV
251 IFVFFLVDLF DSTGTLVGVS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMFS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRTKDVPPM VWIVAVLWAL KFWYLG*
```

m097/a097 99.3% identity in 436 aa overlap

	10	20	30	40	50	60
m097.pep	MDTSKQTLDDGIFKLGKANGT	TVRTELMAGLTTFLTMCYIV	IVNPLILGET	GMDMGAVFVA		
a097	MDTSKQTLDDGIFKLGKANGT	TVRTELMAGLTTFLTMCYIV	IVNPLILGET	GMDMGAVFVA		
	70	80	90	100	110	120
m097.pep	TCIASAIGCFVMGFVGNYP	IALAPGMGLNAYFTFAVV	KGMGVPWQVALGAVFISGLIFIL			
a097	TCIASAIGCFVMGFVGNYP	IALAPGMGLNAYFTFAVV	KGMGVPWQVALGAVFISGLIFIL			
	130	140	150	160	170	180
m097.pep	FSFFKVREMLVNALPMGLKMS	SIAAGIGLFLALISLKGAGI	IVANPATLVGLGDIHQPSAL			
a097	FSFFKVREMLVNALPMGLKMS	SIAAGIGLFLALISLKGAGI	IVANPATLVGLGDIHQPSAL			
	190	200	210	220	230	240
m097.pep	LALFGFAMVVVLGHFRVQGA	IIITILTITVIASLMGLNEF	HGIIGEVPSIAPT	FMQDFE		
a097	LALFGFAMVVVLGHFRVQGA	IIITILTITVIASLMGLNEF	HGIIGEVPSIAPT	FMQDFE		
	250	260	270	280	290	300
m097.pep	GLFTVSMVSVIFVFFLVDLF	DSTGTLVGISHRAGLLVDGK	LPRLKRALLAD	STAIVAGAA		
a097	GLFTVSMVSVIFVFFLVDLF	DSTGTLVGISHRAGLLVDGK	LPRLKRALLAD	STAIVAGAA		
	310	320	330	340	350	360
m097.pep	LGTSSTTPYVESAAAGVSAGG	RTGLTAVTVGVLMACLMFS	PLAKSVPAFATAPALLYVGT			
a097	LGTSSTTPYVESAAAGVSAGG	RTGLTAVTVGVLMACLMFS	PLAKSVPAFATAPALLYVGT			
	370	380	390	400	410	420
m097.pep	QMLRSARDIDWDDMTEAAPA	FLTIVFMPFTYSIADGIAFG	FISYAVVKLLCRTKDVPPM			
a097	QMLRSARDIDWDDMTEAAPA	FLTIVFMPFTYSIADGIAFG	FISYAVVKLLCRTKDVPPM			
	430					
m097.pep	VWIVAVLWALKFWYLGX					
a097	VWIVAVLWALKFWYLGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 345>:

```
g098.seq
1  ATGACCGCCG ACGGTCTCTT CGTCGCTTTC AACTTCAATA CGTTTGCCGT
51  TGTGCGAATA TTGATACCAG TACAGCAGGA TGCTGCCAG GCTGGCGATC
101 AGTTTGTGCG CGATGTCGCG CGCTTCGCTG TCGGGATGGC TTTCGCGTTC
151 GGGATGAACG CAGCCGAGCA TGGACACGCC GGTACGCATC ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAAGTG TGCGACTTCT TCAAACTCGC
351 ATTTTGTGTC CAAATTAGAA TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 346; ORF 098.ng>:

```
g098.pep
1  MTADGLFVAF NFNTFAVVRI LIPVQDAAQ AGDQFVGDDVA RFAVGMFAF
51  GMNAAEHGHA GTHVHRMGM CRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV CDFPKLAFLC QIRMS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 347>:

```
m098.seq
1  ATGACCGCCG ATGGTCTCTT CGTCGCTTTC AACCTCAATG CGTTTGCCGT
51  TGTGCGAATA TTGATACCAG TACAAGAGGA TGCTGCCAG GCTGGCGATC
101 AGTTTGTGCG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTTT
151 AGGATGAACG CAGCCGAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GCGGACTTCT TCAAACTCGC
351 ATTTTGTGTC CAAATCAGAA TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 348; ORF 098>:

```
m098.pep
1  MTADGLFVAF NLNAFAVVRI LIPVQEDAAE AGDQFVGDDVA RFTFRMAFTF
51  RMNAAQHGYA GTHVHRMGM CRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFPKLAFLC QIRMS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 098 shows 89.6% identity over a 125 aa overlap with a predicted ORF (ORF 098.ng) from *N. gonorrhoeae*:

m098/g098

	10	20	30	40	50	60
m098.pep	MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA					
	: : : : : :					
g098	MTADGLFVAFNFNTFAVVRI LIPVQDAAQAGDQFVGDDVARFAVGMFAFAGMNAAEHGHA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m098.pep	GTHVHRMGMC RQAFQNFNHTDRQAAHGFELGFISGQLEFVGQMAVNQQVGDFFKLAFLC					
	: : : : : :					
g098	GTHVHRMGMC RQAFQNFNHTDRQAAHGFELGFISGQLEFVGQMAVNQQVCDFFKLAFLC					
	70	80	90	100	110	120
m098.pep	QIRMSX					
g098	QIRMSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 349>:

```
a098.seq
1  ATGACCGCCG ATGGTCTCTT CGTCGCTTTC AACCTCAATG CGTTTGCCGT
51  TGTGCGAATA TTGATACCAG TACAAGAGGA TGCTGCCAG GCTGGCGATC
```

304

101 AGTTTGTCCG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTC
 151 AGGATGAACG CAGCCCAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
 201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTTAATCAC ACGGATAGGC
 251 AGGCCGCGCA TGGATTTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
 301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GCGGACTTCT TCAAACCTCG
 351 ATTTTGTGC CAAATCAGAA TGTCGTAA

This corresponds to the amino acid sequence <SEQ ID 350; ORF 098.a>:

a098.pep

1 MTADGLFVAF NLNAFAVVRI LIPVQEDAAE AGDQFVGDDVA RFTFRMAFTF
 51 RMNAAQHGYA GTHYVHRMGM CROAFQNFNH TDRQAAHGFE LGFISGQLEF
 101 VGQMAVNQQV GDFFKLAFLC QIRMS*

m098/a098 100.0% identity in 125 aa overlap

	10	20	30	40	50	60
m098.pep	MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA					
a098	MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m098.pep	GTHYVHRMGMCRQAFQNFNHTDRQAAHGFELGFISGQLEFVGQMAVNQQVGDFFKLAFLC					
a098	GTHYVHRMGMCRQAFQNFNHTDRQAAHGFELGFISGQLEFVGQMAVNQQVGDFFKLAFLC					
	70	80	90	100	110	120
m098.pep	QIRMSX					
a098	QIRMSX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 351>:

g099.seq

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTGGA
 51 GCTGACGGGC AAACGGCAGG CGGGCATTAC TGCCACAGAC ATCGTGTGTTG
 101 CACTGACCGA ATTCTTGCGT AAAGAGCGCG TGGTCGGGGC GTTTGTGCGAA
 151 TTTTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
 201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCCATG TTCGCCATCG
 251 ACGCGCAAAC TATTGATTAT TTGAAACTGA CCGGACGTGA CGACGCGCAG
 301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTAT GGGCAGGTGG
 351 CTTGAAAACC GCCGTTTATC CGCGCGTTTT GAAATTTGAT TTGAGCAGCG
 401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCACGCGCG TTTTGCCACC
 451 GCCGATTGCG CGGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCAGA
 501 CGGCCAAATG CCTGACGGTG CAGTGATTAT TGCCGCGATT ACTTCGTGTA
 551 CCAATACTTC CAACCCGCGC AACGTGTGCG CCGCCGCACT GTTGGCACGC
 601 AATGCCAACC GCCTCGGCTT GAAACGCAAA CCTTGGGTGA AATCTTCGTT
 651 TGCCCCGGGT TCAAAAAGTAG CCGGAATCTA TTTGAAAGAA GCAGGCTTGT
 701 TGCCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCATGTACC
 751 ACCTGTAACG GCATGAgcgG CGCGCTGgaC CCGAAAATCC AACAAAGAAAT
 801 CATCGACCGC GAtttgtacg cCACCGCCGT ATTGTcAGGC AACCGCAACT
 851 TCGACGGCCG TATCCATCCG TATGCGAAAC AGGCTTTCTT CGCTTCGCCT
 901 CCTTTGGTCG TTGCCTACGC ATTGGCAGGT AGCATCCGTT TCGATATTGA
 951 AAACGACGTA CTCGGCGTTG CAGACGGCCG CGAAATCCGC CTGAAAGATA
 1001 TCTGGCCGAC AGACGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
 1051 CCGCAACAAT TCCGCGACAT TTATATCCCG ATGTCCGACA CCGGCACAGC
 1101 GCAAAAAGCA CCAAGCCCGC TGTACGACTG GCGACCGATG TCCACCTACA
 1151 TCCGCCGTCC GCCCTATTGG GAAGGCGCAC TGGCAGGGGA ACGTACATTA
 1201 AGAGGTATGC GTCCGCCGGC GATTTTGCCC GACAACATCA CCACCGACCA
 1251 CATCTCgcca tCCAATGCGA TTTTGCGCCG cagTGcGca ggtgaATATT


```

1301 TGGCGAAAAT GGGTTTGCCT GAAGAagaCT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTtcgt
1451 tggcacgcgT tgaacCAGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTT ATCATCATTG CCGGTGCGGA
1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC GGCGAAGGGC GTGCGGCTGG
1601 CGGGTGTGGA AGCCATCGCC GCCGAAGGTT TCGAGCGCAT CCACCGCACC
1651 AACCTCATCG GCATGGGCGT CTTGCCGCTG CAATTCAAAC CCGGCACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGGC CTGACCCTCG TGATTACCG TAAAAACGGA
1801 GAAACCGTCG AAGTTCCGGT TACCTGCCGC CCCGATACCG CAGAAGAAGC
1851 ATTGGTATAT GAAGCCGCGC GCGTATTGCA ACGGTTTGCA CAGGACTTTT
1901 TGAAGGGGAA CGCGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 352; ORF 099.ng>:

g099.pep

```

1 MLGRASMMRL PDIVGVELTG KRQAGITATD IVLALTEFLR KERVVGAFVE
51 FFGEGARSLS IGDRATISNM TPEFGATAAM FAIDAQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWAGGLKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAAKGLAK PYEPPSDGQM PDGAVIIAAI TSCTNTSNPR NVVAAAALLAR
201 NANRLGLKRR PWVKSSFAPG SKVAGIYLKE AGLLPEMEKL GFGIVAFAC
251 TCNGMSGALD PKIQEIIIDR DLYATAVLGS NRNFDGRIHP YAKQAFPLASP
301 PLVVAYALAG SIRFDIENDV LGVADGREIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDIYIP MSDTGTAQKA PSPLYDWRPM STYIRRPPYW EGALAGERTL
401 RGMRPAILP DNITTDHISP SNAILAGSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNKQPL IIIAGADYGQ GSSRDWAAKG VRLAGVEAIA AEGFERIHRT
551 NLIGMGVLP LQFKPGTNRHT LQLDGTETYD VVGERTPRCG LTLVIHRKNG
601 ETVEVPVTCR PDTAEEALVY EAGGVLQRFQ QDFLEGNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 353>:

m099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATG TCGGCGTTGA
51 GCTGAACGGC AAACGCGAGG CGGGCATTAC GGCGACGGAT ATTGTGTTGG
101 CACTGACCGA GTTCTGCGC AAAGAACGCG TGGTCGGGGC GTTTGTCGAA
151 TTCTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCGATG TTGCTATTG
251 ATGAGCAAAC CATTGATTAT TTGAAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAACCTA CGCCAAACC GCAGGCTTGT GGGCAGATGC
351 CTTGAAACC GCCGTTTATC CTCGCGTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCAAGTAACC CGCATGCCCG TTTTGCAGAC
451 GCGGATTTGG CGGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCGGA
501 CGGCCAAATG CCCGACGGCT CGGTCAATCAT CGCCGCGATT ACCAGTTGCA
551 CCAACACTTC CAACCCGCGC AACGTTGTTG CCGCCGCGCT CTTGGCACGC
601 AATGCCAACC GTCTCGGCTT GAAACGCAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGAAATCTA TTGAAAGAA GCGGGCCTGT
701 TGCCCCGAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCCTGCACC
751 ACCTGCAACG GCATGAGTGG CGCGCTGGAT CCGAAAATCC AGAAAGAAAT
801 CATCGACCGC GATTGTACG CCACGCGCGT ATTATCAGGC AACCAGCACT
851 TCGACGGCCG TATCCACCGG TATGCGAAAC AGGCTTTCCT CGCTTCGCTT
901 CCGTTGGTTC TTGCCTACGC GCTGGCAGGC AGTATCCGTT TCGATATTGA
951 AAACGACGTA CTCGCGGTTG CAGACGCAA GGAAATCCGC CTGAAAGACA
1001 TTTGGCCTGC CGATGAAGAA ATCGATGCCG TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAGT TCCGCGATGT GTATGTACCG ATGTTGACA CCGGCACAGC
1101 GCAAAAAGCA CCCAGTCCGC TGTACGATTG GCGTCCGATG TCCACCTACA
1151 TCCGCCGTCC GCCTTACTGG GAAGGCGCGC TGGCAGGGGA ACGCACATTA
1201 AGAGGTATGC GTCCGCTGGC GATTTTGCCC GACAACATCA CCACCGACCA
1251 CCTCTCGCCG TCCAATGCGA TTTTGGCCGT CAGTGCCGCA GGCGAGTATT
1301 TGGCGAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGGACC ACTTGACCGC CCAACGCGCT ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAAAA ACGAAGACGG CAGCGTGC GC CAAGGCTCGT
1451 TCGCCCGCGT CGAACCCGAA GGCGAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGTGCGGA

```

```

1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTAGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACCTTATCG GCATGGGCGT GTTGCCGCTG CAGTTCAAAC CCGACACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTGGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTCG TGATTACCG TAAAAACGGC
1801 GAAACCGTGT AAGTCCCGT TACCTGCTGC CTCGATACTG CAGAAGAAGT
1851 ATTGGTATAT GAAGCCGGCG GCGTGTGCA ACGGTTTGCA CAGGATTTTT
1901 TGAAGGGAA CGCGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 354; ORF 099>:

```

m099.pep
1  MLGRASMMRL PDIVGVELNG KRQAGITATD IVLALTEFLR KERVVGAFVE
51  FFGEGARSLS IGDRATISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAAKGLAK PYEESDQGM PDGSVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLKRK PWKSSFAPG SKVAEIYLKE AGLLPEMEKL GFGIVAFAC
251 TCNGMSGALD PKIQKEIIDR DLYATAVL SG NRNFDGRIHP YAKQAFLAS
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPADEE IDAVVAEYVK
351 PQQFRDVYVP MFDTGTAQKA PSPLYDWRPM STYIRPPYW EGALAGERTL
401 RGMRLAILP DNITDHLSP SNAILAVSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLENE MVKNEDGSRV QGSFARVEPE GETMRMWEAI
501 ETYMNKQPL IIIAGADYGO GSSRDWAAGK VRLAGVEAIV AEGFERIHRT
551 NLIGMGVLP LQKPDNTRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601 ETVEVPVTC LDTAEEVLVY EAGGVLQRF A QDFLEGNA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 099 shows 96.2% identity over a 639 aa overlap with a predicted ORF (ORF 099.ng) from *N. gonorrhoeae*:

m099/g099

	10	20	30	40	50	60
m099.pep	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
	:					
g099	MLGRASMMRLPDIVGVELTGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQTIDYLKLTGRDDAQVKLVETYAKTAGLWADALKT					
	:					
g099	IGDRATISNMTPEFGATAAMFAIDAQTIDYLKLTGRDDAQVKLVETYAKTAGLWAGGLKT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEESDQMPDGSVIIAAI					
	:					
g099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEESDQMPDGAIIAAI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSFAPGSKVAEIYLKEAGLLPEMEKL					
g099	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSFAPGSKVAGIYLKEAGLLPEMEKL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m099.pep	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFLAS					
	:					
g099	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFLAS					
	250	260	270	280	290	300
	310	320	330	340	350	360

m099 . pep	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPADEEIDAVVAEYVKPQQFRDVYVP
g099	PLVVAYALAGSIRFDIENDVLGVADGREIRLKDIWPTDEEIDAIVA EYVKPQQFRDIYIP
	310 320 330 340 350 360
m099 . pep	MFDTGTAQKAPSPLYDWRPMSTYIRRPYWEALAGERTLRGMRPLAILPDNITTDHLS
g099	MSDTGTAQKAPSPLYDWRPMSTYIRRPYWEALAGERTLRGMRPPAILPDNITTDHISP
	370 380 390 400 410 420
m099 . pep	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR
g099	SNAILAGSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR
	430 440 450 460 470 480
m099 . pep	QGSFARVEPEGETMRMWEAIEYTMNRKQPLIIAGADYGQSSRDWAAGVRLAGVEAIV
g099	QGSLARVEPEGQTMRMWEAIEYTMNRKQPLIIAGADYGQSSRDWAAGVRLAGVEAIA
	490 500 510 520 530 540
m099 . pep	AEGFERIHRTNLIGMVLPLQFKPDTNRHTLQLDGTETYDVVGERTPRCDLTLVIHRKNG
g099	AEGFERIHRTNLIGMVLPLQFKPGTNRHTLQLDGTETYDVVGERTPRCGLTLVIHRKNG
	550 560 570 580 590 600
m099 . pep	ETVEVPVTCCLDTAEVLVYEAGGVLRFAQDFLEGNAAX
g099	ETVEVPVTCRPDTAEALVYEAGGVLRFAQDFLEGNAAX
	610 620 630 640

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 355>:

a099 . seq

```

1  ATGCTGGGAC  GCGCGTCCAT  GATGCGCCTG  CCCGATATTG  TCGGCGTTGA
51  GCTGAACGGC  AAACGGAAGG  CGGGCATTAC  GGCGACGGAT  ATTGTGTGG
101 CACTGACCGA  GTTCTGCGC  AAAGAACGCG  TGGTCGGGGC  GTTGTGCGAA
151 TTCTTCGGCG  AGGGCGCGAG  AAGCCTGTCT  ATCGGCGACC  GCGCGACCAT
201 TTCCAACATG  ACGCCGGAGT  TCGGCGCGAC  TGCCGCGATG  TTCGCTATTG
251 ATGAGCAAAC  CATTGATTAT  TTGAAACTGA  CCGGACGCGA  CGACGCGCAG
301 GTGAAATTGG  TGGAAACCTA  CGCCAAAACC  GCAGGCTTGT  GGGCAGATGC
351 CTTGAAAACC  GCCGTTTATC  CGCGCGTTTT  GAAATTGAT  TTGAGCAGCG
401 TAACGCGCAA  TATGGCAGGC  CCGAGCAACC  CGCACGCGCG  TTTTGGCGAC
451 GCCGATTGG  CCGGCAAAGG  CTTGGCTAAA  CCTTACGAAG  AGCCTTCAGA
501 CGGCCAAATG  CCTGACGGTG  CAGTGATTAT  TGCCGCGATT  ACTTCCTGTA
551 CCAATACTTC  CAATCCGCGC  AACGTTGTCG  CCGCCGCGCT  GTTGGCACGC
601 AATGCCAACC  GCCTCGGCTT  GCAACGCAAA  CCTTGGGTGA  AATCTTCGTT
651 TGCCCCGGGT  TCAAAAAGTAG  CCGAAATCTA  TTTGAAAGAA  GCAGATCTGC
701 TGCCCCGAAAT  GGAAAACTC  GGCTTCGGTA  TCGTTGCCTT  CGCATGTACC
751 ACCTGTAACG  GCATGAGCGG  CGCGCTGGAT  CCGAAATCC  AGAAAGAAAT
801 CATCGACCGC  GATTTGTACG  CCACCGCCGT  ATTGTCAGGC  AACC GCAACT
851 TTGACGGCCG  TATCCATCCG  TATGCGAAAC  AGGCTTTCCT  CGCTTCGCCT
901 CCGTTGGTCG  TTGCCTACGC  GCTGGCAGGC  AGCATCCGTT  TCGATATTGA
951 AAACGACGTA  CTCGGCGTTG  CAGACGGCAA  AGAAATCCGC  CTGAAAGACA
1001 TTTGGCTTAC  CGATGAAGAA  ATCGATGCCA  TCGTTGCCGA  ATATGTGAAA
1051 CCGCAGCAAT  TTCGCGACGT  TTATATCCCG  ATGTTTCGAC  CCGGCACAGC
1101 GCAAAAAGCA  CCAAGCCCGC  TGTACGACTG  GCGTCCAATG  TCTACCTATA
1151 TCCGCCGCCC  ACCTTACTGG  GAAGGCGCAC  TGGCAGGGGA  ACGCACATTA
1201 AGCGGTATGC  GTCCGCTGGC  GATTTTGCCC  GACAACATCA  CCACCGACCA

```

```
1251 TCTCTCGCCA TCCAATGCGA TTTTGGCAAG CAGTGCCGCA GGCGAATATT
1301 TGGCAAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGTGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTTTCGC
1451 TGGCACGCGT TGAACCCGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGCGCGGA
1551 CTACGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTGGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACTTGATCG GTATGGGCGT GTTGCCGCTG CAGTTCAAAC CGGGTACCAA
1701 CCGCCACACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTTG TGATTCACCG TAAAAACGGC
1801 GAGACCGTCG AAGTCCCAT TACCTGCCGC CTCGATACCG CAGAAGAAGT
1851 GTTGGTATAT GAAGCCGGTG GCGTATTGCA ACGGTTTGCA CAGGATTTTT
1901 TGAAGGGGAA CCGGCTTAG
```

This corresponds to the amino acid sequence <SEQ ID 356; ORF 099.a>:

a099.pep

```
1  MLGRASMMRL PDIVGVELNG KRKAGITATD IVLALTEFLR KERVVGAFVE
51  FFGEGARSLS IGDRATISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAGKGLAK PYEPPSDGQM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLQRK PWVKSSFAPG SKVAEYLKE ADLLPEMEKL GFGIVAFAC
251 TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFILASP
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDVYIP MFDTGTAQKA PSPLYDWRPM STYIRPPYW EGALAGERTL
401 SGMRLAILP DNITDHLSP SNAIASSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE QOTMRMWEAI
501 ETYMNKQPL IIAAGADYGQ GSSRDWAAKG VRLAGVEAIV AEGFERIHR
551 NLIGMGVLP QFKPGTNRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601 ETVEVPITCR LDTAEVLVY EAGGVLRFA QDFLEGNA*
```

m099/a099 97.5% identity in 639 aa overlap

m099.pep	10	20	30	40	50	60
a099	10	20	30	40	50	60
m099.pep	70	80	90	100	110	120
a099	70	80	90	100	110	120
m099.pep	130	140	150	160	170	180
a099	130	140	150	160	170	180
m099.pep	190	200	210	220	230	240
a099	190	200	210	220	230	240
m099.pep	250	260	270	280	290	300
a099	250	260	270	280	290	300
m099.pep	310	320	330	340	350	360
a099	310	320	330	340	350	360

g102.seq

q102.pap

```

1  MSAKTPSLFG  GAMIIAGKVI  GAGMFPNPTA  NLGDGLIGSL  IVLLYTWFPF
51  SSGALMILEV  NTHNPRGASF  DTMVKDLLGR  GWNIINGIAV  ALVLYGSTYA
101 YILVGGDLTA  KGIGSAVGGK  ISLTVGQLVF  FGILAFVCWA  SARLVDRFTG
151 VLIGGMVLTF  IWATGGLVAD  AKPSVLFDTO  APVGTGYWYI  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWAGT  LVALVIYVLW  QTAIQSNLPR
251 NEFAPVIAAE  RQLSVLNETL  SKFAQTGDMD  KILSLFPYMA  IATSFGLVTL
301 GLFDNIADIF  KWNDMSGRG  TKTVALNFLP  PLISWLLLP  GFFTAIGASG
351 LAATVWDQGI  IPAMLLYVSP  QKIGAGKTYK  VYGLWMLLV  FLFGIANIAA
401 QVLSQMELVP  VFKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 359>:

```

m102.seq
1  ATGCCCAACA  AAACCCCTTC  ACTGTTCCGC  GGCGCGATGA  TTATCGCCGG
51  CACGGTCATC  GCGCGAGGCA  TGCTCGCCAA  CCCGACCGCC  ACATCCGGCG
101 TATGTTTAC  CGGCTCGCTG  GCCGTGTTGC  TGTACACCTG  GTTTTCTATG
151 CTTTCCAGCG  GCCTGATGAT  TTTGGAAGTC  AACACCCATT  ATCCGCACGG
201 CGCAAGTTTC  GACACGATGG  TCAAAGACCT  GCTCGGACGC  GGCTGGAACA
251 TCATCAACGG  CATCGCCGTC  GCCTTCGTTT  TATACCTGCT  TACTTACGCT
301 TATATCTTCG  TCGGCGGCGA  CCTGACCGCC  AAAGGCTTAG  GCAGCGCGGC
351 AGGCGGCGAC  GTTCACTCA  CCGTCGGACA  ACTCGCTTTC  TTCGGCATCC
401 TCGCCTTTTG  CGTATGGGCA  TCCGACCGCT  TGGTCGACCG  CTTACCCGGC
451 GTCCTTATCG  CGGCGATGGT  ATTGACCTTT  ATTGGGCGG  CCGGCGGGCT
501 GATTGCCGAT  GCCAAGCCGT  CCGTCCTCTT  CGATACCCAA  GCCCCGCGCG
551 GCACAACTA  CTGGATTAC  GCCGCCACCG  CCCTGCCCGT  CTGCCTCGCT
601 TCCTTCGGCT  TCCACGGCAA  CGTCTCCAGC  CTGCTCAAAT  ACTTTAAAGG
651 CGACGCGCCC  AAAGTGGCTA  AATCCATCTG  GACGGGCACA  CTGATTGCGC
701 TGGTAATTTA  CGTCCTCTGG  CAAACCGCCA  TCCAAGGCAA  CCTGCCCGCG
751 AACGAGTTTC  CCCCCGTCAT  CGCCGCCGAA  GGGCAAGTCT  CCGTCCTCAT
801 CGAAACCCCTG  TCCAAATTCG  CCCAAACCGG  CAATATGGAC  AAAATATTGT
851 CCCTGTTTTT  CTATATGGCG  ATCGCCACCT  CGTTTTTAGG  CGTAACGCTC
901 GGACTCTTCG  ACTACATCGC  CGACATCTTC  AAATGGAACG  ACAGCATCTC
951 CGGCCCGACC  AAAACCGCCG  CGCTGACCTT  CCTGCCGCC  CTGATTTCTT
1001 GCCTGCTCTT  CCCACCGGC  TTCGTTACCG  CCATCGGCTA  CGTCGGCCTG
1051 GCGGCAACCG  TCTGGACAGG  CATCATCCCC  GCCATGTGTC  TCTACCGTTC
1101 GCGCAAAAAA  TTCGGCGCAG  GCAAAACCTA  TAAAGTTTAC  GCGCGCTTGT
1151 GGCTGATGGT  TTGGGTCTTC  CTTTTCGGCA  TCGTCAACAT  CGCCGCACAG
1201 GTATTGAGCC  AAATGGAAC  CGTCCCCGTA  TTAAAGGAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 360; ORF 102>:

```

m102.pep..
1  MPNKTPSLFG  GAMIIAGTVI  GAGMLANPTA  TSGVWFTGSL  AVLLYTWFSM
51  LSSGLMILEV  NTHYPHGASF  DTMVKDLLGR  GWNIINGIAV  AFVLYLLTYA
101 YIFVGGDLTA  KGLGSAAGGD  VSLTVGQLVF  FGILAFVCWA  SARLVDRFTG
151 VLIGGMVLTF  IWAAGGLIAD  AKPSVLFDTO  APAGTNYWYI  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWGT  LIALVIYVLW  QTAIQNLPR
251 NEFAPVIAAE  QOVSVLIETL  SKFAQTGNMD  KILSLFSYMA  IATSFGLVTL
301 GLFDYIADIF  KWNDISISRT  KTAALTFLEP  LISCLLFTG  FVTAIGYVGL
351 AATVWTGIIP  AMLLYRSRKK  FGAGKTYKVY  GGLWLMVWVF  LFGIVNIAAQ
401 VLSQMELVPV  FK*

```

m102/g102 86.0% identity in 415 aa overlap

	10	20	30	40	50	60
m102.pep	MPNKTPSLFGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
g102	MSAKTPSLFGGAMIIAGKVIAGMFPNPTANLGDGLIGSLIVLLYTWFPFSSGALMILEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m102.pep	NTHYPHGASFDTMVKDLLGRGWNIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD					
g102	NTHNPRGASFDTMVKDLLGRGWNIINGIAVALVLYGSTYAYILVGGDLTAKGIGSAVGGK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m102.pep	VSLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDTO					
g102	ISLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFIATGGLVADAKPSVLFDTO					
	130	140	150	160	170	180
	190	200	210	220	230	240
m102.pep	APAGTNYWYIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWGTIALLVIYVLW					

a102.seq

1	ATGCCACCA	AAACCCCTTC	ACTGTTCCGC	GCGCGATGA	TTATCGCCGG
51	CACGNTCATC	GGCGCAGGTA	TGCTCGCCAA	CCCAGCCGCC	ACATCCGGCG
101	TATGGTTTAC	CGGCTCGCTG	GCCGTGTTGC	TGTACACCTG	GTTTTCCATG
151	CTCTCCAGCG	GCCTGATGAT	TTTGGAAGTC	AACACCACT	ACCCCCACGG
201	CGCGANCTC	GACACCATGG	TAAAGACCT	CTCGGACGG	AGCTGGAACA
251	TCATCAACGG	CATCGCCGTC	GCCTTCTGTT	TATACCTGCT	TACTTACGCT
301	TATATCTTCG	TCGGCGGCGA	CCTGACCGCC	AAAGGCTTAG	GCAGCGCGGC
351	AGGCGGCAAT	GTTTCACTCA	CCGTCCGACA	ACTCGTCTTC	TTCGGCATTTC
401	TCGCCTTTTG	CGTATGGGCA	TCCGCACGCT	TGGTCGACCG	ATTACCCAGC
451	GTCTCTCATG	GCGGCATGGT	ATTAACCTTT	ATTGGGCAA	CGCCCGGCTT
501	GATTGCCGAT	GCCAAACTGC	CCGCTCTCTT	CGACACCCAA	GCCCCTACCG
551	GCACCAACTA	CTGGATTTAT	GTGCCACCG	CCCTGCCCGT	CTGCCTTGCG
601	TCATTTCGTT	TCCACGGCAA	CGTCTCCAGC	CTGCTCAAAT	ACTTTTAAAG
651	CGACGCGCCC	AAAGTGGCTA	AATCCATCTG	GACGGGCACA	CTGTATTGCG
701	TGGTAATTTA	CGTCTCTTGG	CAACCCGCCA	TCCAAGCAA	CTGCGCCGCG
751	AACGAGTTTC	CCCCCGTGAT	TGCCGCCGAA	GCGCAAGTCT	CCGTCTGTAT
801	TGAAACCCCTG	TCCAAATTCG	CCCAAACCGG	CAATATGGAC	AAAATATTGT
851	CCCTGTTTTTC	CTATATGGCG	ATCGCCACCT	CGTTTTTAGG	CGTAACGCTC
901	GGACTCTTCG	ACTACATCG	CGACATCTTC	AAATGGAACG	ACAGCTGTGC
951	CGGCCGACC	AAAACCGCG	CGTGACCTT	CTGCGCCGCT	NTAATTTCTT
1001	GCGTGCTCTT	CCCCACCGGC	TTGTTTACCG	CCATCGGNTA	CGTCGGCCGTG
1051	GCGGCAACCG	TCTGGACAGG	CATCATCCCC	GCCATGCTGC	TNTACCGTTC
1101	GCGCAAAAAA	TTCGGCGCAG	GCAAAACCTA	TAAAGTTTAC	GGCGGCTTGT
1151	GGCTGATGGT	TTGGGTCTTC	CTTTTCGCA	TCNTCAACAT	CGCCGCACAN
1201	GTATTGAGCC	AAATGGAACT	CGTCCCCGTA	TTTAAAGGAT	AA
1202					

This corresponds to the amino acid sequence <SEQ ID 362; ORF 102.a>:

a102.pep

1	MPTKTPSLFG	GAMI IAGTXI	GAGMLANPTA	TSGVWFTGSL	AVLLYTWFMS
51	LSSGLMILEV	NTHYPHGA XF	DTMVKDLLGR	SWNIINGIAV	AFVLYLLTYA
101	YIFVGGDLTA	KGLGSAAGGN	VSLTVFGDLT	FGILAFCVWA	SARLVDRFST
151	VLIGGMVLTIF	IWATGGLIAD	AKLPVGLQVQ	APTGTNYWIY	VATALPVCLA
201	SFGFHGNVSS	LLKYFKGDAP	KVAKSIWTGT	LIALVIYVLW	QTAIQXNLPR
251	NEFAPVIAAE	GQVSVXIETL	SKFAQTGNMD	KILSLFSYMA	IATSFGLVTL
301	GLFDYIADIF	KWNDSVSGRT	KTAALTFLPP	XISCLLFPTG	FVTAIGYVGL
351	AATVWVTGIIP	AMLLYRSRKK	FGAGKTYKVY	GGLWLMVWVF	LFGIXNIAAX
401	VLVSOMELVPV	FKG*			

m102 / a102 95.9% identity in 413 aa overlap

312

m102.pep	10	20	30	40	50	60
	MPNKTPSLFEGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
a102	MPTKTPSLFEGGAMIIAGTXIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
	10	20	30	40	50	60
m102.pep	70	80	90	100	110	120
	NTHYPHGASFDTMVKDLLGRGWNIIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD					
a102	NTHYPHGAXFDTMVKDLLGRSWNIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGN					
	70	80	90	100	110	120
m102.pep	130	140	150	160	170	180
	VSLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDTQ					
a102	VSLTVGQLVFFGILAFVCWASARLVDRFTSVLIGGMVLTFIWATGGLIADAKLPVLFDTQ					
	130	140	150	160	170	180
m102.pep	190	200	210	220	230	240
	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
a102	APTGTNYWIYVATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
	190	200	210	220	230	240
m102.pep	250	260	270	280	290	300
	QTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
a102	QTAIQXNLPNEFAPVIAAEGQVSVXIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
	250	260	270	280	290	300
m102.pep	310	320	330	340	350	360
	GLFDYIADIFKWNDSISGRKTAAALFLPPLISCLLFPTGFVTAIGYVGLAATVWTGIIP					
a102	GLFDYIADIFKWNDSVSGRKTAAALFLPPXISCLLFPTGFVTAIGYVGLAATVWTGIIP					
	310	320	330	340	350	360
m102.pep	370	380	390	400	410	
	AMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIVNIAAQVLSQMEI LVPVFKGX					
a102	AMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIXNIAAXVLSQMEI LVPVFKGX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 363>:

g105.seq

```

1  Atgtccgcag aaaCATACac acAAAtcggc tGGgtaggct taggGcaaat
51  gGgtctgcct atgGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCcgC CAAAGGAGCA
151 AAAGTTTACG GCagcACCGC CGAACTCGTC CGCGCCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTCCGGC ATGTCGGCAA
501 AGGCTCGGGC GCGAACTCG TCTTGAATC GCTCTTAGGC ATTTTCCGGC
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGAAT CGCCTATGTT
651 TCAAACAAAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CCTGCCTTTG
701 CACTCAAACA CGCTTCCAAA GacctTAACC TCGccgtcAA AGAGCTTGAA
751 CAGGCAGGCA ACACCCTGCC CGCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAATTGGC AGAACACTGA

```


1	MSAETYTQIG	WVGLGQMGPL	MVTRLLDGGI	EVGVYNRSPD	KTAPISAKGA
51	KVYGSTAEVL	RACPVIFLMV	<u>SDYAAVCDIL</u>	NGVRDGLAGK	IIVNMSTISP
101	TENLAVKALV	EAAGGQFAEA	PVSGSVGPAT	NGTLLILFGG	SEAVLNFLQK
151	IFSLVGKKT	HFGDGQKGS	AKLVLSLLG	IFGEAYSEAM	LMARQFGIDT
201	DTIVEAIGS	AMDSPMFKTK	KSLWANREFF	PAFALKHASK	DLNLAVKELE
251	QAGTEILPAVE	TVAASYRKAV	EAGYGEODVS	GVYLKLAEH	

m105.seq

1	ATGTCGCGCAA	ACGAATACGC	ACAAATCGGC	TGGaTAGGCT	TAGGGCAAAT
51	GGGTCTGCCT	ATGGTAACGC	GGCTCTTGGA	CGGCGGCATC	GAAGTCGGCG
101	TATACAACCG	CTCGCCCGAC	AAAAC TGCCC	CCATCTCCGC	CAAAGGCGCA
151	AAAGTTTACG	GCAACACCGC	CGAACCTCGT	CGCGACTATC	CCGCTCATTTT
201	CTGTGATGGT	TCGCATATG	CGCCGCTGTG	CGACATCTGT	AACCGAGTCC
251	GGCAGCGAAT	GCCCGCGAAm	ATCATCGTCA	ACATAGCAC	CATCTCCCGC
301	ACCGAAAaGC	TCGCCGTCAA	AGCACTTGTC	GAAGCGCAGm	GaCAGTTTGC
351	CGAAGCACCC	GTTTCCGGAT	CGGTCGGGCC	CGCCACCAAC	GGCACGCTGC
401	TGATTCTGTT	CGGCGGCAGC	GAaCGtTTT	AAACCCGCTG	CAAAAAATAT
451	TTTCCCTCGT	CGGCAAAAAA	GAATTCCATT	TCGGCGATGT	CGGCAAAGGT
501	TCGGGCGCGA	AACTCGTCTT	GAACTCGCTC	TTGGGCATTT	TCGGCGGaaCG
551	TACAGCGAAa	GmTgCTGATG	GCGCGCGAGT	TCGGCATCGA	TACCGACACC
601	ATCGTCGAAG	CCATCGGsGA	CTCGGCAATG	GACTCGCCCA	TGTTCCAAAC
651	CAAAAAATCC	CTGTGGGCAA	ACCGCGAATT	CCCGmCCGmC	TTCCGCCCTCA
701	AACACGCCTC	CAAAGACCTC	AACCTCGCCG	TCAAAGAGCT	TGAACAGGCA
751	GGCAACACCC	TGCCCGCCGT	CGAAACCGTT	GCTGCCAGCT	ACCGCAAAGC
801	AGTCGAAGCC	GGCTACGGGA	CACAGGACGT	TTCCGGCGTT	TACCTGAAAC
851	TGGCAGAAAC	CTGA			

m105.pep

1	MSANEYAQIG	WIGLGQMG	LVTRLLDGGI	EVGVYNRSPD	KTAPISAKGA
51	KVYGNTAELV	RDYPVIFLMV	<u>SDYAAVCDIL</u>	NGVRDLGAGX	IIVNMSTISP
101	TEKLAVKALV	EAQRQFAEAP	VSGSVGPATN	GTLLILFGGS	EPFXTRCKKY
151	FPSSAKKPSI	SAMSAKVRAR	NSSXTRSWAF	SANVQRXXLM	ARQFGIDTDT
201	IVEAIGDSAM	DSPMFQTKKS	LWANREFPXX	FALKHAKSDL	NLAVKELEGA
251	GNTLPVAVETV	AASYRKAVEA	GYGTDVSGV	YLKLAEB	

Homology with a predicted ORF from *N. gonorrhoeae*

m105/g105

	10	20	30	40	50	60
g105.pep	MSAETYYQIGWVGLGQMGLPMVTRLLDGGIEVG VYNRSPDKTAPISAKGAKVYGSTAE L V					
m105	MSANEYAQIGWIGLGQMGLPMVTRLLDGGIEVG VYNRSPDKTAPISAKGAKVYGN T A E L V					
	10	20	30	40	50	60
	70	80	90	100	110	120
g105.pep	RACPFVIFLMVSDYAAVCDILNGVRDGLAGKII VN MSTISP TENLAVKKALVEAAGGF AE A					
m105	RDYPVIFLMVSDYAAVCDILNGVRDGLAGXII VN MSTISP TEKLAVKKALVEAQ R - QFAEA					
	70	80	90	100	110	
	130	140	150	160	170	180
g105.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSL VGKKTFFHGDVKGSGAKLVLSN LL G					
m105	PVSGSVGPATNGTLLILFGGSEFFXTRCKKYFPSS AKKP-SISAMSAKVARNSSX TRSW					
	120	130	140	150	160	170

314

	190	200	210	220	230	240
g105.pep	IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK					
	:	::				
m105	AFSANVQRXXLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPXXFALKHASK					
	180	190	200	210	220	230

	250	260	270	280	289
g105.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEH				
m105	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGTQDVSGVYLKLAEH				
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 367>:

a105.seq

```

1  ATGTCCGCAA  ACGAATACAC  ACAAATCGGC  TGGATAGGCT  TAGGGCAAAT
51  GGGTCTGCCT  ATGGTAACGC  GGCTCTTGGA  CGGCGGCATC  GAAGTCGGCG
101 TATACAACCG  CTCGCCGAC  AAAACTGCCC  CCATCTCCGC  CAAAGGCGCA
151 AAAGTTTACG  GCAACACCGC  CGAACTCGTC  CGCGACTATC  CCGTCATTTT
201 CCTGATGGTT  TCCGACTATG  CCGCCGTGTG  CGACATCCTG  AACGGAGTCC
251 GCGACGGATT  GGCCGGCAAA  ATCATCGTCA  ACATGAGCAC  CATCTCCCCG
301 ACCGAAAACC  TCGCCGTCAA  AGCACTTGTC  GAAGCCGCAG  GCGGACAGTT
351 TGCCGAAGCA  CCCGTTCCG  GATCGGTCGG  GCCCGCCACC  AACGGCACGC
401 TGCTGATTCT  GTTCGGCGGC  AGCGAAGCCG  TTTTAAACCC  GCTGCAAAAA
451 ATATTTTCCC  TCGTCGGCAA  AAAAACCTTC  CATTTCGGCG  ATGTCGGCAA
501 AGGTTTCGGC  GCGAACTCG  TCTTGAACCT  GCTCTGGGC  ATTTTCGGCG
551 AAGCGTACAG  CGAAGCGATG  CTGATGGCGC  GGCAGTTCGG  CATCGATACC
601 GACACCATCG  TCGAAGCCAT  CGGCGGCTCG  GCAATGGACT  CGCCCATGTT
651 CCAAACCAA  AAATCCCTGT  GGGCAAACCG  CGAATTCCTA  CCCGCCTTCG
701 CCCTCAAACA  CGCCTCCAAA  GACCTCAACC  TCGCCGTCAA  AGAGCTTGAA
751 CAGGCAGGCA  ACACCCTGCC  CGCCGTCGAA  ACCGTTGCTG  CCAGCTACCG
801 CAAAGCAGTC  GAAGCCGGCT  ACGGCGAACA  GGACGTTTCC  GCGGTTTACC
851 TGAAATTGGC  AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 368; ORF 105.a>:

a105.pep

```

1  MSANEYTOIG  WIGLGQMLP  MVTLLDGGI  EVGVYNRSPD  KTAPISAKGA
51  KVGNTAELV  RDYPVIFLMV  SDYAAVCDIL  NGVRDGLAGK  IIVNMSTISP
101 TENLAVKALV  EAAGGQFAEA  PVSGSVGPAT  NGTLLILFGG  SEAVLNPLQK
151 IFSLVGKKT  FFGDVGKSG  AKLVNLSLLG  IFGEAYSEAM  LMARQFGIDT
201 DTIVEAIGGS  AMDSPMFQTK  KSLWANREFP  PAFALKHASK  DLNLAVKELE
251 QAGNTLPAVE  TVAASYRKAV  EAGYGEQDVS  GYVLKLAEH*

```

m105/a105 96.5% identity in 289 aa overlap

	10	20	30	40	50	60
m105.pep	MSANEYAQIGWIGLGQMLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
a105	MSANEYTOIGWIGLGQMLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
	10	20	30	40	50	60

	70	80	90	100	110	119
m105.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAG-QFAEA					
a105	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA					
	70	80	90	100	110	120

	120	130	140	150	160	170	179
m105.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVNLSLLG						
a105	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVNLSLLG						
	130	140	150	160	170	180	

	180	190	200	210	220	230
--	-----	-----	-----	-----	-----	-----

315

```

m105.pep    IFGDV-QRXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFFXAFALKHASK
            |||:: :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFFPAFALKHASK
            190      200      210      220      230      240

            240      250      260      270      280
m105.pep    DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
            250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 369>:

g105-1.seq

```

1   ATGTCGCGAG AACATACAC ACAAATCGGC TGGGTAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCCGC CAAAGGAGCA
151 AAAGTTTACG GCAGCACCGC CGAACTCGTC CGCGCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGAG GCGGACAGTT
351 TGCCGAAGCA CCGTTTCCG GATCGGTGCG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTCCGGC ATGTCGGCAA
501 AGGCTCGGGC GCGAACTCG TCTTGAATC GCTCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCTATGTT
651 TCAAAACAAA AAATCACTAT GGGCAAAACG TGAGTTCCCC CCTGCCTTTG
701 CACTCAAAAC CGTTTCCAA GACCTTAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGCGAACA GGACGTTTC GCGGTTTACC
851 TGAAATTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 370; ORF 105-1.ng>:

g105-1.pep

```

1   MSAETTYQIG WVGLQMGLP MVTRLDDGGI EVGVYNRSPD KTAPISAKGA
51  KVYGSTAELV RACPVIPLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
151 IFSLVGKTFE HFGDVGKSG AKLVNLSLG IFGEAYSEAM LMARQFGIDT
201 DTIVEAIGGS AMDSPMFQTK KSLWANREFF PAFALKHASK DLNLAVKELE
251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 371>:

m105-1.seq

```

1   ATGTCGCGAA ACGAATACGC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCCGC CAAAGGCGCA
151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGAG GCGGACAGTT
351 TGCCGAAGCA CCGTTTCCG GATCGGTGCG GCCCGCCACC AACGGCACGC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTCCGGC ATGTCGGCAA
501 AGGTTTCGGC GCGAACTCG TCTTGAATC GCTCTTGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGAGACTCG GCAATGGACT CGCCCATGTT
651 CCAAAACAAA AAATCCCTGT GGGCAAAACG CGAATTCGCC CCGGCTTCG
701 CCCTCAACA CGCTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTC GAAGCCGGCT ACGCGAACA GGACGTTTC GCGGTTTACC
851 TGAAACTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 372; ORF 105-1>:

m105-1.pep

```

1   MSANEYAQIG WIGLQMGLP MVTRLDDGGI EVGVYNRSPD KTAPISAKGA
51  KVYGNTEALV RDYPIVPLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP

```

	10	20	30	40	50	60
m105-1.pep	MSANEYAQIGWIGLQMG	LPMTVRL	LDGGIEVGVN	RS	PDKTAPISAKGAKVY	GN
g105-1	MSAETYYQIGWVGLQMG	LPMTVRL	LDGGIEVGVN	RS	PDKTAPISAKGAKVY	GN
	10	20	30	40	50	60
m105-1.pep	RDYFVIFILMVSDYAAV	CDILNGVRDGLAGK	II	VNMSTISPTENLAVKALVEA	AGGQFAEA	
g105-1	RACPVIFILMVSDYAAV	CDILNGVRDGLAGK	II	VNMSTISPTENLAVKALVEA	AGGQFAEA	
	70	80	90	100	110	120
m105-1.pep	PVSGSVGPATNGTLLIL	FGGSEAVLNPLQKIF	SLVGGKTFHFGDV	GKSGAKLV	NSLIG	
g105-1	PVSGSVGPATNGTLLIL	FGGSEAVLNPLQKIF	SLVGGKTFHFGDV	GKSGAKLV	NSLIG	
	130	140	150	160	170	180
m105-1.pep	IFGEAYSEXMLMARQFG	IDTDTIVEAIGDSAM	DSPMFQTKKSLWAN	REFFPPAFAL	KHASK	
g105-1	IFGEAYSEXMLMARQFG	IDTDTIVEAIGDSAM	DSPMFQTKKSLWAN	REFFPPAFAL	KHASK	
	190	200	210	220	230	240
m105-1.pep	DLNLAVKLEQAGNTLP	AVETVAASYRKAVEA	GYGEQDVSGVYLK	LAEHX		
g105-1	DLNLAVKLEQAGNTLP	AVETVAASYRKAVEA	GYGEQDVSGVYLK	LAEHX		
	250	260	270	280	290	

a105-1.seq

1	ATGTCGCGAA	ACGAATACAC	ACAAATCGGC	TGGATAGGCT	TAGGGCAAAT
51	GGTCTGCGCT	ATGGTAAACG	GGCTCTTGGA	CGCGCGCATC	GAAGTCGGCG
101	TAAACAAACG	CTCGCCCGAC	AAAACCTGCC	CCATCTCCGC	CAAAGCGCTA
151	ATAAGTTACG	GCAACACCGC	CGAACTCGTC	CGCGCATATC	CGGTATTTTT
201	CCTGATGGTT	TCCGACTATG	CCGCCGTGTG	CGACATCTTG	AACGGAGTCC
251	GCGACGGATT	GGCCCGGCAA	ATCATCTGTA	ACATGAGCAC	CATCTCCCCG
301	ACCGAAACCC	TCCGCCGTAA	AGCACTTGTC	GAAAGCCGAG	CGCGACAGTT
351	TGCCGAAGCA	CCCGTTTCCG	GATCGGTCCG	GCCCGCCACC	AACGGCACGC
401	TGCTGATTCT	GTTTCGGCGC	AGCGAAGCCG	TTTTAAACCC	GCTGCAAAAA
451	ATATTTTCCC	TCGTCGGCAA	AAAAACCTTC	GCTTTCGGCG	ATGTCGGCAA
501	AGGTTTCGGC	GCGAAACTCG	TCTTGAACCT	GCTCTTGGGC	ATTTTCGGCG
551	AAGCGTACAG	CGAAGCGATG	CTGATGGCGC	GGCAGTTGCG	CATCGATACC
601	GACACCATCA	TCGAAGGCAT	CGCGGGCTCG	GCAATTGGAT	CGCCCATTCG
651	CCAAACCAA	AAATCCTGTT	GGGCAAAACG	GCAATTCCCA	CCCGGCTTGC
701	CCCTCAAACA	CGCCTCCAAA	GACCTCAACC	TCGCCGTCAA	AGAGCTTGAA
751	CAGGAGGCA	ACACCTTGCC	CGCCGTCGAA	ACGTTTGTGT	CCAGCTACCG
801	CAAAGCAGTC	GAAGCCGGCT	ACGGCGAACA	GGACGTTTCC	GGCGTTTACC
851	TGAAATTTGGC	AGAACACTGA			

a105-1.pap

1	1	MSANEY	TQIG	WIGLGQ	MGLP	MVTRLL	DGGI	EVGVYN	RSPD	KTAPISAK	
51	1	KVYENG	TAELV	RDYPTV	FLMV	SDYA	AAVCDIL	NGVRDL	GLAGK	IIVNMSTG	
101	1	TENLAV	LAKV	EAAAGG	FAVA	PVSGV	SGVPAT	NGRTLL	ILIFGG	SEAVNPLQK	
151	1	IFSLV	GKKTF	HFGDV	GKSG	AKLVN	SLLG	IFGEAY	SEAM	LMARQFG	IDT
201	1	DTIVEA	IGS	AMDS	PMFQTK	KSLWAN	REFP	PAFALK	HASK	DLNLAVKE	LE
251	1	QAGNTL	PAVE	TVAASV	RRKAV	EAGYGE	QDVS	GVYK	KLAEH*		

a105-1.pep MSANEYTGIGWIGLGQMLPMVTRLDDGGIEVGYNRSPDKTAPISAKGAKVYNGTAELV

```

m105-1      MSANEYAQIGWIGLGQMGLPMVTRLDDGGIEVG VYNRSPDKTAPISAKGAKVYGNTAELV
              10      20      30      40      50      60
a105-1.pep  RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA
              70      80      90      100     110     120
m105-1      RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA
              70      80      90      100     110     120
a105-1.pep  PVS GSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVLSLLG
              130     140     150     160     170     180
m105-1      PVS GSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVLSLLG
              130     140     150     160     170     180
a105-1.pep  IFGEAYSEAMLMARQFGIDTD TIVEAIGGSAMDS PMFQTKKSLWANREFPPAFALKHASK
              190     200     210     220     230     240
m105-1      IFGEAYSEXMLMARQFGIDTD TIVEAIGDSAMDS PMFQTKKSLWANREFPPAFALKHASK
              190     200     210     220     230     240
a105-1.pep  DLNLAVKELEQAGNTLPAVETVAASYRKA VEAGYGEQDVSGVYLKLAHX
              250     260     270     280     290
m105-1      DLNLAVKELEQAGNTLPAVETVAASYRKA VEAGYGEQDVSGVYLKLAHX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 375>:

```

g107.seq
1  ATGGTATTAA CCTTTATTTG GGCAACCGGC GGCCTGGTTG CCGATGCCAA
51  ACCGTCCGTC CTCTTCGACA CCAAGCCCC CGTCGGCACC GGCTACTGGA
101 TTTACGCCGC CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTTT CCAGCCTGCT CAAATACTTT AAAGGCGACG cgcCcaaagt
201 GgCGAaATCc atctggGcag gtacattggT TGCcttggtt atttacgtcc
251 TCTggcaaac cgccatCcaa agcaaccTGC cgcgcaacga gttcgcCCCC
301 gtgattgccg ccgagaggca actCTCCGTC CTgaatgaaa cctTgtccaa
351 attcgcccaa accggcgata tggataAaat attgtcccta tttccctaca
401 tggcaatcgc cacctccttt ttaggcgTAA Ccttaggcct gtttgacaac
451 atcgccggac atcttcaaat ggaacgacag tatgtccggg cggcacaaaa
501 accgtcgcgc tga

```

This corresponds to the amino acid sequence <SEQ ID 376; ORF 107.ng>:

```

g107.pep
1  MVLTFIWATG GLVADAKPSV LFDTPAPVGT GYWIYAATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWAGTLVALV IYVLWQTAIQ SNLPRNEFAP
101 VIAAERQLSV LNETLSKFAQ TGDMDKILSL FPYMAIATSF LGVTLGLFDN
151 IAGHLQMERQ YVRAAPKPSR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 377>:

```

m107.seq
1  ATGGTATTGA CCTTTATTTG GGCGGCCGGC GGGCTGATTG CCGATGCCAA
51  GCCGTCCGTC CTCTTCGATA CCAAGCCCC CGCCGGCACA AACTACTGGA
101 TTTACGCCGg CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCGCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTCATCGCCG CCGAAGGGCA AGTCTCCGTC CTCATCGAAA CCCTGTCCAA
351 ATTCGCCCAA ACCGGCAATA TGGACAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCCATC TTCAAATGGA ACGACAGCAT CTCCGGgCCG CACCAAACC
501 GCCGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 378; ORF 107>:

```

m107.pep..
1  MVLTFIWAAG GLIADAKPSV LFDTPAPAGT NYWIYAXTAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP

```

101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
 151 IAHLMQERQH LRAAPKPPR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 107 shows 89.4% identity over a 170 aa overlap with a predicted ORF (ORF 107.ng)
 from *N. gonorrhoeae*:

m107/g107

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	: : : : :					
g107	MVLTFIWAATGGLVADAKPSVLFDTQAPVGTGYWIYAATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
	: : : : :					
g107	KGDAPKVAKSIWAGTLVALVIYVLWQTAIQGNLPRNEFAPVIAAERQLSVLNETLSKFAQ					
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSF LGVTLGLFDYIA-HLMQERQHLRAAPKPPR					
	: : : : :					
g107	TGDMDKILSLFFPYMAIATSF LGVTLGLFDNIAGHLMQERQYVRAAPKPSR					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 379>:

a107.seq

```

1  ATGGTATTAA CCTTTATTG GGCACCGGC GGCCTGATTG CCGATGCCAA
51  ACTGCCCGTC CTCTCGACA CCCAAGCCCC TACCGGCACC AACTACTGGA
101 TTTATGTGCG CACCGCCCTG CCCGTCTGCC TTGCGTCATT CGGTTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTGATTGCCG CCGAAGGGCA AGTCTCCGTC CTGATTGAAA CCCTGTCCAA
351 ATTCGCCCAA ACCGGCAATA TGGACAAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCGACA TCTTCAAATG GAACGACAGC GTGTCCGGCC GCACCAAAC
501 CGCGCGCTG ACCTTCCTGC CGCCTCTAAT TTCCTGCCTG CTCTCCCCA
551 CCGGCTTTGT TACCGCCATC GGCTACGTCG GCCTGGCGGC AACCGTCTGG
601 ACAGGCATCA TCCCCGCCAT GCTGCTCTAC CGTTCGCGCA AAAAATTCGG
651 CGCAGGCAAA ACCTATAAAG TTACGGCGG CTTGTGGCTG ATGGTTTGGG
701 TCTTCCTTTT CGGCATCGTC AACATCGCCG CACAGGTATT GAGCCAAATG
751 GAACTCGTCC CCGTATTAA AGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 380; ORF 107.a>:

a107.pep

```

1  MVLTFIWAATG GLIADAKLPV LFDQAPTGT NYWIYVATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP
101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
151 IADIFKWNDS VSGRTKTAAL TFLPPLISCL LFPTGFVTAI GYVGLAATVW
201 TGIIPAMLLY RSRKKFGAGK TYKVYGLWL MVWVFLFGIV NIAAQVLSQM
251 ELVPVFKG*

```

m107/a107 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	: : : : :					
a107	MVLTFIWAATGGLIADAKLPVLFDTQAPTGTNYWIYVATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60

319

	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
a107	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIAHLQMERQHLRAAPKPPRX					
a107	TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIADIFKWNDSVSGRTKTAALTFLPPLISCL					
	130	140	150	160	170	180
a107	LFPTGFVTAIGYVGLAATVWTGIIPAMLLYRSRKKFGAGKTYKVYGGWLWMVWVFLFGIV					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 381>:

g108.seq

1	ATGttgccgg	gCTTCAACCG	GATATTCAaa	cggTTTGCTC	CAACACTCGG
51	AAcggCGCAT	AAAACGCCgc	ccTTTCGCGT	ATCCCGAACG	GGGCGGCTAA
101	TCAGATCCTA	TCGCCATAAA	AGGCGGGGTT	TCAACCGAAA	AGGAATTGAG
151	ATGAATAAAA	CCTTGCTCTAT	TTTGCCGGCG	GCAATCTTAC	TCGCGGGGTG
201	CGCCGCCGGC	GGCAACACAT	TCGGCAGCTT	AGACGGCGGC	ACGGGTATGG
251	GTGGCAGCAT	CGTCAAAATG	ACGGTAGAAA	gccAATGCCG	TGCGGAATTG
301	GACAGCGCA	GCGAATGGCG	TTTGACCGCG	CTGGCGATGA	GTGCGGAAAA
351	ACAGGCGGAA	TGGGAAAACA	AGATTTCGGG	CTGCGCTACC	GAAGAAGCAC
401	CTAACCAGCT	GACCGGCAAC	GATGTGATGC	AGATGCTGaa	ccagtccacG
451	CGCaatcagg	cacTtgccgc	CctgaccgTC	AAAacgggTT	CcgccctgCTT
501	CAaacgcctg	tACCGCTAA			

This corresponds to the amino acid sequence <SEQ ID 382; ORF 108.ng>:

g108.pep

1	MLPGFNRIK	RFAPTLGTAH	KTPPFALSRT	GRLIRSYRHK	RRGFNRKGIE
51	MNKTLSILPA	AILLGGCAAG	GNTFGSLDGG	TGMGGSIVKM	TVESQCRAEL
101	DRRSEWRLTA	LAMSAEKQAE	WENKICGCAT	EEAPNQLTGN	DVMQMLNQST
151	RNQALAAALTV	KTVSACFKRL	YR*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 383>:

m108.seq

1	ATGTTGCCGG	GCTTCAACCG	GATATTCAAA	CGGTTTGTTT	CAACACTCGG
51	AACGGCGCAT	AAAACGCCGC	CCTTCGCGTT	ATCCCGAACG	GGGCGGCTAA
101	TCAGATTCTA	TCGCCATAAA	AGGCGGGGTT	TCAACCGAAA	AGGAATTGAG
151	ATGAATAAAA	CCTTGCTCTAT	TTTGCCGGTG	GCAATCTTAC	TCGCGGGCTG
201	CGCCGCCGGA	GGCGGTAACA	CATTCCGCAG	CTTAGACGGT	GGCACAGGCA
251	TGGCGGCAG	CATCGTCAA	ATGGCGGTTG	GGAGCCAATG	CCGTGCGGAA
301	TTGGACAAAC	GCAGCGAATG	GCGTTTGACC	GCGCTGGCGA	TGAGTGCCGA
351	AAAACAGGCG	GAGTGGGAAA	ACAAGATTG	CGCTTGCGTC	GCCCAAGAAG
401	CACCCGAACG	GATGACCGGC	AACGATGTGA	TGCAGATGCT	GGCTCCGTCC
451	ACGCGCAATC	AGGCACTTGC	CGCCCTGACC	GCCAAAACGG	TTTCCGCCTG
501	CTTCAAACAC	CTGTACCGCT	AA		

This corresponds to the amino acid sequence <SEQ ID 384; ORF 108>:

m108.pep

1	MLPGFNRIK	RFVPTLGTAH	KTPPFALSRT	GRLIRFYRHK	RRGFNRKGIE
51	MNKTLSILPV	AILLGGCAAG	GGNTFGSLDG	GTGMGGSIVK	MAVGSQCRAE
101	LDKRSEWRLT	ALAMSAEKQA	EWENKICACV	AQEAPERMTG	NDVMQMLAPS
151	TRNQALAAAL	AKTVSACFKH	LYR*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 108 shows 89.6% identity over a 173 aa overlap with a predicted ORF (ORF 108.ng) from *N. gonorrhoeae*:

m108/g108

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 385>:

1	ATGTTGCCGG	GCTTCAACCG	GATATTCAAA	CGGTTTGTC	CAACACTCGG
51	AACGGCGCAT	AAAACGCCG	CCTTCGCGTT	ATCCCGAACG	GGGCGGCTAA
101	TCAGATTCTA	TCGCCATAAA	AGGCGGGGTT	TCAACCGAAA	AGGAATTGAG
151	ATGAATAAAA	CCTTGTCTAT	TTTGCCGGTG	GCAATCTTAC	TCGGCGGGTG
201	CGCCGCGCGG	GGCGGTAACA	CATTCGGCAG	CTTAGACGGC	GCGACAGGTA
251	TGGGCGCGAG	CATCGTCAAA	ATGGCGGTAG	AAAGCCAATG	CCGTGCGGAA
301	TTGAACAAAC	GCAGCGAATG	GCGTTTGACC	GCGCTGGCGA	TGAGTGCCGA
351	AAAACAGGCG	GAATGGGAAA	ACAAGATTTG	CGCTTGCGTC	GCCCAAGAAG
401	CACCCAACCA	GCTGACCGGC	ACGATGTGA	TGCAGATGCT	GGATCCGCTC
451	ACGCGCAATC	AGGCACCTGC	CGCCTTGACC	GCCAAACGG	TTTCCGCTCG
501	CTTCAAAAC	CTGTACCCT	AA		

This corresponds to the amino acid sequence <SEQ ID 386; ORF 108.a>:

1 MLPGFNRIFK RFVPTLGTAH KTPPFALSRT GRLIRFYRHK RRGFNRRKGIE
51 MNKTLSILPV AILGGCAAG GGNTFGSLDG GTMGGSIVK MAVESQCRAE
101 LNKRSEWRLT ALAMSAEKQA EWENKICACV AQEAPNQLTG NDMVMQLDPS
151 TRNQAALALT AKTVSACFKH LYR*

m108/a108 96.5% identity in 173 aa overlap

	10	20	30	40	50	60
m108.pep	MLPGFNRIFKRFVPTLGTAHKTPPFALSRTGRLIRFYRHKRRGFNRKGIEMNKTL					
a108	MLPGFNRIFKRFVPTLGTAHKTPPFALSRTGRLIRFYRHKRRGFNRKGIEMNKTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m108.pep	AILLGGCAAGGGNTFGSLDGGTGMGGSIIVKMAVGSQCRAELDKRSEWRITALAMSAEKQA					
a108	AILLGGCAAGGGNTFGSLDGGTGMGGSIIVKMAVESQCRAELNKRSEWRITALAMSAEKQA					
	70	80	90	100	110	120
	130	140	150	160	170	
m108.pep	EWENKICACVAQEAPERMTGNDVMQMLAPSTRNQALAAALTAKTVSACFKHLYRX					
a108	EWENKICACVAQEAPNQLTGNDVMQMLDPSTRNQALAAALTAKTVSACFKHLYRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 387>:

g109.seq

```

1  ATGTATTATC GCCGGGTTGT GGGGCTATCC GATGGACTTG GCGATTGGC
51  AGCCGGTATT GATCGTAGGC GTATGCTTAC CGCTTTTGA AGCGGGCATG
101 GAAATGACGC GCAAAGGCAA AACCACCAA TCCGCCGCCA TCGTGGTGTG
151 CTCTTCCGTC TGGTCAATCC GGTTCGCGC TGGGCGTTGA CGATGCTGTT
201 GGATAATTG GGCTTAATCG GCTGCAAAGA ACGCAGCGCG CAATTAGGTT
251 TTGTCGGACG AGTATTGATA CCCGCAGTAG GTTCTTAAT CTTGTGTGTG
301 GCGATGGGTG CGGTCGGGAT GCTGCCCGGT ATCCCTCCGT TTTTGGAGCA
351 GTTCAAATCT TTGGGCTAG

```

This corresponds to the amino acid sequence <SEQ ID 388; ORF 109.ng>:

g109.pep

```

1  MYRRRVVGLS DGLGDLAAGI DRRRLMTAFG SHHGNDARQ NHPIRRHRGV
51  LFRLVNPVFG WALTMLLDNL GLIGCKERSA QLGFVGRVLI PAVGFLILCV
101 AMGAVGMLPG IPPFLEQFKS LG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 389>:

m109.seq

```

1  ATGTATTATC GCCGGGTTAT GGGGCTATCC GATGGACTTG GCGATTGGC
51  AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG
101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC
151 CATCGTGGTG TTCTCTCCG CTTGTCAAT CCGGTTTTCG GCTGGGCGTT
201 GACGATGCTG TTGGATAATT TGGGCTTAAT CGGCTGCAAA GAGCGCAGTG
251 CGCAATTAGG TTTCGCCGA GCGGTGTTGA TACCCGAGT AGGTTTCTTG
301 ATCTTGTGTG TGGCGATGGG TGCGGTGCGG ATGCTGCCCG GTATCCCGCC
351 GTTTTGGAA CACTTCAAT CTTTGGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 4; ORF 109>:

m109.pep

```

1  MYRRVMGLS DGLGDLAAGI ERSGLRRRIL TAFSGHGND AQRQNHPIRR
51  HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSAQLGFAG RVLIPAVGFL
101 ILCVAMGAVG MLPGIPPFLE HFKSLG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 109 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 109.ng) from *N. gonorrhoeae*:

m109/g109

	10	20	30	40	50	60
m109.pep	MYRRVMGLSDGLGDLAAGIERSLGRRIILTAFGSHHGNDARQNHPIRRHRGVLFRLVN					
	: : :					
g109	MYRRRVVGLSDGLGDLAAGIDR----RRMLTAFSGSHHGNDARQNHPIRRHRGVLFRLVN					
	10	20	30	40	50	
	70	80	90	100	110	120
m109.pep	PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLI PAVGFLILCVAMGAVGMLPGIPPFLE					
	: :					
g109	PVFGWALTMLLDNLGLIGCKERSAQLGFVGRVLI PAVGFLILCVAMGAVGMLPGIPPFLE					
	60	70	80	90	100	110
m109.pep	HFKSLGX					
	:					
g109	QFKSLGX					
	120					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 391>:

a109.seq

```

1  ATGTATTATC GCCGGGTTGT GGGGCTATCC GATGGACTTG GCGATTGGC
51  AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG
101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC
151 CACCGTGGTG TTCTCTCCG CTTGGTCAAT CCGGTTTTCG GCTGGGCGTT

```

a109.pep

1 MYRRRVVGLS DGLGDLAAGI ERSLGRRRIL TAFSGHGND AQRQNHPIRR
51 HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSAQLGFTG RVLIPVVGFL
101 ILCVAMGAVG MLPGIPFFLE HFKSLG*

m109/a109 97.6% identity in 126 aa overlap

		10	20	30	40	50	60
m109.pep		MYYRRVMGLSDGLGDLAAGIERSLGRRRILTAFGSGHGNDAGRQNHPIRRHRGVLFRLVN					
		:					
a109		MYYRRVVGLSDDLGLAAGIERSLGRRRILTAFGSGHGNDAGRQNHPIRRHRGVLFRLVN					
		10	20	30	40	50	60
		70	80	90	100	110	120
m109.pep		PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLIPAVGFLILCVAMGAVGMLPGIPPFLE					
		:					
a109		PVFGWALTMLLDNLGLIGCKERSAQLGFTGRVLIPVVGFLILCVAMGAVGMLPGIPPFLE					
		70	80	90	100	110	120
m109.pep		HFKSLGX					
a109		HFKSLGX					

g111.seq

```

seq
1   ATGCCGTCGTG AAACACGCCT GCGGAACCTT ATCCGCGCCT TGATATTTGC
51  CTTGGGTTC ATCTTCTGA ACGCTGTTC GGAacaaac GCGCAaaccg
101 TTACCCTGCA AGGCGAAACG ATGGGTACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCCCCT GCCAAATAC AAAAGCGCAT
201 TGATGATGCG CTTAAAGAAG TCAACCGGCA GATGtccaCC TACCAGACCG
251 ATTCCGAAAT CAGCCGGCTTt atacagacan atgctggaga gctcttcgcr
301 tntcatgcag ntctataac tgattccgcc gaagactgtc tgcctaatac
351 qcttatctca tcggcgctct ga

```

g111.pap

```

1  MPSETRLPNL IRALIFALGF IFLNACSEQT AQTVTLQGET MGTTYTVKYK
51  SNNRDKLPSP AKIQKRIDDA LKEVNRQMST YQTDSEISRF IQTAGELFAH
101 ASITDSAEDC LPNTPISSAL *

```

m111.seq

1	ATGCCGTCTG	AAACACGCCT	GCCGAACTTT	ATCCGCGTCT	TGATATTTGC
51	CCTGGGTTTC	ATCTTCTGA	ACGCTGTTC	GGAACAAACC	GCGCAAACCG
101	TTACCCTGCA	AGGCGAAACG	ATGGGCACGA	CCTATATCGT	CAAATACCTT
151	TCAAATAATC	GGGACAAACT	CCCCTACCTT	GCCGAAATAC	AWAAACGCAT
201	CGATGACGCG	CTTAAAGAAK	TCAACCGGyA	GATGTCTACC	TATCAGCCCG
251	ACTCCGAAT	CAGCCGGTTC	AACCAACACA	CAGCCGGCAA	GCCCTCCGC
301	ATTTCAGCG	ACTTCGCACA	CGTTACTGCC	GAAGCCGTCC	GCCTGAACCG
351	CCTGACACAC	GGCGCGCTGG	ACGTAACCGT	CGGCCCTTGG	GTCAACCTTT
401	GGGGATTTCG	CCCCGACAAA	TCCGTTTACC	GTGAACCGTC	GCCGGAAACA
451	ATCAAAACAG	CGGCATCTTA	TACGGTGACCA	GACAAAATCA	TTTTGAAACA
501	AGGCAAGAGT	TACGTTCTCT	TGAGCAAAAC	CCACCCCAAG	GCCTATTGGG
551	ATTATCTCTC	GATTCGCAAA	GGCTTCGGCG	TTGATAAAGT	TGCGGGCGAA

```

601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GGCGGCAATA CGCAGATTAT CGTCCCCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCA
801 TAAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACG
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTCG TGTTCCTCTG ATTGTCAGGG
1001 ATAAAGCGG CTACCGCACC GCCATGTCTT CCGAATTGTA AAAAGTGC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 396; ORF 111>:

```

m111.pep
1  MPSETRLPNF IRVLIFALGF IFLNACSEQT AQTVTLOGET MGTTYXVKYL
51  SNNRDKLPSP AEIXKRIDDA LKEXNRXMSY YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFDPK SVTREPSPEQ
151 IKQAASYTGI DKIIKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPWR IGIEQPNIVQ CGNTQIIVPL
251 NNRLATSGD YRIFHVDKNG KRLSHIINPN NKRPIHNLA SISVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

ORF 111 shows 88.7% identity over a 97 aa overlap with a predicted ORF (ORF 111.ng) from *N. gonorrhoeae*:

```

m111.pep/g111.pep

      10      20      30      40      50      60
m111.pep  MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLOGETMGTTYXVKYLSNNRDKLPSP
          |||||:|:|||||
g111      MPSETRLPNLIRALIFALGFIFLNACSEQTAQTVTLOGETMGTTYTVKYLSNNRDKLPSP
          10      20      30      40      50      60

      70      80      90      100     110     120
m111.pep  AEIXKRIDDALKEXNRXMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVRLNRLTH
          |:| ||||| || ||||| ||||| |:|:
g111      AKIQKRIDDALKEVNROMSTYQTDSEISRFIQTXAGELFAXHAXSITDSAEDCLPNTPI
          70      80      90      100     110     120

      130     140     150     160     170     180
m111.pep  GALDVTVGPLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKIIKQKGDYASLSKTHPK
g111      SALX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 397>:

```

a111.seq
1  ATGCCGCTCG AAACACGCCT GCCGAACCTT ATCCGCACCT TGATATTTGC
51  CCTGAGTTTT ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201 CGATGACGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAT CAGCCGGTTC AACCACACA CAGCCGGCAA GCCCTCCCG
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG
351 CCTGACACAC GCGCGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCCG CCCGACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAAG CAGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGCGCAA
601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCTTGGCGC ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GGCGGCAATA CGCAGATTAT CGTCCCCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCA

```

801 TAAAAGCGGC AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
 851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG
 901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
 951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTGC TGTTCCTG ATTGTCAGGG
 1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGA AAAAGTCTC
 1051 CGCTAA

This corresponds to the amino acid sequence <SEQ ID 398; ORF 111.a>:

a111.pep

1 MPSETRLPNF IRTLIFALS IFLNACSEQT AQTVTLOGET MGTITYTVKYL
 51 SNNRDKLPSP AEIQKRIDDA LKEVNRQMS YQPDSEISRF NQHTAGKPLR
 101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPEQ
 151 IKQAASYTGI DKILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
 201 LEKYGIQNYL VEIGGELHGK GKNARGEPRW IGIEQPNIVQ GGNTQIIVPL
 251 NNRLATSGD YRIFHVDKSG KRLSHIINPN NKRPIHNLAS ISVVDASAM
 301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
 351 R*

m111/a111 97.7% identity in 351 aa overlap

m111.pep	10	20	30	40	50	60
	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLQGETMGTITYXVKYLSNNRDKLPSP					
a111	MPSETRLPNFIRTLIFALSFIPLNACSEQTAQTVTLQGETMGTITYTVKYLSNNRDKLPSP					
	10	20	30	40	50	60
m111.pep	70	80	90	100	110	120
	AEIXKRIDDALKEXNRXMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVRLNRLTH					
a111	AEIQKRIDDALKVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVHLNRLTH					
	70	80	90	100	110	120
m111.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFPGDKSVTREPSPEQIKQAASYTGIDKIILKQKGDYASLSKTHPK					
a111	GALDVTVGPLVNLWGFPGDKSVTREPSPEQIKQAASYTGIDKIILKQKGDYASLSKTHPK					
	130	140	150	160	170	180
m111.pep	190	200	210	220	230	240
	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRWIGIEQPNIVQ					
a111	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRWIGIEQPNIVQ					
	190	200	210	220	230	240
m111.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRLATSGDYRIFHVDKNGKRLSHIINPNKRPIHNLASISVVDASAM					
a111	GGNTQIIVPLNNRLATSGDYRIFHVDKSGKRLSHIINPNKRPIHNLASISVVDASAM					
	250	260	270	280	290	300
m111.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
a111	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 399>:

g111-1.seq

1 ATGCCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTTGC
 51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
 101 TTACCCTGCA AGGCGAAACG ATGGGTACGA CCTATACCGT CAAATACCTT
 151 TCAAATAATC GGGACAAACT CCCCTCCCTT GCCAAAATAC AAAAGCGCAT
 201 TGATGATGCG CTTAAGAAG TCAACCGCA GATGTCCACC TACCAGACCG

326

	10	20	30	40	50	60
m111-1.pep	70	80	90	100	110	120
	AEIQKRIDDALKEVNRQMSTYQPDSEISRFNQHTAGKPLRISSDFAHVTAEEAVRLNRLTH					
g111-1	AKIQKRIDDALKEVNRQMSTYQTDSEISRFNQHTAGKPLRISSDFAHVTAEEAVRLNRLTH					
	70	80	90	100	110	120
m111-1.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFGPKSVTREPSPQIKQAASVTGIDKIILKQKDYASLSKTHPK					
g111-1	GALDVTVGPLVNLWGFGPKSVTREPSPQIKQAASVTGIDKIILQKQKDYASLSKTHPK					
	130	140	150	160	170	180
m111-1.pep	190	200	210	220	230	240
	AYLDLSSIAKGFVGVKAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQ					
g111-1	AYLDLSSIAKGFVGVKAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIIQ					
	190	200	210	220	230	240
m111-1.pep	250	260	270	280	290	300
	GGNTQIIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPIHNLASISVVADSAM					
g111-1	GGNTQIIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPIHNLASISVVSAMSAM					
	250	260	270	280	290	300
m111-1.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAFLIVRDKGGYRTAMSSEFEKLLRX					
g111-1	TADGLSTGLFVLGETEALRLAEQEKLAFLIVRDKGGYRTAMSSEFAKLLRX					
	310	320	330	340	350	

g111-1/p44550

sp|P44550|YOJL_HAEIN HYPOTHETICAL LIPOPROTEIN HI0172 PRECURSOR >gi|1074292|pir||C64144
 hypothetical protein HI0172 - Haemophilus influenzae (strain Rd KW20) >gi|1573128 (U32702)
 lipoprotein, putative [Haemophilus influenzae Rd] Length = 346
 Score = 349 bits (885), Expect = 2e-95
 Identities = 177/328 (53%), Positives = 240/328 (72%), Gaps = 4/328 (1%)

Query: 23 LNACSEQTAQTVTLQGETMTGTTYXVKYLSNNRDKLPSPAEIXKRIDDALKEVNRQMSTYQ 82
 L AC ++T + ++L G+TMGTTY VKYL + S + + I+ LK+ N MSTY+
 Sbjct: 17 LAACQKET-KVISLSGKTMGTTYHVKYLDGSGITATS-EKTHEEIEAILKDVNAKMSTYK 74

Query: 83 PDSEISRFNQHT-AGKPLRISSDFAHVTAEEAVRLNRLTHGALDVTVGPLVNLWGFGPKS 141
 DSE+SRFNQ+T P+ IS+DFA V AEA+RLN++T GALDVTVG+VNLWGFGP+K
 Sbjct: 75 KDSLSRFNQHTQVNTPIEISADFAKVLAEAIRLNKVTGALDVTVGPPVNLWGFGPEKR 134

Query: 142 VTREPSPQIKQAASVTGIDKIILKQKDYASLSKTHPKAYLDLSSIAKGFVGVKAGELE 201
 ++P+PEQ+ + ++ GIDKI L K+ A+LSK P+ Y+DLSSIAKGFVGV+VA +L
 Sbjct: 135 PEKQPTPEQLAERQAWVGIDKITLDTNKEKATLSKALPQVYVDLSSIAKGFVGVQVAEKL 194

Query: 202 EKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQGGNTQIIIVPLNNRSLATSGDY 261
 E+ QNY+VEIGGE+ KGKN G+PW+I IE+P + ++ LNN +A+SGDY
 Sbjct: 195 EQLNAQNYMVEIGGEIRAKGNIEGKWPQIAIEKPTTGERAVEAVIGLNNMGMASSGDY 254

Query: 262 RIFHVDKNGKRLSHIINPNKRPIHNLASISVVADSAMTADGLSTGLFVLGETEALKLA 321
 RI+ ++NGKR +H I+P PI H+LASI+V+A ++MTADGLSTGLFVLGE +AL++A
 Sbjct: 255 RIY-FEENGKRFHEIDPKTGYPHQHLASITVLAPTSMTADGLSTGLFVLGEDKALEVA 313

Query: 322 EREKLAFLIVRDKGGYRTAMSSEFEKL 349
 E+ LAV+LI+R G+ T SS F+KL
 Sbjct: 314 EKNNLAVYLIIRTDNGFVTKSSSAFKKL 341

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 403>:

a111-1.seq

```

1  ATGCCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCACCT TGATATTGTC
51  CCTGAGTTTT ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201 CGATGACGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGGAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCTCCGC
301 ATTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG

```

```

351 CCTGACACAC GCGCGCTGG ACGTAACCGT CGGCCCTTG GTCACCTTT
401 GGGGATTCCG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAAACAAG CAGCATCTTA TACGGGCATA GACAAATCA TTTTGAAACA
501 AGGCAAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTTGG
551 ATTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGCGGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCACAAAAC GCGCGGCGA ACCTTGGCGC ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACACCGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAAGCGGC AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGAGA CAGTCCGATG
901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAATCGC TGTTCCTG ATTGTCAGG
1001 ATAAAGCGCG CTACCGCACC GCCATGTCTT CCGAATTGA AAACTGCTC
1051 CGTAA

```

This corresponds to the amino acid sequence <SEQ ID 404; ORF 111-1.a>:

a111-1.pep

```

1  MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLQGET MGTITYTVKYL
51  SNNRDKLPSP AEIQKRIDDA LKEVNRQMSY YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPQ
151 IKQAASYTGI DKIIKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPWR IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKSG KRLSHIINPN NKRPISHNLA SISVVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

a111-1/m111-1 98.9% identity in 351 aa overlap

a111-1.pep	10	20	30	40	50	60
	MPSETRLPNF	IRTLIFALSF	IFLNACSEQT	AQTVTLQGET	MGTITYTVKYL	SNNRDKLPSP
m111-1	10	20	30	40	50	60
	MPSETRLPNF	IRTLIFALSF	IFLNACSEQT	AQTVTLQGET	MGTITYTVKYL	SNNRDKLPSP
a111-1.pep	70	80	90	100	110	120
	AEIQKRIDDA	LKEVNRQMSY	YQPDSEISRF	NQHTAGKPLR	ISSDFAHVTA	EAVHLNRLTH
m111-1	70	80	90	100	110	120
	AEIQKRIDDA	LKEVNRQMSY	YQPDSEISRF	NQHTAGKPLR	ISSDFAHVTA	EAVHLNRLTH
a111-1.pep	130	140	150	160	170	180
	GALDVTVGPL	VNLWGFPGDK	SVTREPSPQ	IKQAASYTGI	DKIIKQKGD	YASLSKTHPK
m111-1	130	140	150	160	170	180
	GALDVTVGPL	VNLWGFPGDK	SVTREPSPQ	IKQAASYTGI	DKIIKQKGD	YASLSKTHPK
a111-1.pep	190	200	210	220	230	240
	AYLDLSSIAK	GFGVDKVAGE	LEKYGIQNYL	VEIGGELHGK	GKNARGEPWR	IGIEQPNIVQ
m111-1	190	200	210	220	230	240
	AYLDLSSIAK	GFGVDKVAGE	LEKYGIQNYL	VEIGGELHGK	GKNARGEPWR	IGIEQPNIVQ
a111-1.pep	250	260	270	280	290	300
	GGNTQIIVPL	NNRSLATSGD	YRIFHVDKSG	KRLSHIINPN	NKRPISHNLA	SISVVADSAM
m111-1	250	260	270	280	290	300
	GGNTQIIVPL	NNRSLATSGD	YRIFHVDKSG	KRLSHIINPN	NKRPISHNLA	SISVVADSAM
a111-1.pep	310	320	330	340	350	
	TADGLSTGLF	VLGETEALKL	AEREKLAVFL	IVRDKGGYRT	AMSSEFEKLL	RX
m111-1	310	320	330	340	350	
	TADGLSTGLF	VLGETEALKL	AEREKLAVFL	IVRDKGGYRT	AMSSEFEKLL	RX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 405>:

g114.seq

```

1  ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCAGCAGG AATGCAGCAA
51  GACTTTTTTA TGTCCGCCGG GCGGGACGAG TATGGGGCGG TCAATGTCGG

```

g114.pap

m114.seq

m114.pcp

m114/g114 90.0% identity over a 140 aa overlap

a114.seq

1	ATGCCGGAGG	CAAGCATCGC	CTCCATCACT	TCGCCGCTGC	ACGGGGCGCA
51	ACAGGAATGC	AGCAAGACTT	TTTTATGTCC	GCCGGGCGGG	ACGAGTATGG
101	GGCGGTCAAT	GTCGGTAAAC	GTAGGTTTGT	TTTGTGTTTC	CATTAACCTA
151	ACGATAATCTG	TCGAATACGG	TTGAAGCGGC	TATTTTATCA	GAGCCGCCGC
201	ATGTA AAAACA	GGGTGTCAGG	GCATCAGCCC	GAGCTCGCTG	AACGAACCGA
251	CGGTTTGCGC	CGTTACGATA	AAATGGTCGA	GCAGCGACAC	ATCGACCAGC
301	GACATTTGCC	TGCGCCAGCC	CCTTGTGAAC	ATGATGTCTT	CCTGCGAAGG
351	TTGCGGGCGAG	CCGCCCGGAT	GGTTGTGCGC	GATAATCAGG	CTGTCCGCAT
401	ATTCTGCCAA	TGCCAGTTTG	ACAATTTTCA	GGATGTAA	

1 MPEASIASIT SPLHGAQQEC SKTFLCPPGG TSMGRMSVTV VGLFCVSINL
51 TISVEYG*SG YFIRAAACKT GCQGISPSCL NERTVCAVTI KWSSSDTSTS
101 DIACASRLVN MMSSCEGSGE PPGWLCAIIR LSAYSSNASL TISM*

```

10      20      30      40      50
m114.pep MASITSPLHGAHRECSKTFLCPPGGTSGRSM SVTVGLFCVSINLTISVEYGXSG
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114      MPEASIASITSPLHGAQEC SKTFLCPPGGTSMGRSM SVTVGLFCVSINLTISVEYGXSG
10      20      30      40      50      60

60      70      80      90      100     110
m114.pep YFIRAAACKTECQGINPSC LNEQTLCXVTIKWSSSDTSTSDIACASRLVNMSSCEXSGE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114      YFIRAAACKTGCGISP SC LNERTVCAVTIKWSSSDTSTSDIACASRLVNMSSCEGSGE
70      80      90      100     110     120

120     130     140
m114.pep PPGWLCAIIRLSAYSSNASLTISRMX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114      PPGWLCAIIRLSAYSSNASLTISRMX
130     140

```

g117.seq

1	atggtcgacg	aactcgacCT	GCTGCCCGAT	GCCGTGCGCG	CCACCTGTCT
51	TGCCGACATC	GGACGCTACG	TCCCCGATTG	GAACCTATTG	GTTTCCGAGC
101	GCTGCAACAG	CACCTGCGCC	GAGCTGGTCA	AAGGTgtgga	CGAAGTGCAG
151	AAACTTACCC	ACTTCGCCCC	GGTGGACAGC	GCTGCCACGC	CGGAAGAACG
201	CGCAGACCAA	GCGGAAACCA	TGCGGAAAAAT	CTCTGTGGCG	atggttaccg
251	Acatccgcgt	cgtaTTAATC	AAACTGGCGA	TGCGTaccgcg	caccCTGcta
301	ttTTtaaGCA	ACGCCCCCGA	CAGCCCTGAA	AAACgcgccg	TCgccaaAga
351	aacccTCGAC	ATCTTCGCCC	CGCTCGCCAA	CCGCTTGGGC	GTGTGGCAGC
401	TCAAAATGGCA	GCTCGAAGAT	TTGGGCTTCC	GCCATCAAGA	ACC CGAAAAA
451	TACCGCGAAA	TCGCCCTGCT	TTTGGACGAA	AAACCGCACG	ACACGCTCGA
501	ATACATCGAA	AACTTCTCTG	ATATCTCTCG	TACGGAACCT	AAAAAATACA
551	ATATCCAATT	TGAAGTCGCC	GGCCGTCCGA	AACACATCTA	CTCCATTTAC
601	AAAAAAATGG	TGAAGAAAAA	ACTCAGCTTC	GACGgccTGT	TCGACATCCG
651	CGCCGTGCGG	ATTCTGTGTC	ATACCGTCCC	CGaGTGTTAC	ACCACGCTGG
701	gcaTCGTCCA	CAGCCTCTGG	CAGCCCATTTC	CCGGCGagtt	CGAcgactAC
751	ATCGCCCAACC	CCAAAGGcaA	CGgttATAAA	AGtTTGCACA	CCGTCTCATGT
801	cggccccGGAA	gacaaaggta	tggaAGtgCA	AATCGCGACC	TTCGAtatGC
851	accAATTCAa	CgaatTCggT	gtgcgcgCCC	ATTCGCGtta	caaagaaggc
901	ggcaaaggcg	attccGCCTa	cgaacaaaAAA	ATcgccTggt	TGcgccaaACT
951	CTTGGACTGG	CGCGAAAAATA	TGCGGGAAG	CGGCAAGGAA	GACCTCGCCG
1001	CCGCTTCAA	AACCGAGCTT	TTCAACGACA	CGATTTATGT	TTTGACCCCG
1051	CACGGCAAG	TCCTCTCTCT	GCCAACGGGC	GCAACCCCCA	TCGACTTCGC
1101	CTACGCCCTG	CACGACGCA	TcggCGACCG	CTCGCGGGGC	GCGAAAGTCG
1151	AaggGCGAGAT	TGTGCCCGTG	TCCACCCCGC	TCGAAAAACG	ACAGCGCGTC
1201	GAAATcatta	cCGCcaaAGA	AGGGCATCCT	TCCGTCAACT	GGCTTTACGA
1251	AGGctgG3tc	aAATCCGCA	AGGCCATCGG	caaAATCCGC	GCCTAcatCC
1301	GCCAGcaaaAa	cgCgaCACC	GTGCGCGAAG	AAGGCCGTGT	CCAACTCGAC
1351	AAGCAGCTTG	CCAAACTCAC	GCCCCAACCC	AACCTGCAAG	AGCTTgccga
1401	aaATCTCTGGC	tacaaAAAGC	cagaagacct	ctacacCGCc	gtcggaacaag
1451	gcgaatttcc	caaccgcgcc	atCcaaaaag	ctcgcggcac	GCTggaacgaa
1501	cgccccccCG	TGCCCGTFCAG	CGCAACCACC	ATCGTCAAAAT	AGTCCAAAAT

```

1551 CAAAAAAGGT GGCAAAACCG GCGTGCTCAT CGACGGCGAA GACGGCTTGA
1601 TGACCACGCT TGCCAAATGC TGCAAACCCG CGCCGCCCGA CGATATTGCC
1651 GGCTTCGTTA CCCGCGAGCG CGGCATTTCG GTCCACCGCA AAACCTGCCC
1701 CTCTTTCCGA CACCTTGCCG AACACGCGCC CGAAAAAGTA CTGGACGCAA
1751 GTTGGGCGGC GTTGCAGGAA GGGCAAGTGT TCGCCGTCGA TATCGAAATC
1801 CGCGCCCAAG ACCGCTCCGG GCTTTTGCGC GACGTATCCG ACGCGCTCGC
1851 CCGCCACAAA CTCAACGTTA CCGCCGTGCA AACCCAGTCC CGCGACTTGG
1901 AAGCCAGCAT GAGGTTACAG CTCGAAGTCA AACAAGtCAA CGacCTCCCC
1951 CGCGTCCTCG CCGGCCTCGG CGATGTCAAA GCGGTATTGA GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 412; ORF 117.ng>:

g117.pep

```

1 MVDELDDLFD AVAATLLADI GRYVPDWNLL VSERCNSTVA ELVKGVDEVQ
51 KLTHFARVDS LATPEERAQQ AETMRKMLLA MVTDIRVLI KLAMRTRTLL
101 FLSNAPDSPE KRAVAKETLD IFAPLANRLG VWQLKWQLED LGFRHOEPEK
151 YREIALLLDE KRTERLEYIE NFLDILRTEL KKYNIHFEVA GRPKHIYSIY
201 KKMVKKKLSF DGLFDIRAVR ILVDTVPECY TTLGIVHSLW QPIPGFDDY
251 IANPKGNGYK SLHTVIVGPE DKGVEVQIRT FDMHQFNEFG VAAHWRYKEG
301 GKGDSAYEQK IAWLRQLLDW RENMAESGKE DLAAAFKTEL FNDTIYVLT
351 HGKVLSLPTG ATPIDFAYAL HSSIGDRCRG AKVEGQIVPL STPLENGQVR
401 EIITAKEGHP SVNWLYEGWV KSGKAIGKIR AYIRQONADT VREEGRVQLD
451 KQLAKLT PKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLNE
501 PPPVPVSATT IVKQSKI KKG GKTGVLIDG DGLMTTLAKC CKPAPPDDIA
551 GFVTRERGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFAVDIEI
601 RAQDRSGLLR DVSDALARHK LNVTA VQTQS RDLEASMRFT LEVKQVNDLP
651 RVLAGLGDVK GVLSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 413>:

m117.seq (partial)

```

1 ..GTGAACTCA AGAAATACAA TGTCCATTTC GAAGTCGCCG GCCCGCCGAA
51 ACACATCTAC TCCATTTACA AAAAAATGGT GAAGAAAAAA CTCAGCTTCG
101 ACGGCCTCTT TGACATCCGC GCCGTGCGAA TTCTGGTTGA TACCGTCCCC
151 GAGTGTTACA CCACGCTGGG TATCGTCCAC AGCCTCTGGC AGCCCATTC
201 CGGCGAGTTC GACGACTACA TCGCCAATCC CAAAGGCAAC GGCTATAAAA
251 GTTTGCACAC CGTCATCGTC GGCCCGGAAG ACAAGGCGT GGAAGTACAA
301 ATCCGCACCT TCGATATGCA CCAATTCAAC GAATTCGGTG TCGCGCCCA
351 CTGgCGTTAC AAAGAGGGCG GCAAGGGCGA TTCCGCCTAC GAACAGAAAA
401 TCGCCTGGTT GCGCCAATC TTGGACTGGC GCGAAAACAT GCGCGAAAGC
451 GGCAAGGAAG ACCTCGCCGC CGCCTTCAAA ACCGAGCTTT TCAACGACAC
501 GATTTATGTT TTGACCCCGC ACGGCAAGT CCTCTCCCTG CCCACGGGCG
551 CGACCCCAT CGACTTCGCC TACGCCCTGC ACAGCAGCAT CGGCGACCGT
601 TGCCGCGGTG CGAAAGTCGA AGGGCAGATT GTGCCGCTGT CCACCCCGCT
651 CGAAAACGGA CAGCGCGTCG AAATCATTAC CGCCAAAGAA GGGCATCCTT
701 CCGTCAACTG GCTTTACGAA GGCTGGGTCA AATCCAACAA GGCAATCGGC
751 AAAATCCGCG CCTACATCCG CCAGCAAAAC GCCGACACCG TGCGCGAAGA
801 AGGCCGCGTC CAACTCGACA AACAGCTTGC CAAACTCACG CCCAAACCCA
851 ACCTGCAAGA GCTTGCCGAA AATCTCGGCT ACAAAAAGCC AGAAGACCTC
901 TACACCGCCG TCGGACAAGG CGAAATTTCC AACCGCGCCA TCCAAAAAGC
951 CTGCGGCACg CTGAACGAAC CGCCGCCCGT ACCCGTCAGC GAAACCAACA
1001 TCGTCAAAAC GTCCAAAATC AAAAAAGGCG GCAAAAACGG CGTGCTCATC
1051 GACGGCGAAG ACGGTCTGAT GACCACGCTT GCCAAATGCT GCAAACCCGC
1101 GCCGCCCGAC GATATTATCG GCTTCGTTAC CCGCGAGCGC GgCATTTCAG
1151 TGCACCGCAA AwyyTkCyCG TCTTTCCAAC ACCTCGCCGA ACACGCGCCC
1201 GAWAAAGTGC TGGACGCAAG CTGGGCGGCA TTGCAGGAAG GACAAGTATT
1251 CGCCGTCGAT ATCGAAATCC GCGCCCAAGA CCGCTCCGGG CTTTTGCGCG
1301 ACGTATCCGA CGCGCTCGCC CGCCACAAAC TCAACGTTAC CGCCGTGCAA
1351 ACCCAGTCCC GCGACTTGGA AGCCAGCATG AGGTTACAGC TCGAAGTCAA
1401 ACAAGTCAAC GACCTCCCGC GCGTCCTCGC CAGCCTCGGC GACGTCAAAG
1451 GCGTATTGAG CGTTACCCGG CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 414; ORF 117>:

m117.pep (partial)

```

1....VKLKKYNVHF EVAGRPKHIY SIYKKMVKKK LSFDGLFDIR AVRILVDTV
51  ECYTTLGIVH SLWQPIGGEF DDYIANPKGN GYKSLHTVIV GPEDKGVEVQ
101 IRTFDMHQFN EFGVAAHWRY KEGGKGDSAY EQKIAWLRQL LDWRENMAES
151 GKEDLAAAFK TELFNDTIYV LTPHGKVLSL PTGATPIDFA YALHSSIGDR
201 CRGAKVEGQI VPLSTPLENG QRVETITAKE GHPSVNWLYE GWVKSNAIG
251 KIRAYIROQN ADTVREGRV QLDKQLAKLT PKPNLQELAE NLGYKKPEDL
301 YTAVGQGEIS NRAIQACGT LNEPPVPVPS ETTIVKQSKI KKGKNGVLI
351 DGEDGLMTTL AKCKPAPPD DIIGFVTRER GISVHRKXXX SFQHLAEHAP
401 XKVLDASWAA LQEGQVFAVD IEIRAQDRSG LLRDVSDALA RHKLNVTAVQ
451 TQSRDLEASM RFTLEVQVN DLPRVLASLG DVKGVLSVTR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 117 shows 97.6% identity over a 490 aa overlap with a predicted ORF (ORF 117.ng) from *N. gonorrhoeae*:

m117/g117

m117.pep				10	20	30
				VKLKKYNVHF	EVAGRPKHIY	SIYKKMVKKK
g117				:	:	:
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
		SFDGLFDIR	AVRILVDTV	PECYTTLGIVH	SLWQPIGGEF	DDYIANPKGN
g117						
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
		PEDKGVEVQ	IRTDFDMHQ	FNEFGVAAHWRY	KEGGKGDSAYE	QKIAWLRQL
g117						
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
		KEDLAAAFK	TELFNDTIYV	LTPHGKVL	SLPTGATPID	FAYALHSSIG
g117						
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
		PLSTPLENG	QRVETITAKE	GHPSVNWLYE	GWVKSNAIG	KIRAYIROQN
g117						
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
		LDKQLAKLT	PKPNLQELA	ENLGYKKPED	LYTAVGQGEI	SNRAIQACGT
g117						
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
		TTIVKQSKI	KKGKNGVL	IDGEDGLMTT	LAKCKPAPPD	DIIGFVTRER
g117						
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
		FOHLAEHAP	XKVLDASWAA	LQEGQVFAVD	IEIRAQDRSG	LLRDVSDALA

a117.seq

This corresponds to the amino acid sequence <SEQ ID 416; ORF 117.a>:

a117.pep

1	MVHELDLLPD	AVAATLLADI	GRYPDWNLL	VSERCNSTVA	ELVGKGVDEVO
51	KLTHFARVDS	LATPEERAQO	AETMRKMLLA	MVTDIRVULL	KLAMRTTQLQ
101	FLSNAPDSPE	KRAVAKETLD	IFAPLANRLG	VQWLKHWQLED	LGRFRHQEPEK
151	YREIALLLDE	KRTERLEYIE	NFLNILRTEL	KVYNKHFEVA	GRPKHIYSIY
201	KKMVKKKLSF	DGLFDIRAVR	ILVDTVPECY	TTLGIVHSLW	QPIPGFEDDY
251	IANPKNGGYK	SLHTVIVGPE	DKGVEVQIRT	FDMHQFNEFG	VAAHWRYKEG
301	KGKDSAYEOK	IAWLRQLLDW	RENMAESGKE	DLAAAFKTEL	FNDTIYVLPT
351	HGKVLSLPTG	ATPIDFAYAL	HSSIGDRCRG	AKVEGOIVPL	STPLENGORV

401 EIITAKEGHP SVNWLYEGWV KSNKAIGKIR AYIRQONADT VREEGRVQLD
 451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLNE
 501 PPPVPVSETT IVKQSKI KKG GKNGLIDGE DGLMTTLAKC CKPAPPDDIV
 551 GFVTRDRGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GOVFAVDIEI
 601 RAQDRSGLLR DVSDALARHK LNVAVQTQS RDLEASMRFT LEVKQVTDLP
 651 RVLASLGDKV GVLVTRL*

m117/a117 98.0% identity in 490 aa overlap

m117.pep				10	20	30
				VKLKKYNVHFEVAGRPKHIYSIYKKMVKKKL		
a117	EKYREIALLLDEKRTERLEYIENFLNILRTELKKYNHFEVAGRPKHIYSIYKKMVKKKL					
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
		SFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVG				
a117	SFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVG					
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
		PEDKGVQVQIRTFDMHQFNEFGVAHWRYKEGKGDSAYEQKIAWLRLQLDWRENMAESG				
a117	PEDKGVQVQIRTFDMHQFNEFGVAHWRYKEGKGDSAYEQKIAWLRLQLDWRENMAESG					
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
		KEDLAAAFKTELFNDTIYVLTPHGKVLSTPTGATPIDFAYALHSSIGDRCRGAKVEGQIV				
a117	KEDLAAAFKTELFNDTIYVLTPHGKVLSTPTGATPIDFAYALHSSIGDRCRGAKVEGQIV					
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
		PLSTPLENGQORVEIITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQONADTVREEGRVQ				
a117	PLSTPLENGQORVEIITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQONADTVREEGRVQ					
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
		LDKQLAKLTPKPNLQELAENLGKYPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSE				
a117	LDKQLAKLTPKPNLQELAENLGKYPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSE					
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
		TTIVKQSKI KKGKNGVLIDGEDGLMTTLAKCCKPAPPDDIIGFVTRERGISVHRKXXXS				
a117	TTIVKQSKI KKGKNGVLIDGEDGLMTTLAKCCKPAPPDDIVGFVTRDRGISVHRKTCPS					
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
		FOHLAEHAPXKVLDASWAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAVQT				
a117	FRHLAEHAPEKVLDAWAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAVQT					
	570	580	590	600	610	620
m117.pep		460	470	480	490	
		QSRDLEASMRFTLEVQVNDLPRVLASLGDKVGVLSVTRLX				
a117	QSRDLEASMRFTLEVQVTDLPRVLASLGDKVGVLSVTRLX					
	630	640	650	660		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 417>:

g117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CCCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCCG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTCGCTGG CGCAGGAACA TTATCTGCCC
151 GATGCCGCCA CGCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GGCAGAAATG GTCGACGAAC TCGACCTGCT GCCCGATGCC GTCGCCGCCA
251 CCCTGCTTGC CGACATCGGA CGTACGTCC CCGATTGGAA CCTATTGGTT
301 TCCGAGCGCT GCAACAGCAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTTACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAAGCGCG ACAGCAAGCG GAAACCATGC GGAAAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT ATTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCAGACAG CCCTGAAAAA CGCGCCGTCG
551 CCAAAGAAAC CCTCGACATC TTCGCCCCGC TCGCCAACCG CTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCGCGC ATCAAGAACC
651 CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAAC TTCTCGATA TCCTGCGTAC GGAACCAAAA
751 AAATACAATA TCCACTTTGA AGTCGCGCGC CGTCCGAAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAAACT CAGCTTCGAC GGCCTGTTTC
851 ACATCCGCGC CGTGCAGATT CTGGTCGATA CCGTCCCGCA GTGTTACACC
901 ACGCTGGGCA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCGagttCGA
951 cgactACATC GCCAACCCCA AAGgcaACGg ttATAAAAGt TTGCACACCG
1001 TCATCGTcgg cccGGAagaa aaaggtgtgg aagtgcAAAT CCGCACCTTC
1051 GATATGCacc AATTcCaaCga ATTcGGTgTC GCCGCCCACT GGCgTTACAA
1101 AGAAGGCGGC AAAGGCGATT CCGCCTACGA ACAAAAAATC GCCTGGTTGC
1151 GCCAACTCTT GGAAGTGGCG GAAATATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCGC CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCGCGAC GGCAAAGTCC TCTCTCTGCC AACGGGCGCA ACCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGCTG CCGGGGCGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCCGCTCG AAAACGGACA
1401 GCGCGTCGAA ATCATTACCG CCAAAGAAGG GCATCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAAA TCCGGCAAGG CCATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGTGTCCA
1551 ACTCGACAAG CAGCTTGCCA AACTCACGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCGCTC
1651 GGACAAGGCG AAATTTCCAA CCGCGCCATC CAAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTGC CCGTCAGCGC AACCACCATC GTCAAAACAGT
1751 CCAAAATCAA AAAAGGTGGC AAAACCGGCG TGCTCATCGA CGCGGAAGAC
1801 GGCTTTGATG CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 TATTGCCGGC TTCGTTACCC GCGAGCGCGG CATTTCGCTC CACCGCAAAA
1901 CCTGCCCTCT TTTCCGACAC CTTGCCGAAC ACGCGCCCGA AAAAGTACTG
1951 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKS LHTVIVGPee KGEVQIRTF
2001 CGAAATCCGC GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAACTC AACGTTACCG CCGTGCAAAC CCAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCGCGC GTCTCGCGG GCCTCGGCGA TGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTA

```

This corresponds to the amino acid sequence <SEQ ID 418; ORF 117-1.ng>:

g117-1.pep

```

1  MTAISPIQDT QSATLQELRE WFDSYCAALP DNDKNLIGTA WSLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VDELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLDILRTELK
251 KYNIHFEVAG RPKHIYSYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKS LHTVIVGPee KGEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGRED
401 LAAAFKTELF NDTIYVLTPH GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGOIVPLS TPLENGQVRE IITAKEGHPS VNWLYEGWVK SGRKIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSATTI VKQSKIKKGG KTGVLIDGED
601 GLMTTLAKCC KPAPPDDIAG FVTRERGISV HRKTCPSFRH LAEHAPERVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLAGLGDVKG VLSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 419>:

m117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA

```

```

51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCCG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTTGCTGG CGCAGGAACA TTACCCCGCC
151 GATGCCGCCA CGCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GCGGCAATG GTTCATGAAC TCGACCTGCT CCCGATGCC GTCCGCCCA
251 CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGACTGGAA CCTATTGGTT
301 TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTCACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAACCGCG CCAGCAGGCA GAAACTATGC GGAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCAGACAG CCCGAAAAA CGCGCCGTCG
551 CCAAAGAAAC CCTCGACATC TTCGCCCGC TCGCCAAACG TTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCCGCC ATCAAAAGCC
651 CGAAAAATAC CGCGAAATCG CGCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAC TTCTCAACA TCCTGCGCGG TGAACCTAAG
751 AAATACAAAT TCCATTTTCA AGTCGCCGGC CGCCGAAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAAACT CAGCTTCGAC GGCCTCTTTG
851 ACATCCCGCG CGTGCGAATT CTGGTTGATA CCGTCCCGCA GTGTTACACC
901 ACGCTGGGTA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCGA
951 CGACTACATC GCCAATCCCA AAGGCAACGG CTATAAAAGT TTGCACACCG
1001 TCATCGTCTCG CCCGGAAGAC AAAGGCGTGG AAGTACAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTCCGGTGTG GCCGCCCACT GGCCTTACAA
1101 AGAGGGCGCG AAGGGCGATT CCGCCTACGA ACAGAAAAAT GCCTGGTTGC
1151 GCCAACTCTT GGAATGGCGC GAAACATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCCGCG CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAGTCC TCTCCCTGCC CACGGGCGCG ACCCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCGGCTCG AAAACGGACA
1401 GCGCGTCGAA ATCATTACCG CCAAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCAACAAGG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGCGTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCACGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCCGTC
1651 GGACAAGGCG AAATTTCCAA CCGGCCATC CAAAAGCCT CCGGCACGCT
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCGA AACCACCAT GTCAACACGT
1751 CCAAAATCAA AAAAGGCGG AAAAACGGCG TGCTCATCGA CGCGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 TATTATCGGC TTCGTTACCC GCGAGCGCGG CATTTCAGTG CACCGCAAAA
1901 CCTGCCCGTC TTTCCAACAC CTCGCCGAAC ACGCGCCCGA AAAAGTGCTG
1951 GACGCAAGCT GGGCGGCATT GCAGGAAGGA CAAGTATTCT CCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAACTC AACGTTACCG CCGTGCAAAC CCAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCCGCGC GTCCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTA

```

This corresponds to the amino acid sequence <SEQ ID 420; ORF 117-1>:

m117-1.pep

```

1  MTAISPIQDT QSATLQELRE WFD SYCAALP DNDKNLIGTA WLLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VHELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WOLKWQLEDL GFRHQKPEKY REIALLLDEK RTERLEYIEN FLNLRGELK
251 KYNVHFEVAG RPKHIYSYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKGNGYKS LHTVIVGPED KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGKED
401 LAAAFKTELF NDTIYVLTPH GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGORVE IITAKEGHPS VNWLYEGWVK SNKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKKGG KNGVLIDGED
601 GLMTTLAKCC KPAPPDDIIG FVTRERGISV HRKTCPSFQH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLASLGDVKG VLSVTRL*

```

m117-1/g117-1 98.2% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
g117-1	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWSLAQEHYPADAATPYGEPL					
	10	20	30	40	50	60
	70	80	90	100	110	120

m117-1.pep PDHFLGAAQMVHEDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDVQK
|||||
g117-1 PDHFLGAAQMVDELDPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDVQK
70 80 90 100 110 120

m117-1.pep 130 140 150 160 170 180
LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK
|||||
g117-1 LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK
130 140 150 160 170 180

m117-1.pep 190 200 210 220 230 240
RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFHQQPEKYREIALLLDEKRTTERLEYIEN
|||||
g117-1 RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFHQQPEKYREIALLLDEKRTTERLEYIEN
190 200 210 220 230 240

m117-1.pep 250 260 270 280 290 300
FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
|||||
g117-1 FLDILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
250 260 270 280 290 300

m117-1.pep 310 320 330 340 350 360
TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV
|||||
g117-1 TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEEKGVEVQIRTFDMHQFNEFGV
310 320 330 340 350 360

m117-1.pep 370 380 390 400 410 420
AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH
|||||
g117-1 AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH
370 380 390 400 410 420

m117-1.pep 430 440 450 460 470 480
GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
|||||
g117-1 GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
430 440 450 460 470 480

m117-1.pep 490 500 510 520 530 540
VNWLYEGWVKSNAIGKIRAYIROQNADTVREEGRVQDKQLAKLTPKPNLQELAENLGY
|||||
g117-1 VNWLYEGWVKSNAIGKIRAYIROQNADTVREEGRVQDKQLAKLTPKPNLQELAENLGY
490 500 510 520 530 540

m117-1.pep 550 560 570 580 590 600
KKPEDLYTAVGQGEISNRAIQACGTLNEPPVPVSETTIVKQSKIKGGKNGVLIDGED
|||||
g117-1 KKPEDLYTAVGQGEISNRAIQACGTLNEPPVPVSATTIVKQSKIKGGKGTGVLIDGED
550 560 570 580 590 600

m117-1.pep 610 620 630 640 650 660
GLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAWALQEG
|||||
g117-1 GLMTTLAKCKPAPPDDIAGFVTRERGISVHRKTCPSFRHLAEHAPEKVLDAWALQEG
610 620 630 640 650 660

m117-1.pep 670 680 690 700 710 720
QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTAQTQSRDLEASMRFTLEVQVNDLPR
|||||
g117-1 QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTAQTQSRDLEASMRFTLEVQVNDLPR
670 680 690 700 710 720

m117-1.pep 730
VLASLGDVKGVLVSVTRLX
|||||
g117-1 VLAGLGDVKGVLVSVTRLX
730

m117-1/RelA

sp|P55133|RELA_VIBSS GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) >gi|537617 (U13769) ppGpp synthetase I [Vibrio sp.] Length = 744
Score = 536 bits (1366), Expect = e-151
Identities = 288/685 (42%), Positives = 432/685 (63%), Gaps = 31/685 (4%)

Query: 74 LDLLPDAVAATILLADI---GRYVPDWNLLVSERCNSTVAELVKGVDDEVQKLTHFARVDSL 130
L + D + A LL + G Y D + E + T+ LV+GV+++ ++ ++ S
Sbjct: 68 LSMDADTLIAALLYPLVEGGCYSTD---ALKEEYSGTILHLVQGVQMCAS---QLKST 121

Query: 131 ATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRLQFLSNAPDSPEKRAVAKETLDI 190
A +A Q + +R+MLL+MV D R V+IKLA R L+ + + PD +RA A+E +I
Sbjct: 122 AEETAQAQVDNIRRMLLSMVDDFRVCVVKLAERICNLREVKDQDEV-RRAAQECANI 180

Query: 191 FAPLANRLGVWQLKWQLEDLGFRRHQKPEKYREIALLLDEKRTERLEYIENFLNIRGELK 250
+APLANRLG+ QLKW++ED FR+Q P+ Y++IA L E+R +R +YI +F++ L +K
Sbjct: 181 YAPLANRLGIGQLKWEIEDYAFRYQHPDITYKQIAKQLSERRIDREDYITHFVDDLSDAMK 240

Query: 251 KYNVHFEVAGRPKHIYSIYKMKVKKLSFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQ 310
N+ EV GRPKHIYSI++KM KK L FD LFD+RAVRI+ + + +CY LG+VH+ ++
Sbjct: 241 ASNIRAEVQGRPKHIYSIWRKMQKKSLEFDELFDVRAVRIVAEELQDCYAALGVVHTKYR 300

Query: 311 PIPGEFDDYIANPKGNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFVAAHWRYKEG- 369
+P EFDDY+ANPK NGY+S+HTV++GPE K +E+QIRT MH+ +E GVAHW+YKEG
Sbjct: 301 HLPKEFDDYVANPKPNQYQSIHTVVLGPEGKTIETIQTQKMHSEELGVAAHWRYKEGT 360

Query: 370 --GKGDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPHGKVLSP 427
G SAY++KI WLR+LL W+E M++SG ++ +++++F+D +Y TP G V+ LP
Sbjct: 361 ASGGAQSAYDEKINWLRKLLAWQEEMSDSG--EMLDELRSQVDDRVAFTPKGDVVDLP 418

Query: 428 TGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQRVEIITAKEGHPSVNWLYE- 486
+ ATP+DFAY +HS +G RC GAKVEG+IVP + L+ G +VEIIT KE +PS +WL
Sbjct: 419 SNATPLDFAYHIHSEVGHRCIGAKVEGRIVPFTYHLQMGDQVEIITQKEPNPSRDWLNPN 478

Query: 487 -GWVKSNAIGKIRAYIRQONADTVREEGRVQLDKQLAKL--TPKPNLQELAENLGYKKP 543
G+V S++A K+ A+ R+Q+ D G+ L+ +L K+ T K A+ K P
Sbjct: 479 LGFVTSSRARAKVHAWFRKQDRDKNIIAGKEILEAEVKIATLKDAQYAAKRFNVKSP 538

Query: 544 EDLYTAVGQGEIS-NRAIQKACGTLEPPVPVSETTIVKQSKI-----KKGKNGV 594
E+LY +G G++ N+ I +N+P + + K S+ KK ++ V
Sbjct: 539 EELYAGIGSGDLRINQVINHINALVNKPTAEEDQQLLEKLSEASNKQATSHKKPQDAV 598

Query: 595 LIDGEDGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAW 654
+++G D LMT LA+CC+P P DDI GFVT+ RGISVHR C + L HAPE+++D W
Sbjct: 599 VVEGVNDLMTLHARCCQPIPGDDIQGFVTQGRGISVHRMDCEQLEELRHAPERIIDTVW 658

Query: 655 AALQEQGVFAVDIEIRAQDRSGLLRDVSALARHKLNVAVQTQ--SRDLEASMRFTLEV 712
G + + + + A +R+GLL++++ L K+ V +++++ + + M F LE+
Sbjct: 659 GGGFVGN-YTITVRVTASERNGLLKELTNTLMNEKVKVAGMKSRVDYKKQMSINDFELEL 717

Query: 713 KQVNDLPRVLASLGDVKGVLVSVTRL 737
+ L RVL + VK V RL
Sbjct: 718 TDLEVLGRVLKRIEQVKDVAEAKRL 742

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 421>:

all17-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCAC CGCGCTGCCG AACAAACGATA
101  AAAAATTGT CTTAGCCGCC CGTTCGCTGG CGGAAGCACA TTACCCCGCC
151  GATGCCGCCA CGCCGTATGG CGAACCGCTG CCCGACCACT TCCTCGGCGC
201  GGCGCAAATG GTTCATGAAC TCGACCTGCT CCCCAGTGCC GTCGCGCCA
251  CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGACTGGAA CCTATTGGTT
301  TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351  AGTGCAGAAA CTCACCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401  AAGAACGCGC CCAGCAGGCA GAACTATGC GGAAAATGCT GCTGGCGATG
451  GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACCGGCAC
501  CCTGCAATTT TTAAGCAACG CCCCAGCAG CCCCAGAAA CGCGCCGTCG
551  CCAAGAAAC CCTCGACATC TTCGCCCGC TCGCCAACCG TTTGGGCGTG
601  TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCGCC ATCAAGAACC
651  CGAAAATAC CGCGAAATCG CCCTGCTTT GGACGAAAA CGCACCAGAAC
701  GCCTCGAATA CATCGAAAC TTCCTTAATA TCCTGCGTAC GGAACCTCAA
751  AAATACAATA TCCACTTTGA AGTCGCCGGC CGTCCGAAAC ACATCTACTC
801  CATTACAAA AAAATGGTGA AGAAAAAAT CAGCTTCGAC GGGTTGTTGC

```

```

851 ACATCCGCGC CGTGCGGATT CTGGTTGATA CCGTCCCCGA GTGTTACACC
901 ACACTGGGCA TTGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCGA
951 CGACTACATC GCCAACCCGA AAGGCAACGG CTATAAAGT TTGCACACCG
1001 TCATCGTCGG CCCGGAAGAC AAAGGCGTGG AAGTGCAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTCTGGTGC GCCGCGCACT GCGGTTACAA
1101 AGAGGGCGGC AAAGGCGATT CCGCCTACGA ACAAATAATC GCCTGGTTAC
1151 GCCAATTTT GGAATGGCGC GAAAACATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCCGCG CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAGTCC TCTCCCTGCC CACAGGCGCG ACCCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAAGTCGAAG GGCAGATTGT GCGCTGTGCC ACCCGCTCG AAAACGGACA
1401 GCGTGTCCGA ATCATTACCG CCAAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCAACAAGG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGGAAGAAG GCCGCGTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCACGCC CAAACCCAACT CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCCGTC
1651 GGACAAGCGG AAATTTCCAA CCGCGCCATC CAAAAGCCT GCGGCGTCCA
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCGA AACCACCATC GTCAACAGT
1751 CCAAAATCAA AAAAGCGGCG AAAAACGCGG TGCTCATCGA CGCGGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 CATGTGCGGC TTCGTTACCC GCGATCGCGG CATTTCGGTA CACCGCAAAA
1901 CCTGCCCTTC TTCCGACAC CTCGCCAAC ACGCGCCGA AAAAGTACTG
1951 GACGCAAGTT GGGCGCGGTT GCAGGAAGGA CAAGTGTTCG CCGTCGATAT
2001 CGAAATCCCG GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAACTC AACGTTACCG CCGTGCAAAAC CCAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTACGCTC GAAGTCAAAAC AAGTTACCGA
2151 CCTCCACGCG GTCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTA

```

This corresponds to the amino acid sequence <SEQ ID 422; ORF 117-1.a>:

a117-1.pep

```

1  MTAISPIQDT QSATLQELRE WFDSYCTALP NNDKKLVLA RSLAEAHYPA
51  DAATPYGEPL PDHFLGAAQM VHELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLNLRTELK
251 KYNIHFEVAG RPKHIYSYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKS LHTVIVGPED KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGKED
401 LAAAFKTELE NDTIYVLTPL GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGORVE IITAKEGHPS VNWLYEGWVK SNKAIGKIRA
501 YIROONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKGG KNGVLIDGED
601 GLMTTLAKCC KPAPPDDIVG FVTRDRGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVTDLPR VLASLGDVKG VLSVTRL*

```

a117-1/m117-1 97.7% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
a117-1	MTAISPIQDTQSATLQELREWFD SYCTALPNNDKKLVLAARSLAEAHYPADAATPYGEPL					
	10	20	30	40	50	60
m117-1.pep	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLV SERCNSTVAELVKGVDEVQK					
a117-1	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLV SERCNSTVAELVKGVDEVQK					
	70	80	90	100	110	120
m117-1.pep	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIK LAMRTRTLQFLSNAPDSPEK					
a117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIK LAMRTRTLQFLSNAPDSPEK					
	130	140	150	160	170	180
m117-1.pep	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQPEKYREIALLLDEKRTERLEYIEN					
a117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQPEKYREIALLLDEKRTERLEYIEN					
	190	200	210	220	230	240
m117-1.pep	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQPEKYREIALLLDEKRTERLEYIEN					
a117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQPEKYREIALLLDEKRTERLEYIEN					

```
g118.seq
  1  ATGTGCGAGT  TCAAGGATTT  TAGAAGAAAC  ATCCCTTGTT  TTGAAGAGTA
51  TGACGAAAAA  TCATTATTG  GCAAAATGGT  TGTAGACGGG  GTGTGGGATG
101 ATGAAGAATA  TTGGAAGCTG  GAGAAATGAT  TAATcgaGGT  TAGGAGAAAA
151 TATCCTTATC  CGATGGATAT  ACCAAGGGAT  ATTGTGATTG  GAATCGGTAC
201 CATTATTGAT  TTTTAAATGG  TTCCAAATTG  GGAGCTTTTT  GAAATTAAG
251 CTTCCCCTTG  GTTGCCGTAT  AGCGTGGGAA  TTCATGAACG  TTATGAAAGA
301 TTCACAACGA  TGCTCCGTTA  TATTTTACC  GAGAAAGACA  TAGTCAACGT
351 GCGATTTGAT  TATTACAaCa  AAAAATAG
```

g118.pep

1	MCEFKDFRRN	IPCFFEYDEN	SFIGKWYDDG	VWDDEEYVKL	ENDLIEVRRK
51	YPYPMDIPRD	<u>IVIGIGTIID</u>	FLMPVNWELF	EIKASFWLPD	SVGIHERYER
101	FTTMLRYIFT	<u>EKDIVNVRED</u>	YYNKK*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 425>:

```
m118.seq
1  ATGTGTGAGT TCAAGGATAT TATAAGAAAC GTTCCTTATT TTGAGGGGTA
51  TGACGAAAAT TCATTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAATTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGACAT ACCAAGATAT GTTGTGATTG GAATCGGTAC
201 CATTATTGAT TTCTTAATGG TTCCAAATTG GAACTTTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 426; ORF 118>:

```
m118.pep
1  MCEFKEIIRN VPYFEGYDEN SFIGKYYDDG VWDDEEYWLK ENDLIEVRKK
51  YPYPMIDIPRY VVIGIGTIID FLMVPNWKL F EIKASPWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVREF YNNKK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 118 shows 92.8% identity over a 125 aa overlap with a predicted ORF (ORF 118.ng) from *N. gonorrhoeae*:

```
m118/g118

          10          20          30          40          50          60
m118.pep  MCEFKEIIRNVPYFEGYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPMIDIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g118       MCEFKEIIRNVPYFEGYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPMIDIPRD
          10          20          30          40          50          60

          70          80          90          100         110         120
m118.pep  VVIGIGTIIDFLMVPNWKLFEIKASPWLPDSVGIHERYERFTTMLRYIFTEKDIVNVREF
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g118       IVIGIGTIIDFLMVPNWELFEIKASPWLPDSVGIHERYERFTTMLRYIFTEKDIVNVREF
          70          80          90          100         110         120

m118.pep  YNNKKX
          |||||
g118       YNNKKX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 427>:

```
a118.seq
1  ATGTGTGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAAT TCATTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAATTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201 CATTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 428; ORF 118.a>:

```
a118.pep
1  MCEFKEIIRN IPCFEEYDEN SFIGKYYDDG VWDDEEYWLK ENDLIEVRKK
51  YPYPMIDIPRD IVIGIGTIID FLMVPNWEL F EIKASPWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVREF YNNKK*
```

m118/a118 93.6% identity in 125 aa overlap

```
m118.pep  MCEFKEIIRNVPYFEGYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPMIDIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a118       MCEFKEIIRNIPCFEEYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPMIDIPRD
          10          20          30          40          50          60
```

341

	70	80	90	100	110	120
m118.pep	VVIGIGTIIDFLMVPNWKLFEIKASPWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD					
a118	IVIGIGTIIDFLMVPNWELFEIKASPWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD					
	70	80	90	100	110	120
m118.pep	YYNKXX					
a118	YYNKXX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 429>:

g120.seq

```

1   ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAAGGCTACC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAATCC GCGGTACGG TTGTCGGCAA TACCCTGCAC CCTGCCTACT
251 ATAAAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTGTGTTCA CGCTTGCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGTCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGCC TGAATAAGGC GGTACGGGA AAATACAGCA Tagggggcgt
501 gGAAACCGAA GTCGTCAAAT ATCGGGTGCG GCGCGCGAC GATACGGTAA
551 CGTATTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGAcgaCG GCAAACCTA TACGCTGAAG CTCAAATCGG TGCAGATCAA
651 CGGACAGGCC GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 430; ORF 120.ng>:

g120.pep

```

1   MMKTFKNIFS AAILSAAALPC AYAARLPQSA VLHYSYSGYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PAYYKDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DTVTYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 431>:

m120.seq

```

1   ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGmACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GCGGTACGG TTGTCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CTTACGGCAA AGCGGGCGAG AGCAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTGTGTTCA CGCTTGCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGCG GCGCGCGAC GATGCGGTAA
551 TGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCG

```

This corresponds to the amino acid sequence <SEQ ID 432; ORF 120>:

m120.pep

```

1   MMKTFKNIFS AAILSAAALPC AYAAGLPQSA VLXYSYSGYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PTYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 120 shows 97.3% identity over a 223 aa overlap with a predicted ORF (ORF 120.ng) from *N. gonorrhoeae*:

m120/g120

	10	20	30	40	50	60
m120 . pep	MMKTFKNIFSAAILSAALPCAYAAGLPQSAVLXYSYGI PATMTFERSGNAYKIVSTIK					
g120	MMKTFKNIFSAAILSAALPCAYAARLPQSAVLHYSYGI PATMTFERSGNAYKIVSTIK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m120 . pep	VPLYNIRFESGGTVVGNLHPTYYRDIRRGKLYAEAKFADGSVTY GKAGESKTEQSPKAM					
g120	VPLYNIRFESGGTVVGNLHPAYYKDIRRGKLYAEAKFADGSVTY GKAGESKTEQSPKAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m120 . pep	DLFTLAWQLAANDAKLPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE VVKYRVRRGD					
g120	DLFTLAWQLAANDAKLPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE VVKYRVRRGD					
	130	140	150	160	170	180
	190	200	210	220		
m120 . pep	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLSVQINGQA AAKP					
g120	DTVTYFFAPSLNNIPAQIGYTDDGKTYTLKLSVQINGQA AAKPX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 433>:

a120 . seq

```

1  ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTCCGCTAT ACAATATCCG
201 TTTCGAGTCC GCGCGTACGG TTGTCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CTAACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAGCCCC
351 CAAGGCTATG GATTGTGTTCA CGCTTGCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGCG GCGCGGCGAC GATGCGGTAA
551 TGTATTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 434; ORF 120.a>:

a120 . pep

```

1  MMKTFKNIFS AAILSAAALPC AYAAGLPQSA VLHYSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLH PTYYRDIRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

m120/a120 99.6% identity in 223 aa overlap

	10	20	30	40	50	60
m120 . pep	MMKTFKNIFSAAILSAALPCAYAAGLPQSAVLXYSYGI PATMTFERSGNAYKIVSTIK					
a120	MMKTFKNIFSAAILSAALPCAYAAGLPQSAVLHYSYGI PATMTFERSGNAYKIVSTIK					

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	10	20	30	40	50	60
m120.pep	70	80	90	100	110	120
	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTYKGAGESKTEQSPKAM					
a120	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTYKGAGESKTEQSPKAM					
	70	80	90	100	110	120
m120.pep	130	140	150	160	170	180
	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVVKYRVRGD					
a120	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVVKYRVRGD					
	130	140	150	160	170	180
m120.pep	190	200	210	220		
	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAPX					
a120	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAPX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 435>:

g121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATTATG TCGGGAACCA GTATGGACGG
51  GCGGATGCC GTGCTGGTAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCTGACC GGTTGCGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCAC AGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCTCCGTGC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTtac AGCATACAGC TTGCCGATTT
351 GCGCTGCTG GCGGAACTGa cgcggatttt TACCGTCggc gacttcCGCA
401 GCCGCGACCT TGCTGCCGGC GgacaAGGTG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCGCGA TGACAGGGAA ACACGCGTGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAcgcgtg gacgcaggca
601 cacTGGcagc TGCCTTACGA CAAAaaccgt gcAAAGgcgg cacAAGGCAA
651 catatTGCcg cAACTGCTCG gcaggctGCT CGCCcaccCG TATTCTCAC
701 AACCCcacc aaAAAGCACG GGgcGCGaac TgtttgcccT AAattggtc
751 gaaacctAcc ttgacggcgg cgaaaaccga tacgacgtat tgcggacgt
801 tccccgattc accgcgcaaA ccgTttggga cgccgtctca CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGCGG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gccgCATTtg
1001 cgtggttggc GCGGTGTTGG ATTAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCGACCGGCG CATCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 436; ORF 121.ng>:

g121.pep

```

1  METQLYIGIM SGTSMGDADA VLVRMDGGKW LGAEGHAFTP YPDRLRRKLL
51  DLQDTGTDEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPC DITALGCHGQ
101 TVRHAPENGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAPLVPFAF
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGFDTPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRF TAQTVWDVAV HAAADARQMY ICGGIRNFV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWLAACW INRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 437>:

m121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCG CCAATTGCTG

```

```

151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCCTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxXcAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACGCCACCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCCGCGCAA CCGTTTGCGA CGCCGCTCA CACGCAGCGG
851 CAGATGCCCG TCAAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCTGCGACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACGGCGC CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 438; ORF 121>:

m121.pep

```

1 METQLYIGIM SGTSMGDGADA VLIRMDGGKW LGAEGHAFTF YPGRLLRRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL Axxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
151 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDGADAVLIRMDGGKWLGAEGHAFTFPYPGRLLRRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGDGADAVLVRMDGGKWLGAEGHAFTFPYDRLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
m121.pep	HRSRILSQELSRLYAQTAAELLCSONLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
g121	HRSRMLSQELSRLYAQTAAELLCSONLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	70	80	90	100	110	120
m121.pep	AXXX					
g121	AELTRIFTVGDFRSRDLAAGGQGAFLVPFHEALFRDDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
g121	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDAVSHAAADARQMYICDGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
g121	LMADLAECFGTRVSLHSTAE LNLDPOWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
g121	GAGYYYYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 439>:

```

a121.seq
1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCGCTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCGGGA ACACAGTTAC AGCGTACAGC TTGCCGATT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TGCGGCGCGC GGACAAGGCG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGCGGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGCCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCCG TATTTCCGAC
701 AACCACCCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCCT AATTGGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATT ACCCGCGCAA CCGTTTTCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 440; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCQNLAAPS DITALGCHGQ
101 TVRHAPESY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121/a121 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLDLQDTGADEL					
a121	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLDLQDTGADEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCQNLAAPSDITALGCHGQTVRHAPHEHGYISQLADLPLL					
a121	HRSRILSQELSRLYAQTAAELLCQNLAAPSDITALGCHGQTVRHAPHEHGYISQLADLPLL					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m121.pep	XX					
a121	: : : : :					
	130	140	150	160	170	180
	AERTQIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRAVLNIGGIANISVLPPDA					
m121.pep	190	200	210	220	230	240
	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
a121	: : : : :					
	190	200	210	220	230	240
	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
m121.pep	250	260	270	280	290	300
	GRELFAINWLETYLDGGENRYDVLRTLRSRFTAQTVCDVASHAAADARQMYICDGGIRNPV					
a121	: : : : :					
	250	260	270	280	290	300
	GRELFAINWLETYLDGGENRYDVLRTLRSRFTAQTVFVDAVSHAAADARQMYICGGGIRNPV					
m121.pep	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
a121	: : : : :					
	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTAE LNLDPOWVEAAAFWMAACWVNRI PGSPHKATGASKPCIL					
m121.pep	XAGYYYY					
a121						
	GAGYYYY					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 441>:

m121-1.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGGACCG CTTTACCCCC TACCCCGGCA GGTTACGCCG CCAATTGCTG
151 GATTTGCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCTTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCGCAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CGCGGATTTT TACCGTCGGC GACTTCGCGA
401 GCCCGGACCT TCGGCGCGGC GGACAAGGCG CGCCACTCGT CCGCGCCTTT
451 CACGAAGCCC TGTTCGCGCA CAACAGGGAA ACACGCGCGG TACTGAACAT
501 CGCGGGGATT GCCAACATCA GCGTACTCCC CCGCGACGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGACGCGTG GACGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCCACCC TAAAGCAGC GGGCGCGAAC TGTTCGCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGC GAACGCTCTCA CACGACGCG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTC CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCGC CATCCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 442; ORF 121-1>:

m121-1.pep

```

1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRQLL
51  DLQDTGADEL HRSRILSOEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AERTRITVG DFRSRDLAAG GGAPLVPAF
151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRSR TAQTVCDVAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPOWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

m121-1/g121 95.6% identity in 366 aa overlap

10 20 30 40 50 60

```

m121-1.pep  METQLYIGIMSGTSMGDADVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL
              |||||
g121         METQLYIGIMSGTSMGDADVLVRMDGGKWLGAEGHAFTPYPDRLRRKLLDLQDTGTDEL
              10      20      30      40      50      60

              70      80      90      100     110     120
m121-1.pep  HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPHEHGYSIQLADLPLL
              |||||
g121         HRSRILSQELSRLYAQTAELLCSQNLAPCDITALGCHGQTVRHAPHEHGYSIQLADLPLL
              70      80      90      100     110     120

              130     140     150     160     170     180
m121-1.pep  AERTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA
              |||||
g121         AELTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDDRETRVVLNIGGIANISVLPPGA
              130     140     150     160     170     180

              190     200     210     220     230     240
m121-1.pep  PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST
              |||||
g121         PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
              190     200     210     220     230     240

              250     260     270     280     290     300
m121-1.pep  GRELFALNWLETYLDGGENRYDVLRTLRSRFTAQTVCDVASHAAADARQMYICGGGIRNPV
              |||||
g121         GRELFALNWLETYLDGGENRYDVLRTLRSRFTAQTVWDVASHAAADARQMYICGGGIRNPV
              250     260     270     280     290     300

              310     320     330     340     350     360
m121-1.pep  LMDLAECFGRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL
              |||||
g121         LMDLAECFGRVSLHSTAEINLDPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL
              310     320     330     340     350     360

m121-1.pep  XAGYYYY
              |||||
g121         GAGYYYY

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 443>:

```

a121-1.seq
1  ATGGAACAC  AGCTTTACAT  CGGCATCATG  TCGGGAACCA  GCATGGACGG
51  GGCGGATGCC  GTACTGATAC  GGATGGACGG  CGGCAATGG  CTGGGCGCGG
101  AAGGGCAGCG  CTTTACCCCG  TACCCCGGCA  GGTACGCCG  CAAATTGCTG
151  GATTTGCAGG  ACACAGGCGC  GGACGAACTG  CACCGCAGCA  GGATGTTGTC
201  GCAAGAACTC  AGCCGCCTGT  ACGCGCAAAC  CGCCGCCGAA  CTGCTGTGCA
251  GTCAAAACCT  CGCGCGCTCC  GACATTACCG  CCCTCGGCTG  CCACGGGCAA
301  ACCGTCAGAC  ACGCGCCGGA  ACACAGTTAC  AGCGTACAGC  TTGCCGATTT
351  GCCGCTGCTG  GCGGAACGGA  CTCAGATTTT  TACCGTCGGC  GACTTCCGCA
401  GCCGCGACCT  TCGCGCCGCG  GGACAAGGCG  CGCCGCTCGT  CCCCCTTTT
451  CACGAAGCCC  TGTTCGCGCA  CGACAGGGAA  ACACGCGCGG  TACTGAACAT
501  CGCGGGGATT  GCCAACATCA  GCGTACTCCC  CCCCAGCGCA  CCGCCTTCG
551  GCTTCGACAC  AGGACCGGGC  AATATGCTGA  TGGACGCGTG  GATGCAGGCA
601  CACTGGCAGC  TTCCTTACGA  CAAAAACGGT  GCAAGGCGG  CACAAGGCAA
651  CATATTGCCG  CAACTGCTCG  ACAGGCTGCT  CGCCACCCG  TATTTGCGAC
701  AACCCACCC  TAAAGCACG  GGGCGCGAAC  TGTTTGCCCT  AAATTGGCTC
751  GAAACCTACC  TTGACGGCGG  CGAAAACCGA  TACGACGTAT  TCGCGACGCT
801  TTCCCGATT  ACCGCGCAA  CCGTTTTCGA  CGCGCTCTCA  CACGAGCGG
851  CAGATGCCCG  TCAATGTAC  ATTTGCGGCG  GCGGCATCCG  CAATCCTGTT
901  TTAATGGCGG  ATTTGGCAGA  ATGTTTGGGC  ACACGCGTT  CCCTGCACAG
951  CACCGCCGAA  CTGAACCTCG  ATCCGCAATG  GGTAGAAGCC  GCCGCGTTG
1001  CATGGATGGC  GCGGTGTTGG  GTCAACCGCA  TTCCCGGTAG  TCCGCACAAA
1051  GCAACCGCG  CATCCAAACC  GTGTATTCTG  GCGCGGGAT  ATTATTATTG
1101  A

```

This corresponds to the amino acid sequence <SEQ ID 444; ORF 121-1.a>:

```

a121-1.pep
1  METQLYIGIM  SGTSMDGADA  VLIRMDGGKW  LGAEGHAFTP  YPGRLRRKLL
51  DLQDTGADEL  HRSRILSQEL  SRLYAQTAEE  LLCSQNLAPS  DITALGCHGQ
101  TVRHAPESY  SVQLADLPLL  AERTQIFTVG  DFRSRDLAAG  GQGAPLVPF
151  HEALFRDRE  TRAVLNIGGI  ANISVLPPDA  PAFGFDTPG  NMLMDAWMQA

```

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201 HWQLPYDKNG AKAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
 251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
 301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
 351 ATGASKPCIL GAGYYY*

m121-1/a121-1 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAF	TPYPGR	LRQLLDLQDT	GADEL
a121-1	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAF	TPYPGR	LRQLLDLQDT	GADEL
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSR	LYAQTAELLCSQ	NLAPSDIT	ALGCHGQTV	RHAP	EHGYSIQ
a121-1	HRSRILSQELSR	LYAQTAELLCSQ	NLAPSDIT	ALGCHGQTV	RHAP	EHGYSIQ
	130	140	150	160	170	180
m121-1.pep	AERTTRIFTVGDF	RSRDLAAGGQGA	PLVPAFHEAL	FRDNR	RETRAVLN	IGGIANISV
a121-1	AERTTRIFTVGDF	RSRDLAAGGQGA	PLVPAFHEAL	FRDNR	RETRAVLN	IGGIANISV
	190	200	210	220	230	240
m121-1.pep	PAFGFDTGPGNML	MDAWTQAHWQL	PYDKNGAKA	AQGNILPQ	LLDRLLAHP	YFAQPHPKST
a121-1	PAFGFDTGPGNML	MDAWTQAHWQL	PYDKNGAKA	AQGNILPQ	LLDRLLAHP	YFAQPHPKST
	250	260	270	280	290	300
m121-1.pep	GRELFALNWL	ETYLDGGENR	YDVLRTLSR	FTAQTV	CDVSHAA	ADARQMYIC
a121-1	GRELFALNWL	ETYLDGGENR	YDVLRTLSR	FTAQTV	CDVSHAA	ADARQMYIC
	310	320	330	340	350	360
m121-1.pep	LMADLAECFG	TRVSLHSTAD	NLDPQWVEA	AXFAWLA	ACWINRIP	GSPHKATG
a121	LMADLAECFG	TRVSLHSTAD	NLDPQWVEA	AXFAWLA	ACWINRIP	GSPHKATG
m121-1.pep	XAGYYYY					
a121	GAGYYYY					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 445>:

g122.seq

```

1  ATGGCTTTAC TGAGCATCCG CAAGCTGCAC AAACAATACG GCAGCGTAAC
51  CGCCATCCAA TCCTTAGACT TGGACTTGGA AAAAGGCGAA GtcatCGTAC
101 TGCTGGGCCG gTccggtgc ggCAAATCCA CCCTcctgcg ctgcgtcaac
151 GGTTTGGAGC CGCACCAagg cgGCAGCATC GTGATGGACG GTgtcgGCGA
201 ATTCggcAAA GACGTTTCCT GGCAAACCGC CCGGCAAAAa gtcggtatgg
251 tctttcaaag taacgAactg Tttgccaca tgaccgtcat cgAaaacatc
301 ttcttAggcC CGGTAAagga aCAAAACgc gaccgtgccg aagcaGAGGC
351 gCAAGCCGGC AAactGttgg aacgcgTCGG actgctAGAC CGCAAAAACG
401 CCTATCCGCG CGAACTTTCC GGCGGTCAGA AACAGCGCAT CGCCATTGTC
451 CGCGCCCTGT GCCTGAATCC GGAAGTCATC CTGCTGGACG AAATCACC GC
501 CGCACTTGAC CCCGAAATGG TGCGCGAAGT CTGGAAGTG GTTTTGAAC
551 TCGCCCGCGA AGGATGAGT ATGCTCATCG TAACCCACGA AATGGGGTTC
601 GCACGCAAAG TTGCCGACCG CATCGTCTTT ATGGACAAAG GCGGCATCGT
651 CGAATCGTCC GACCCCGAAA CCTTTTTTTC CGCACAAAAG AGCGAACGCG
701 CCCGCCAATT TCTGGCAGGT ATGGACTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 446; ORF 122.ng>:

1	MALLSIRKLH	KQYGSVTAIQ	SLDLDLEKGE	VIVLLGPSGC	GKSTLLRCVN
51	GLEPHQGGSI	VMDGVGEFGK	DVSQQTARQK	VGMVFQSNEL	FAHMTVIENT
101	FLGPVKEQNR	DRAEAEAQAD	KLLERVGLLD	RKNAYPRELS	GGQKQRTAIV
151	RALCLNPEVI	LLDEITAAAL	PEMVEVLEVL	VLELAREGMS	MLIVTHEMGF
201	ARKVAIDRVF	MDKGGIVESS	DPETFFSAPK	SERAROFAGL	MDY*

m122.seq

1	GTTGTCATGA	TTAAATCCG	CAATATCCAT	AAGACCTTTG	GCGAAAACAC
51	TATTTTGC	GGCATCGATT	TGGATGTGTG	CAAAGGGCAG	GTGGTCGTCA
101	TCCTCGGGc	TTCCGGCTCA	GGCAAAACGA	CGTTTCTGCG	ATGCCTTAAAC
151	GCGTTGGAAA	TGCCCAAGA	CGGACAAATC	GAGTTCGACA	ACGAGCGACC
201	GCTGAAATC	GATTTTCTA	AAAAACCAAG	CAAAACGAT	ATTTTGGCAC
251	TGCGCCGCAA	GATCAKGCAT	GTGTTTCAAC	AATACAAyCT	CTTTCCGCAG
301	AAAACCGCCT	TGGAAAACGT	AATGGAAGGA	CCGGTTGCCG	TACAgGGCAA
351	GCTGCCCGCC	CAAGCGCGCG	AAGAGGCTCT	GAAACTGCTG	GAAAAAGTCG
401	GCTTGGGCGA	CAAAGTGGAT	TGTATCCCT	ACAGCTTTTC	CGGCGGTCAG
451	CAGCAGCGCG	TCGGCATATG	CCGCGCATTG	GCGATTTCAG	CTGAACATGAT
501	CTGTGTTGAC	GAACCGACTT	CCGCGCTCGA	TCCTGAATTG	GTGCAAGATG
551	TTTTGGATmC	CATGAAGGAA	TTGGCGCAAG	AAGGCTGGAC	CATGGTTTGT
601	GTTACGCATG	AAATCAAGTT	CGCCTTAGAA	GTGGCAACCA	CCGwCGTGT
651	GATGGACrGC	GGCGTTATTG	TCGAACAAGG	CAGCCCGCAA	GATTTGTTCG
701	ACCACCCCAA	ACCGAACGG	ACGCGGAGAT	TTTTAAGCCA	AATCCAATCT
751	ACCAAGATT	GA			

m122.pep

1	VVMIKIRNIH	KTFGENTILR	GIDLDVCKGQ	VVVI LGPSGS	GKTTFLRCLN
51	ALEMPEDGQI	EFDNERPLKI	DFSKKPSKHD	ILALRRKSXM	VFQQYNLFPH
101	KTALENVMBG	PVAVQGGKPA	QAREEALKLL	EKVGLGDKVD	LYPYQLSGGQ
151	QQRVGIARAL	AIQPELMLFD	EPTSALDPEL	VQDVLDXMKE	LAQEGWTMVV
201	VTHEIKFALE	VATTXVVM DX	GVIVEQGS PQ	DLDFHPKHER	TRRFLS IQS
251	TKI*				

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 122 shows 47.2% identity over a 246 aa overlap with a predicted ORF (ORF 122.ng) from *N. gonorrhoeae*:

m122/q122

[illegible]

350

	180	190	200	210	220	230
		250				
m122.pep	TRRFLSQIQSTKIX					
	: : :					
g122	ARQFLAGMDYX					
	240					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 449>:

```
a122.seq
1   GTTGTTCATGA TTAAATCCG CAATATCCAT AAGACCTTCG GCAAAAATAC
51  CATTGTGCGC GGCATCAATT TGGATGTGTG CAAAGGGCAG GTGGTCGTCA
101 TCCTCGGGCC TTCCGGCTCA GGCAAAACGA CGTTTCTGCG ATGCCTAAAC
151 GCGTTGGAAA TGCCCGAAGA CGGACAAATC GAGTTCGACA ACGAGCGACC
201 GCTGAAAATC GATTTTCTA AAAACCAAG CAAACACGAT ATTTTGGCAC
251 TGCGCCGCAA ATCAGGCATG GTGTTCAAC AATACACCT CTTCCGCAC
301 AAAACCGCCT TGGAAAACGT GATGGAAGGA CCGGTTGCCG TACAGGGCAA
351 GCCTGCCGCC CAAGCGCGCG AAGAGGCTCT GAAACTGCTG GAAAAAGTCG
401 GCTTGGGCGA CAAAGTGGAT TTGTATCCCT ACCAGCTTTC CGGCGGTCAG
451 CAGCAGCGCG TCGGCATTGC CCGAGCATTG GCGATTGAGC CCGAGCTGAT
501 GTTGTTCGAC GAACCCACTT CCGCGCTTGA CCCCAGTTG GTGCAAGACG
551 TGTTGAACGC CATGAAGGAA TTGGCGCGGG AAGGTTGGAC GATGGTCGTC
601 GTTACCCACG AAATCAAGTT CGCGCTGGAA GTTGCCACGA CCGTTGTCGT
651 GATGGACGGC GCGGTTATCG TAGAGCAGGG CAGCCCGAAA GAGTTGTTCC
701 ACCACCCCAA ACACGAACGG ACGCGGAGAT TTTAAGCCA AATCCAATCT
751 ACCAAGATT GA
```

This corresponds to the amino acid sequence <SEQ ID 450; ORF 122.a>:

```
a122.pep
1   VVMIKIRNIH KTFGKNTILR GINLDVCKGQ VVVLGPGSGS GKTTFILRLN
51  ALEMPEDGQI EFDNERPLKI DFSKKPSKHD ILALRRKSGM VFQQYNLFPH
101 KTALENVMEG PVAVQGKPAA QAREEALKLL EKVLGDKVD LYPYQLSGGQ
151 QORVGIARAL AIQPELMLFD EPTSALDPEL VQDVNLAMKE LAREGWTMVV
201 VTHEIKFALE VATTVVVMDG GVIVEQGSFK ELFDHPKHER TRRFLSQIQS
251 TKI*
```

m122/a122 96.0% identity in 253 aa overlap

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKT	FGENTILRGID	LDVCKGQVV	VILGPGSGK	TTFLRLCNA	LEMPEDGQI
a122	VVMIKIRNIHKT	FGKNTILRGIN	LDVCKGQVV	VILGPGSGK	TTFLRLCNA	LEMPEDGQI
	10	20	30	40	50	60
m122.pep	EFDNERPLKID	FSKKPSKHDIL	ALRRKSXMF	QQYNLFPHK	TALENVMEG	PVAVQGKPAA
a122	EFDNERPLKID	FSKKPSKHDIL	ALRRKSGMV	FQQYNLFPH	KTALENVME	GPPVAVQGKPAA
	70	80	90	100	110	120
m122.pep	QAREEALKLLE	KVGLGDKVDL	YPYQLSGGQ	QORVGIARAL	AIQPELMLF	DEPTSALDPEL
a122	QAREEALKLLE	KVGLGDKVDL	YPYQLSGGQ	QORVGIARAL	AIQPELMLF	DEPTSALDPEL
	130	140	150	160	170	180
m122.pep	VQDVLDXMKEL	AQEGWTMVV	VTHEIKFALE	VATTXVVM	DXGVIVEQGS	PQDLFDHPKHER
a122	VQDVNLAMKEL	AREGWTMVV	VTHEIKFALE	VATTVVVMD	GGVIVEQGS	FKELFDHPKHER
	190	200	210	220	230	240
m122.pep	TRRFLSQIQST	KIX				

a122 |||||
 TRRFLSQIQSTKIX
 250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 451>:

g122-1.seq
 1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACCATTTT
 51 GCGCGGCATC GATTGGATG TGGCAAAGG GCAGGTGGTC GTCATCCTCG
 101 GGCCTTCCGG CTCGGGTAAA ACAACATTTC TGCGCTGCCT AAACGCGTTG
 151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGCGC GGCCGTTACG
 201 CATTGATTTT TCCAAAAAAA CAAGCAAACA CGATATTTTG GCACTGCGCC
 251 GCAAGTCCGG AATGGTATTC CAACAATACA ACCTCTTCCC GCATAAAACC
 301 GTGTTGGAAC ACGTGATGGA AGGGCCGGTT GCCGTACAGG GCAAGCCTGC
 351 CGCCCAAGCG CGCGAAGAGG CTTTGAAACT GCTGGAAAAA GTCGGCTTGG
 401 GCGATAAAGT GGATTTGTAT CCCTACCAGC TTTCCGCGCG TCAGCAGCAG
 451 CGTGTGCGTA TCGCCCGCGC ACTGGCGATT CAGCCTGAAT TGATGCTGTT
 501 TGACGAACCC ACTTCCGCGC TGGACCCCGA GTTGGTGCAA GACGTGTTGG
 551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC
 601 CACGAAATCA AGTTCACGCT GGAAGTTGCC ACGAACGTCG TCGTGATGGA
 651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC
 701 TCAAACACGA ACGGACGCGG AGATTTTAA GCCAATCCA ATCTGCCAAG
 751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 452; ORF 122-1.ng>:

g122-1.pep
 1 MIKIRNIHKT FGENTILRGI DLDVKGQVV VILGPSGSGK TTFRLCLNAL
 51 EMPEDGQIEF DNARPLRIDF SKKTSKHDIL ALRRKSGMVF QQYNLFPHKT
 101 VLENVMEGPV AVQGKPAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ
 151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDMKELA REGWTMVVVT
 201 HEIKFTLEVA TNVVMDGGV IVEQSPKEL FDHLKHERTR RFLSQIQSAK
 251 I*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 453>:

m122-1.seq
 1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACATATTT
 51 GCGCGGCATC GATTGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
 101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TGCGATGCCT AAACGCGTTG
 151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA
 201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC
 251 GCAATCAGG CATGGTGTTC CAACAATACA ACCTCTTCCC GCACAAAACC
 301 GCCTTGGAAC ACGTAATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC
 351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAAAA GTCGGCTTGG
 401 GCGACAAAGT GGATTTGTAT CCCTACCAGC TTTCCGCGCG TCAGCAGCAG
 451 CGCGTCCGCA TTGCCGCGC ATTGGCGATT CAGCCTGAAC TGATGCTGTT
 501 TGACGAACCG ACTTCCGCGC TCGATCCTGA ATTGGTGCAA GATGTTTGG
 551 ATACCATGAA GGAATTGGCG CAAGAAGGCT GGACCATGGT TGTGCTTACG
 601 CATGAAATCA AGTTCGCCTT AGAAGTGGCA ACCACCGTCG TCGTGATGGA
 651 CGGCGGCGTT ATTGTGCAAC AAGGCAGCCC GCAAGATTTC TTCGACCACC
 701 CCAACACGA ACGGACGCGG AGATTTTAA GCCAATCCA ATCTACCAAG
 751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 454; ORF 122-1>:

m122-1.pep
 1 MIKIRNIHKT FGENTILRGI DLDVCRQVV VILGPSGSGK TTFRLCLNAL
 51 EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT
 101 ALENVMEGPV AVQGKPAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ
 151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDTMKELA QEGWTMVVVT
 201 HEIKFALEVA TTVVMDGGV IVEQSPQDL FDHPKHERTR RFLSQIQSTK
 251 I*

m122-1/g122-1 94.8% identity in 251 aa overlap

	10	20	30	40	50	60
m122-1.pep	MIKIRNIHKTFFGENTILRGIDLDVCRQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
g122-1	MIKIRNIHKTFFGENTILRGIDLDVKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					

352

	10	20	30	40	50	60
m122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFFQYNNLFPHKTALENVMEGPFVAVQGKPAQA					
g122-1	DNERPLKIDFSKKPSKHDILALRRKSGMVFFQYNNLFPHKTVLENVMEGPFVAVQGKPAQA					
	70	80	90	100	110	120
m122-1.pep	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMFLFDEPTSLDPELVQ					
g122-1	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMFLFDEPTSLDPELVQ					
	130	140	150	160	170	180
m122-1.pep	190	200	210	220	230	240
	DVLDTMKELAQEGWMTVVVTHEIKFALEVATTVVMDGGVIVEQGSPODLFDHPKHETR					
g122-1	DVLDTMKELAQEGWMTVVVTHEIKFTLEVATNVVMDGGVIVEQGSPODLFDHPKHETR					
	190	200	210	220	230	240
m122-1.pep	250					
	RFLSQIQSTKIX					
g122-1	RFLSQIQSAKIX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 455>:

a122-1.seq

```

1  ATGATTAAAA TCCGCAATAT CCATAAGACC TTCGGCAAAA ATACCATTTT
51  GCCCGGCATC AATTGGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCAGGCCAA ACGACGTTTC TGCGATGCCT AAACGCGTTG
151 GAAATGCCCC AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAATCAGG CATGGTGTTC CAACAATACA ACCTCTTTCC GCACAAAACC
301 GCCTTGGAAA ACGTGATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGACAAAGT GGATTGTAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
451 CGCGTCGGCA TTGCCCGAGC ATTGGCGATT CAGCCCGAGC TGATGTTGTT
501 TGACGAACCC ACTTCCGCGC TTGACCCCGA GTTGGTGCAA GACGTGTTGA
551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC
601 CACGAAATCA AGTTCGCGCT GGAAGTTGCC ACGACCGTTG TCGTGATGGA
651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC
701 CCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTACCAAG
751 ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 456; ORF 122-1.a>:

a122-1.pep

```

1  MIKIRNIHKT FGKNTILRGI NLDVCKGQVV VILGPSGSGK TFLRCLNAL
51  EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMV FQYNNLFPHK
101 ALENVMEGPV AVQGKPAQA REEALKLEK VLGDKVDLY PYQLSGGQQ
151 RVGIARALAI QPELMFLFDEP TSALDPELVQ DVLNAMKELA REGWMTVVVT
201 HEIKFALEVA TTVVMDGGV IVEQGSPEL FHPKHETR RFLSQIQSTK
251 I*

```

a122-1/m122-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
a122-1.pep	MIKIRNIHKTFGKNTILRGINLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
m122-1	MIKIRNIHKTFGKNTILRGIDLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
	10	20	30	40	50	60
a122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFFQYNNLFPHKTALENVMEGPFVAVQGKPAQA					
m122-1	DNERPLKIDFSKKPSKHDILALRRKSGMVFFQYNNLFPHKTALENVMEGPFVAVQGKPAQA					
	70	80	90	100	110	120
a122-1.pep	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMFLFDEPTSLDPELVQ					
m122-1	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMFLFDEPTSLDPELVQ					

q125.seq

1	ATGTCGGGCA	ATGCCTCCTC	TCCTTCATCT	TCCGCCGCCA	TCCGGCTGGT
51	TTGGTTCGGC	GCGGCGGTAT	CGATTGCCGA	AATCAGCACG	GGTACGCTGC
101	TCGCCCCCTT	GGGCTGGCAG	CGCGGTCTGG	CGGCCCTGCT	TTTGGGT CAT
151	GCCGTCGGCG	GCGCGCTGTT	TTTTCGCGCG	GCGTATATCG	GCGCACTGAC
201	CGGACGCGAG	TCGATGGAAA	GTGTGCGCCT	GTGTTCCGGC	AAATGCGGTT
251	CAGTGCTGTT	TTCCGTGGCG	AATATGCTGC	AAC TCGCCG	CTGGACGGCG
301	GTGATGATT	ACGTCGCGCG	AacggTCAGC	TCGCTTTTGG	GCAAAGTGTT
351	GTGGGACggc	gaATCCTTTG	TCTGGTGGGC	ATTGGCAAAC	GGCGCACTGA
401	TCGTGCTGTG	GCTGGTTTTC	GGCGCACGCA	GAACGGGCGG	GCTGAAAACC
451	GTTTCGATGC	TGCTGATGCT	GCTTGCCGTG	TTGTGGTTGA	GCGTCGAAGT
501	GTTTCGTTTC	TCCGGCACAA	ACGCCGCGCC	CGCCGTTTCA	GACGGCATGA
551	CCTTCGGAAC	GGCAGTCGAA	CTGTCCGCGC	TCATGCCGCT	TTCTGGGCT
601	CCGCTGGCGC	CCGACTACAC	GCGCCAAGCA	CGCCCGTCGT	TTGCCGCAAC
651	CTGACGGCGA	ACGCTCGCCT	ATACGCTGAC	GCGCTGCTGG	ATGTATGCCT
701	TGGGTTTGGC	GGCGGCTCTG	TTTACCGGAG	AAACCGACGT	GGCGAAAAATC
751	CTGTTGGGCG	CGGGCTTGGG	CATAACGGGC	ATTCTGGCAG	TCGTCTCTCTC
801	CACCGTTACC	ACAACGTTTC	TCGATACCTA	TTCCGCCGGC	GCGAGTGC GA
851	ACAACATTTC	CGCGCGTTTT	GCGGAAATAC	CCGTCTGTGT	CGGCGTTACC
901	CTGATccgca	ccgtgcttgc	cgtcatgttg	cccgttaccg	aatataaaaa
951	cttctctgctg	cttatccgct	cggatatttg	gccgatggcg	gggtggttttg
1001	attgccaact	TTTTtttctt	AAAACGGCGT	GA	

This corresponds to the amino acid sequence <SEQ ID 458: ORF 125.ng>:

m125.seq

1	ATGTCGGGCA	ATGCCTCCTC	TCCTTCATCT	TCCTCCGCCA	TCGGGCTGAT
51	TTGGTTCGGC	GCGGCGGTAT	CGATTGCCGA	AATCAGCACG	GGTACGCTGC
101	TTGCGCCTTT	GGGCTGGCAG	CGCGGTCTGG	CGGCTCTACT	TTTGGGTTCAT
151	GCCGTCGCG	GCGCGCTGTT	TTTTGCGGCG	GCGTATATCG	GCGCACTGAC
201	CGGACGCGC	TCGATGAAA	GCGTGCGCCT	GTCGTTCCGC	AAACGCGGTT
251	CAGTGCTGTT	TTCGCTGGCG	AAATAGTCTC	AAC TGCCCG	CTGGACGGCG
301	GTGATGATT	ACGCGCGCG	AACGGTCAGC	TCGCTTTTGG	GCAAAGTGTT
351	GTGGGACGCG	GAATCTTTTG	TCTGTGTGGC	ATTGCAAAAC	GGCGCGCTGA
401	TTGTGCTGTG	GCTGGTTTTC	GGCGCACGCA	AAACAGGCGG	GCTGAAAACC
451	GTTTCGATGC	TGCTGATGCT	GTTGGCGGTT	CTGTGGCTGA	GTGCCGAAGT
501	CTTTTCCACG	GCAGGCAGCA	CCGCGCACCA	GGTTTCAGAC	GGCATGAGTT
551	TCGGAACGGC	AGTCGAGCTG	TCCGCCGTGA	TGCCGCTTTC	CTGGCTGCCG
601	CTTGCCGCCG	ACTACACGCG	CCACGCGCGC	CGCCCGTTTG	CGGCAACCTT
651	GACGGCAACG	CTCGCCTATC	CGCTGACAGG	CTGCTGGATG	TATGCCTTGG
701	GTTTGGCAGC	GGCGTTTGTC	ACCGGACAAA	CCGACGTGGC	AAAAATCCAC
751	CTGGGCGCAr	GTTTG ₉ GTGC	GGCAGGCATT	TGGCGGCTGC	TCCTCTCTCC
801	CGTTACCACA	ACGTTTCTCG	ATGCCTATTC	CGCGCGCGCG	AGTGCGAACC

354

851 ACATTTCCGC GCGTTTTCG GAAACACCCG TCGCTGTCrG CGTTACCCCTG
 901 ATCGGCACCG TACTTGCCGT CATGCTGCCC GTTACCGAAT ATGAAAACCTT
 951 CCTGCTGCTT ATCGGCTCGG TATTTGCGCC GATGGCGGgC GGTTTTGATT
 1001 GCCGACTTTT TCGTCTTGAA ACGGCGTGA

This corresponds to the amino acid sequence <SEQ ID 460; ORF 125>:

m125.pep
 1 MSGNASSPSS SSAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH
 51 AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFSVA NMLQLAGWTA
 101 VMIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
 151 VSMLLMLLAV LWLSAEVFST AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
 201 LAADYTRHAR RPPAATLTAT LAYTLTGCM YALGLAAALF TGETDVAKIL
 251 LGAXLGAAGI LAVVLSTVTT TFLDAYSAGA SANNISARFA ETPVAVXVTL
 301 IGTVLAVMLP VTEYENFLLL IGSVFAPMAG GFDCRLFRLE TA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 125 shows 92.1% identity over a 343 aa overlap with a predicted ORF (ORF 125.ng) from *N. gonorrhoeae*:

m125/g125

	10	20	30	40	50	60
m125.pep	MSGNASSPSSSSAIGLIWFGAAVSVIAEISTGTLLAPLGWQRGLAALLLGHAVGGALFFAA					
g125	MSGNASSPSSSSAIGLVWFGAAVSVIAEISTGTLLAPLGWQRGLAALLLGHAVGGALFFAA					
	10	20	30	40	50	60
m125.pep	AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG					
g125	AYIGALTGRSSMESVRLSFGKCGSVLFSVANMLQLAGWTAVMIYVAGTSSALGKVLWDG					
	70	80	90	100	110	120
m125.pep	AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG					
g125	AYIGALTGRSSMESVRLSFGKCGSVLFSVANMLQLAGWTAVMIYVAGTSSALGKVLWDG					
	70	80	90	100	110	120
m125.pep	ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQ-VS					
g125	ESFVWWALANGALIVLWLVFGARRTGGLKTVSMLLMLLAVLWLSVEVFASSGTNAAPAVS					
	130	140	150	160	170	179
m125.pep	ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQ-VS					
g125	ESFVWWALANGALIVLWLVFGARRTGGLKTVSMLLMLLAVLWLSVEVFASSGTNAAPAVS					
	130	140	150	160	170	180
m125.pep	DGMSFGTAVELSAVMPLSWPLAADYTRHARRPFAATLTATLAYTLTGCMYALGLAAL					
g125	DGMTFGTAVELSAVMPLSWPLAADYTRQARRPFAATLTATLAYTLTGCMYALGLAAL					
	180	190	200	210	220	230
m125.pep	DGMSFGTAVELSAVMPLSWPLAADYTRHARRPFAATLTATLAYTLTGCMYALGLAAL					
g125	DGMTFGTAVELSAVMPLSWPLAADYTRQARRPFAATLTATLAYTLTGCMYALGLAAL					
	180	190	200	210	220	230
m125.pep	DGMSFGTAVELSAVMPLSWPLAADYTRHARRPFAATLTATLAYTLTGCMYALGLAAL					
g125	DGMTFGTAVELSAVMPLSWPLAADYTRQARRPFAATLTATLAYTLTGCMYALGLAAL					
	190	200	210	220	230	240
m125.pep	FTGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVT					
g125	FTGETDVAKILLGAGLGITGILAVVLSTVTTTFLDTYSAGASANNISARFAEIPVAVGVT					
	240	250	260	270	280	290
m125.pep	FTGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVT					
g125	FTGETDVAKILLGAGLGITGILAVVLSTVTTTFLDTYSAGASANNISARFAEIPVAVGVT					
	240	250	260	270	280	290
m125.pep	FTGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVT					
g125	FTGETDVAKILLGAGLGITGILAVVLSTVTTTFLDTYSAGASANNISARFAEIPVAVGVT					
	250	260	270	280	290	300
m125.pep	LIGTVLAVMLPVTEYENFLLLLIGSVFAPMAGGFDCRLFRLETAX					
g125	LIRTVLAVMLPVTEYKNFLLLLIRSVFPGMAGGFDCRLFCCLKTAX					
	300	310	320	330	340	
m125.pep	LIGTVLAVMLPVTEYENFLLLLIGSVFAPMAGGFDCRLFRLETAX					
g125	LIRTVLAVMLPVTEYKNFLLLLIRSVFPGMAGGFDCRLFCCLKTAX					
	300	310	320	330	340	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 461>:

a125.seq
 1 ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCGCCGCCA TCGGGCTGAT
 51 TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACACTGC
 101 TTGCGCCTTT GGGCTGGCAG CGCGGTCTGG CGGCTCTGCT TTTGGGTCAT

```

151 GCCGTCGGCG GCGCGCTGTT TTTTGGCGCG GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAG GCGTGCGCCT GTCGTTCCGC AAACGCGGTT
251 CAGTGCTGTT TTCCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGCCGGCGC AACGGTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACGGC GAATCTTTTG TCTGGTGGGC ATTGGCAAAC GCGCGCGTGA
401 TTGTGCTGTG GCTGGTTTTT GCGCGACGCA AAACAGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GTTGGCGGTT CTGTGGCTGA GTGCCGAAGT
501 CTTTTCCACG GCAGGCAGCA CCGCCGACCA GGTTCAGAC GGCATGAGTT
551 TCGGAACGGC AGTCGAGCTG TCCGCCGTGA TGCCGCTTTC TTGGCTGCCG
601 CTGGCCGCCG ACTACACGCG CCACGCGCGC CGCCCGTTTG CGGCAACCCT
651 GACGGCAACG CTCGCCTACA CGCTGACCGG CTGCTGGATG TATGCCTTGG
701 GTTTGGCAGC GCGGTTGTTT ACCGGAGAAA CCGACGTGGC AAAATCCTG
751 CTGGGCGCAG GTTGGGTGTC GGCAGGCATT TTGGCGTGC TCCTGTGCGC
801 CGTTACCAAC ACTTTTCTCG ATGCCTACTC CGCCGGCGTA AGTGCCAACA
851 ATATTTCCGC CAACTTTTCG GAAATACCCA TCGCCGTTGC CGTCGCCGTT
901 GTCGGCACAC TGCTTGCCGT CCTCCTGCCC GTTACCGAAT ATGAAACTT
951 CCTGCTGCTT ATCGGCTCGG TATTGCGGCC GATGGCG.GC GGTTTTGATT
1001 GCCGACTTTT TCGTCTTGAA ACGGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 462; ORF 125.a>:

```

a125.pep
1 MSGNASSPSS SAAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH
51 AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFSA NMLQLAGWTA
101 VMIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
151 VSMLLMLLAV LWLSAEVFT AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
201 LAADYTRHAR RFAATLTAT LAYTLTGCWM YALGLAAALF TGETDVAKIL
251 LGAGLGAAGI LAVVLSTVTT TFLDAYSAGV SANNISAKLS EIPIAVAVAV
301 VGTLLAVLLP VTEYENFLLI IGSVFAPMAX GFDCRLFRLT TA*

```

m125/a125 95.6% identity in 342 aa overlap

```

m125.pep      10      20      30      40      50      60
MSGNASSPSSSSAIGLIWFGAAVVSIAEISTGTLLAPLGWQORGLAALLLGHAVGGALFFAA
|||||:|||||
a125          10      20      30      40      50      60
MSGNASSPSSSSAIGLIWFGAAVVSIAEISTGTLLAPLGWQORGLAALLLGHAVGGALFFAA

m125.pep      70      80      90      100     110     120
AYIGALTGRSSMESVRLSFGKRGSVLFSSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG
|||||:|||||
a125          70      80      90      100     110     120
AYIGALTGRSSMESVRLSFGKRGSVLFSSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG

m125.pep     130     140     150     160     170     180
ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFTAGSTAAQVSD
|||||:|||||
a125         130     140     150     160     170     180
ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFTAGSTAAQVSD

m125.pep     190     200     210     220     230     240
GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCWMYALGLAAALF
|||||:|||||
a125         190     200     210     220     230     240
GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCWMYALGLAAALF

m125.pep     250     260     270     280     290     300
TGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVTL
|||||:|||||
a125         250     260     270     280     290     300
TGETDVAKILLGAGLGAAGILAVVLSTVTTTFLDAYSAGVSANNISAKLSEIPIAVAVAV

m125.pep     310     320     330     340
IGTVLAVMLPVTEYENFLLIIGSVFAPMAGGFDCRLFRLTAX
:||||:|||||
a125         310     320     330     340
VGTLLAVLLPVTEYENFLLIIGSVFAPMAXGFDCRLFRLTAX

```

310 320 330 340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 463>:

```
g126.seq
  1  AtgccgtcTG AAaccCcaaa ggcACGCCGC CGGCTTTCAG ACGGCATCGC
 51  GTCCGACAAC CATACCAAAG AATCCATCAT GCTCACCctg tacggcGAAA
101  CTTTCCCTTC GCGGCTGCTg ctcggcacgG cggcctacCC GACCCCTGAA
151  ATCCTCAAAC AATCCGTCCG AACCGCCCGG CCCGCGATGA ttaccGTCTC
201  GCTGCGCCGC ACGGGATGCG GCGGCGAGGC GCACGGTCAG GGGTTTGTGT
251  CGCTGCTTCA AGAAACCGGC GTTCCCGTCC TGCCGAACAC GGCAGGCTGC
301  CAAAGCGTGC AGGAAGCGGT AACGACGGCG CAAATGGCGC GCGAAGTGTT
351  TGAAACCGAT TGGATAAAAT TGGAACTCAT CGGCGACGAC GACACCTTGC
401  AGCCGGACGT GTTCCAATC GTCGAAGCGG CGGAAATCCT GATTAAAGAC
451  GGCTTCAAAG TGCTGCCTTA TTGCACCGAA GACCTGATTG CCTGCCGCCG
501  CCTGCTCGAT GCGGGCTGTC AGGCGTTGAT GCCGTGGGCG GCTCCCATCG
551  GCACGGGTTT GGGGGCGGTT CACGCCTATG CGCTCAAAAT CCTGCGCGAA
601  GCGCTGCCCG ACACGCCGCT GATTATCGAC GCGGGCTTGG GTTTGCGTTC
651  CCAAGCGGCA CAAGTGATGG AATGGGGTTT TGACGGCGTA TTGTTAAACA
701  CCGCCGTTTC CCGCAGCGGC GACCCCGTCA ACATGGCGCG CGCCTTCGCA
751  CTCGCCGTCG AATCCGGACG GCTGGCATTG GAAGCCGGGC CGGTCGAAGC
801  GCGAACCAAA GCCCAAGCCA GCACGCCGAC AGTCGGACAA CCGTTTGTGG
851  ATTCGGCGGA ATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 464; ORF 126.ng>:

```
g126.pep
  1  MPSETPKARR RLSGDIASDN HTKESIMLTL YGETFPSRL LGTAAYPTPE
 51  ILKQSVRTAR PAMITVSLRR TCGGGEAHGQ GFWSLLQETG VVPLPNTAGC
101  QSVQEAHTTA QMAREVFETD WIKLELIGDD DTLQPDVFQL VEAAILIKD
151  GFKVLPYCTE DLIACRRLLD AGCQALMPWA APIGTGLGAV HAYALKILRE
201  RLPDTPLIID AGLGLPSQAA QVMEWGFQDV LLNTAVSRSG DPNVNMARAF
251  LAVESGRLAF EAGPVEARTK AQAAPTPTVGQ PFWHSAEY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 465>:

```
m126.seq (partial)
  1  ..CACTATACAA AGGAACCCAT TATGCTCACC CTATACGGCG AAACTTTCCC
 51  CTCGCGGCTG CTGCTCGGCA CGGCTGCCTA CCCGACCCCG GAAATCCTCA
101  AACAATCCAT CCAAACCGCC CAGCCTGCGA TGATTACCGT CTCGCTGCGC
151  CGCGCGGGAA GCGGCGGCGA GCGCGACGGT CAGGGGTTTT GGTGCTGCT
201  TCAAGAAACC GCGGTTCCCG TCCTGCCGAA CACGGCAGGC TGCCAAAGCG
251  TGCAGGAAGC GGTAACGACG GCGCAAATGG CGCGCGAAGT GTTTGAAACC
301  GATTGGATAA AATTGGAAC TATCGGAGAT GACGACACCT TGCAGCCGGA
351  TGTGTTCCAG CTGTGCGAAG CGGCGGAAAT CCTGATTAAA GACGGCTTCA
401  AAGTGCTGCC TTATTGCACC GAAGACCTGA TTGCCTGCCG CCGCTGCTC
451  GACGCGGGCT GTCAGGCGTT GATGCCGTGG GCGGCCCGA TCGGCACGGG
501  TTTGGGCGCG GTTACGCCTT ACGCGTTGAA CGTCTGCGC GAACGCCTGC
551  CCGACACGCC GCTGATTATC GACGCGGGCT TGGGTTTGCC CTCACAGGCG
601  GCACAAGTGA TGAATGGGG CTTTGACGGC GTGCTTTTGA ATACTGCCGT
651  TTCCCGCAGC GCGGATCCGG TCAATATGGC ACGGCGCTTC GACTCGCCG
701  TCGAATCCGG ACGGCTGGCA TTTGAAGCCG GACCGGTGCA AGCAGCGGAC
751  AAAGCGCAAG CCAGCACGCC GACAGTCGGA CAACCGTTTT GGCATTGCGC
801  GGAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 466; ORF 126>:

```
m126.pep (partial)
  1  ..HYTKEPIMLT LYGETFPSRL LLGTAAYPTP EILKQSIQTA QPAMITVSLR
 51  RAGSGGEAHG QGFWSLLQET GVPVLPNTAG QSVQEAHTT AQMAREVFET
```

```

101 DWIKLELIGD DDTLQPDVFQ LVEAAEILIK DGFKVLPYCT EDLIACRRLI
151 DAGCQALMPW AAPIGTGLGA VHAYALNVLR ERLPDTPLII DAGLGLPSQA
201 AQVMWGFDFG VLLNTAVSRS GDPVNMAF ALAVESGRLA FEAGPVEARD
251 KAQASTPTVG QPFWHSAEY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 126 shows 95.9% identity over a 269 aa overlap with a predicted ORF (ORF 126.ng) from *N. gonorrhoeae*:

m126/g126

```

                                10      20      30      40
m126.pep      .  HYTKPEIMLTLYGETFPSRLLLGTAAAYPTPEILKQSIQTAQ
                  ::||| ||||| ||||| ||||| ||||| ||||| ||||| ::|||
g126      MPSETPKARRRLSDGIASDNHTKESIMLTLYGETFPSRLLLGTAAAYPTPEILKQSVRTAR
                  10      20      30      40      50      60

                                50      60      70      80      90      100
m126.pep      PAMITVSLRRAGSGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      PAMITVSLRRTGCGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                  70      80      90      100      110      120

                                110      120      130      140      150      160
m126.pep      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                  130      140      150      160      170      180

                                170      180      190      200      210      220
m126.pep      APIGTGLGAVHAYALNVLRERLPDTPLIIDAGLGLPSQAAQVMWGFDFGVLLNTAVSRSG
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      APIGTGLGAVHAYALKILRERLPDTPLIIDAGLGLPSQAAQVMWGFDFGVLLNTAVSRSG
                  190      200      210      220      230      240

                                230      240      250      260      270
m126.pep      DPVNMAFALAVESGRLA FEAGPVEARDKAQASTPTVGQPFWHSAEYX
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      DPVNMAFALAVESGRLA FEAGPVEARTKAQASTPTVGQPFWHSAEYX
                  250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 467>:

a126.seq

```

1  TTGTTAATCC ACTATACAAA GGAACCCATT ATGCTCACCC TGTACAGCGA
51  AACTTTCCT TCGCGGCTGC TGCTCGGCAC AGCCGCCTAC CCGACCCCTG
101 AAATCCTCAA ACAATCCGTC CGAACC GCCCGCGAT GATTACCGTC
151 TCGCTGCGCC GCGCGGGATG CCGCGGCGAG GCGCACGGTC AGGGGTTTGT
201 GTCGCTGCTT CAAGAAACCG GCGTTCCTCGT CCTGCCGAAC ACGGCAGGCT
251 GCCAAGCGT GCAGGAAGCG GTAACGACGG CGCAAATGGC GCGCGAAGTG
301 TTTGAAACCG ATTGGATTAA ACTCGAACTC ATCGGCGACG ACGACACCTT
351 GCAGCCGAT GTGTTCCAAC TTGTCGAAGC GCGGAAATC CTGATTAAAG
401 ACGGCTTCAA AGTGCTGCCT TATTGCACCG AAGACCTGAT TGCCTGCCGC
451 CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG ATGCCGTGGG CGGCCCGAT
501 CGGCACGGGT TTGGGCGCGG TTCACGCCTA CGCGTTGAAC GTCCTGCGCG
551 AACGCCTGCC CGACACGCCG CTGATTATCG ACGCGGGCTT GGGTTTGCCG
601 TCACAGCGCG CACAAGTGAT GGAATGGGGC TTTGACGGCG TGCTTTTGAA
651 TACTGCCGTT TCCCGCAGCG GCGATCCGGT CAATATGGCA CGCGCCTTCG
701 CACTCGCGT CGAATCCGGA CGGCTGGCAT TTGAAGCCGG ACCGGTCGAA
751 GCACGCGACA AAGCGCAAGC CAGCAGCCG ACAGTCGGAC AACCGTTTTG
801 GCATTCGGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 468; ORF 126.a>:

```
a126.pep
1  LLIHYTKEPI MLTYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV
51 SLRRAGCGGE AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV
101 FETDWIKLEL IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR
151 RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP
201 SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE
251 ARDKAQASTP TVGQPFWSHA EY*
```

m126/a126 98.1% identity in 269 aa overlap

```

              10      20      30      40      50
m126.pep      HYTKEPIMLTLYGETFP SRLLLGTAAYPTPEILKQSIQTAQPAMITVSLRRAGSGGE
              |||||
a126           LLIHYTKEPIMLTLYSETFP SRLLLGTAAYPTPEILKQSVRTARPAMITVSLRRAGCGGE
              10      20      30      40      50      60

              60      70      80      90      100     110
m126.pep      AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREVFETDWIKLELIGDDDTLQPD
              |||||
a126           AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREVFETDWIKLELIGDDDTLQPD
              70      80      90      100     110     120

              120     130     140     150     160     170
m126.pep      VFQVLEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWAAPIGTGLGAVHAYALN
              |||||
a126           VFQVLEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWAAPIGTGLGAVHAYALN
              130     140     150     160     170     180

              180     190     200     210     220     230
m126.pep      VLRERLPDTP LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG
              |||||
a126           VLRERLPDTP LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG
              190     200     210     220     230     240

              240     250     260     270
m126.pep      RLAFEAGPVEARDKAQASTPTVGQPFWSHA EYX
              |||||
a126           RLAFEAGPVEARDKAQASTPTVGQPFWSHA EYX
              250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 469>:

```
g126-1.seq
1  ATGCTCACCC TGTACGGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51  GGCCGCTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACC GCCC
101 GGCCCGCGAT GATTACCGTC TCGCTGCGCC GCACGGGATG CGGCGGCGAG
151 GCGCACGGTC AGGGGTTTGT GTGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAATC
301 ATCGGCGACG ACGACACCTT GCAGCCGGAC GTGTTC AAC TCCTCGAAGC
351 GGCGGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ATGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCTCCCAT CGGCACGGGT TTGGGGGCGG TTCACGCCTA
501 TCGGCTCAAA ATCCTGCGCG AACGCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTGCTT TCCCAAGCGG CACAAGTGAT GGAATGGGGT
601 TTTGACGGCG TATTGTTAAA CACCGCCGTT TCCCGCAGCG GCGACCCCGT
651 CAACATGGCG CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG GCCGGTCGAA GCGCGAACCA AAGCCCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTGT GCATTGCGCG GAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 470; ORF 126-1.ng>:

```
g126-1.pep
1  MLTYGETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRTGCGGE
```

```

51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALK ILRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARTKAQASTP
251 TVGQPFWWSA EY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 471>:

m126-1.seq

```

1 ATGCTCACCC TATACGGCGA AACTTTCCCC TCGCGGCTGC TGCTCGGCAC
51 GGCTGCCTAC CCGACCCCGG AAATCCTCAA ACAATCCATC CAAACCGCCC
101 AGCCTGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGAAG CGGCGGCGAG
151 GCGCACGGTC AGGGGTTTGT GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAACCTC
301 ATCGGAGATG ACGACACCTT GCAGCCGGAT GTGTTCCAGC TTGTCGAAGC
351 GGCGGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCTT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC GCGCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCGCAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CCGCTTGAAC GTCCTGCCGC AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCT TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCAGCGCG
751 ACAGTCGGAC AACCGTTTGT GCATTGCGG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 5; ORF 126-1>:

m126-1.pep

```

1 MLTYGETFP SRLLGTAAY PTPEILKQSI QTAQPAMITV SLRRAGSGGE
51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

m126-1/g126-1 96.9% identity in 262 aa overlap

	10	20	30	40	50	60
m126-1.pep	MLTYGETFP SRLLGTAAYPTPEILKQSIQTAQPAMITVSLRRAGSGGEAHGQGFWSLL					
g126-1	MLTYGETFP SRLLGTAAYPTPEILKQSVRTARPAMITVSLRRTGCGGGEAHGQGFWSLL					
	10	20	30	40	50	60
m126-1.pep	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPDVFQVLEAAEI					
g126-1	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPDVFQVLEAAEI					
	70	80	90	100	110	120
m126-1.pep	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPDVFQVLEAAEI					
g126-1	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPDVFQVLEAAEI					
	70	80	90	100	110	120
m126-1.pep	LIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALNVLRERLPDTP					
g126-1	LIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALKILRERLPDTP					
	130	140	150	160	170	180
m126-1.pep	LIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALNVLRERLPDTP					
g126-1	LIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALKILRERLPDTP					
	130	140	150	160	170	180
m126-1.pep	LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG RLAFEAGPVE					
g126-1	LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
m126-1.pep	LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG RLAFEAGPVE					
g126-1	LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
m126-1.pep	ARDKAQASTPTVGQPFWWSAEYX					
g126-1	ARTKAQASTPTVGQPFWWSAEYX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 473>:

a126-1.seq

```

1 ATGCTCACCC TGTACAGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51 AGCCGCTTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCGCCC
101 GGCCCGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGATG CGGCGGCGAG

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151 GCGCACGGTC AGGGGTTTTG GTCGCTGCTT CAAGAAACCG GCGTTCCTGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATTAA ACTCGAACTC
301 ATCGGCGACG ACGACACCTT GCAGCCGGAT GTGTTCCAAC TTGTCGAAGC
351 GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCCG CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCCGAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CGCGTTGAAC GTCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTTG GCATTGCGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 474; ORF 126-1.a>:

```

a126-1.pep
  1 MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE
 51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCOAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSQDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

a126-1/m126-1 98.14 identity in 262 aa overlap

	10	20	30	40	50	60
a126-1.pep	MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE AHGQGFWSLL					
m126-1	MLTLYGETFP SRLLLGTAAY PTPEILKQSIQTAQPAMITV SLRRAGSGGE AHGQGFWSLL					
	10	20	30	40	50	60
a126-1.pep	QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQVLEAAEI					
m126-1	QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQVLEAAEI					
	70	80	90	100	110	120
a126-1.pep	QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQVLEAAEI					
m126-1	QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQVLEAAEI					
	70	80	90	100	110	120
a126-1.pep	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGT GLGAVHAYALN VLRERLPDTP					
m126-1	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGT GLGAVHAYALN VLRERLPDTP					
	130	140	150	160	170	180
a126-1.pep	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGT GLGAVHAYALN VLRERLPDTP					
m126-1	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGT GLGAVHAYALN VLRERLPDTP					
	130	140	150	160	170	180
a126-1.pep	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSQDPVNMA RAFALAVESG RLAFEAGPVE					
m126-1	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSQDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
a126-1.pep	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSQDPVNMA RAFALAVESG RLAFEAGPVE					
m126-1	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSQDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
a126-1.pep	ARDKAQASTP TVGQPFWWSA EYX					
m126-1	ARDKAQASTP TVGQPFWWSA EYX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 475>:

g127.seq

```

  1 ATGGAAATAT GGAATATGTT GAACACTTGG CCCGATGCCG TCCCGATACG
 51 CGCGGAGGCG GCCGAATCCG TGGCGGCGGT CGCGGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAGAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GCGGGTTTTT GGTTCAGAC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GCGCAAATT CAAACGCTGG
251 CTTTGTGCGAT GTTTCGGGTG GCGGCGCGG TCGTCGTGGC GACAAAAGAA
301 CTGATTATGT GTCTGTGCGG CAGTATTTTA aggtctGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAATCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TTCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAT GTCATCCATA

```



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551 CGGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCCGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 TCAGCGGTAT TTGGAACG TGCAGGCGGA AAAACTGTTT ATCAGCCCCG
701 CCGCCAGGCC GCGCGTTACC CCGGTACCGT ACGACGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCCTC CCCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GCGCGTTATG GACGAATTTT TCGCGTACA ATACCGCTG TTAAATCATC
851 CCGCCGgctc cgAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 476; ORF 127.ng>:

g127.pep

```

1 MEIWNMLNTW PDAVPIRAEA AESVAAVAAL LLARALLNI HFRRHDPFGI
51 ESKRRFLVAS RNITLLLVL FSLAFIWSAQI QTLALSMFAV AAUVVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNLLLLSH VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVS KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 477>:

m127.seq

```

1 ATGGAATAT GGAATATGTT GGACACTTGG CTCGGTGCCG TCCCGATACG
51 TGCGGAGGCG GTCGAATCCG TGGCGGCGGT TGCGGCTTGT CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAAAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GCGGTTTTT GGTGCGCAGC CGCAATATAA CGTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GCGCAAATC CAAACGCTGG
251 CTTTGTGAT GTTTCGGTG GCGGCGCGG TCGTCGTGGC GACGAAGGAA
301 CTGATTATGT GTCTGTCCGG CAGTATTTTA AGGTCTGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAACCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TCCCCAACA GCCTGTGTGT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAT GTCATCCATA
551 CGGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCCGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 CCAACGGsAT TTGGAACG TGCAGGCGGA AAAACTGTTT ATCAGCCCCG
701 CCGCCAGACC GCGCGTTACC CCGTGCCGT ACGATGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCTTC CCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GCGCGTTATG GACGAATTTT TCGCGTACA ATACCGCTG TTAAATCACC
851 CCGCCGGCTC CGAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 478; ORF 127>:

m127.pep

```

1 MEIWNMLDTW LGAVPIRAEA VESVAAVAAL LLARALLNI HFKRHDPFGI
51 ESKRRFLVAS RNITLLLVL FSLAFIWSAQI QTLALSMFAV AAUVVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNLLLLSH VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVS KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 127 shows 97.9% identity over a 290 aa overlap with a predicted ORF (ORF 127.ng) from *N. gonorrhoeae*:

m127/g127

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAVESVAAVAALLARALLNIHFKRHDPFGIESKRRFLVAS					
	: : : : : : :					
g127	MEIWNMLNTWPDVPIRAEAESVAAVAALLARALLNIHFRRHDPFGIESKRRFLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAUVVATKELIMCLSGSILRSATQQYSVG					
	: : : : : : :					
g127	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAUVVATKELIMCLSGSILRSATQQYSVG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
g127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRYLENVQAEKLFITPAARPRVT					
g127	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRYLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLNHPAGSETLX					
g127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLNHPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 479>:

```
a127.seq
1  ATGGAAATAT  GGAATATGTT  GGACACTTGG  CTCGGTGCCG  TCCCGATACG
51  TCGCGAGGCG  GTCGAATCCG  TGGCGGTGGT  CGCGGCTTTG  CTGCTGGCGC
101 GCGCCCTTCT  GTTGAATATC  CACTTCAAAC  GGCATCCGGA  TTTCGGCATC
151 GAAAGCAAGC  GCGGTTTTTT  GGTGCCAGC  CGCAATATAA  CGCTGCTTTT
201 GGTGCTGTTT  TCGCTGGCAT  TTATCTGGTC  GCGCGAAATC  CAAACGCTGG
251 CTTTGTGCGT  GTTTGCGGTG  GCGGCGGCGG  TCGTCGTGGC  GACGAAGGAA
301 CTGATTATGT  GTCTGTCGGG  CAGCATTTTA  AGGTCGTCCA  CCCAGCAATA
351 CTCGGTCGGC  GACTATATCG  AAATCAACGG  CCTGCGCGGG  CGCGTGGTCG
401 ACATCAACCT  GTTGAACACG  CTGATGATGC  AGGTCGGTCC  GAACCCCTTG
451 GTCGGACAGC  TTGCGGGAAC  CACCGTTTCT  TTCCCAACA  GCCTGTTGTT
501 GAGCCACCCC  GTGCGCCGCG  ACAATATTTT  GGGCGACTAC  GTCATCCATA
551 CGGTGCAAT  CCCGGTCCC  ATCCATTTGG  ATTCGGATGA  AGCCGTATGC
601 CGTCTGAAAG  CCGTACTCGA  GCCCTTGTGC  GCGCCCTACA  TCCCGGCCAT
651 CCAACGGCAT  TTGGAACACG  TGCAGGCGGA  AAACTGTTT  ATCAGCCCGC
701 CCGCCAAACC  GCGCGTTACC  CGCGTGCCGT  ACGATGACAA  GGCATACCGC
751 ATCATCGTCC  GCTTCGCCTC  CCCCGTTTCA  AAGCGGCTGG  AAATCCAACA
801 GCGGTTATG  GACGAATTT  TGCGGTACA  ATACCGCTG  TTAAATTACC
851 CCGCCGGCTC  CGAACACTT  TAA
```

This corresponds to the amino acid sequence <SEQ ID 480; ORF 127.a>:

```
a127.pep
1  MEIWNMLDTW  LGAVPIRAEA  VESVAVVAAL  LLARALLNI  HFKRHPDFGI
51  ESKRRFLVAS  RNITLLLVLF  SLAFIWSAQI  QTLALSMFAV  AAHVVVATKE
101 LIMCLSGSIL  RSATQQYSVG  DYIEINGLRG  RVVDINLLNT  LMMQVGNPL
151 VGQLAGTTVS  FPNSLLLSHP  VRRDNILGDY  VIHTVEIPVP  IHLDSDEAVC
201 RLKAVLEPLC  APYIPAIQRH  LENVQAEKLF  ITPAAKPRVT  RVPYDDKAYR
251 IIVRFASPV  SRLEIQQAVM  DEFLRVQYRL  LNYPAGSETL  *
```

m127/a127 98.6% identity in 290 aa overlap

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLNIHFKRHPDFGIESKRRFLVAS					
a127	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLNIHFKRHPDFGIESKRRFLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAHVVVATKELIMCLSGSILRSATQQYSVG					
a127	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAHVVVATKELIMCLSGSILRSATQQYSVG					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
a127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
a127	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRHLENVQAEKLFITPAAKPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLNHPAGSETLX					
a127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLNYPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 481>:

g128.seq

1	atgattgaca	acgCActgct	ccacttgggc	gaagaaccCC	GTTTaatca
51	aatccaaacc	gaagACatca	AACCCGCCGT	CCAAACCGCC	ATCGCCGAAG
101	CGCGCGGACA	AATCGCCGCC	GTCAAAGCGC	AAACGCACAC	CGGCTGGGCG
151	AACACCGTCG	AGCGTCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTTG
201	GGGCGTCGTG	TCCCATCTCA	ACTCCGTCGT	CGACACGCCC	GAACCTGCGCG
251	CCGTCTATAA	CGAACTGATG	CCTGAAATCA	CCGTCTTCTT	CACCGAAATC
301	GGACAAGACA	TGAACTGTGA	CAACCGCTTC	AAAACCATCA	AAAATTCCCC
351	CGAATTTGCA	ACGCTTTCCC	CCGCACAAAA	AACCAAGCTC	GATCACGACC
401	TGCGCGATTT	CGTATTGAGC	GGCGCGGAAC	TGCCGCCCGA	ACGGCAGGCA
451	GAACCTGGCAA	AACCTGCAAA	CGAAGGCGCG	CAACTTTCCG	CCAAATTCTC
501	CCAAAACGTC	CTAGACGCGA	CCGACGCGTT	CGGCATTTC	TTTGACGATG
551	CCGCACCGCT	TGCCCGCATT	CCCAGAGACG	CGCTCGCCAT	GTTTGCCGCC
601	GCCGCGCAAA	GCGAAGGCAA	AACAGGTTAC	AAAATCGGCT	TGCAGATTCC
651	GCACTACCTT	GCCGTTATCC	AATACGCCGG	CAACCGCGAA	CTGCCGGAAC
701	AAATCTACCG	CGCCTACGTT	ACCCGTGCCA	GCGAACTTTC	AAACGACGGC
751	AAATTCGACA	ACACCGCCAA	CATCGACCGC	ACGCTCGAAA	ACGCATTGAA
801	AACCGcctaa	cTGCTCGGCT	TTAAAAATTA	CGCCGAATTG	TCGCTGGCAA
851	CCAAAATGGC	GGACACGCCC	GAACAGGTTT	TAAACTTCCT	GCACGACCTC
901	GCCCCCGCG	CCAAACCCTA	CGCCGAAAAA	GACCTCGCCG	AAGTCAAAGC
951	CTTCGCCCGC	GAACACCTCG	GTCTCGCCGA	CCCGCAGCCG	TGGGACTTGA
1001	GCTACGCCGG	CGAAAAACTG	CGCGAAGCCA	AATACGCATT	CAGCGAAACC
1051	GAAGTCAAAA	AATACTTCCC	CGTCGGCAAA	GTTCTGGCAG	GCCTGTTCCG
1101	CCAAATCAAA	AAACTCTACG	GCATCGGATT	CGCCGAAAAA	ACCGTTCCCC
1151	TCTGGCACAA	AGACGTGCGC	TATTTTGAAT	TGCAACAAAA	CGGCAAAACC
1201	ATCGGCGGCG	TTTATATGGA	TTTGTACGCA	CGCGAAGGCA	AACGCGGCGG
1251	CGCGTGGATG	AACGACTaca	AAGGCCGCGG	CCGCTTTGCC	GACGgcacGC
1301	TGCAACTGCC	CACCGCCTAC	CTCGTCTGCA	ACTTCGCCCC	GCCCCGTCCG
1351	GGCAAAGAAG	CGCGTTTAAG	CCACGACGAA	ATCCTCACCC	TCTTCCACGA
1401	AacCGGCCAC	GGACTGCACC	ACCTGCTTAC	CCAAGTGGAC	GAAGTGGGCG
1451	TGTCCGGCAT	CAAcggcgta	GAATGGGACG	CGGTGGAAGT	GCCCAAGCCAG
1501	TTTATGGAAA	ACTTCGTTTG	GGAATACAAT	GTATTGGCAC	AAATGTCGCG
1551	CCACGAAGAA	AccgGCGAGC	CCCTGCCGAA	AGAACTCTTC	GACAAAATGC
1601	TcgcCGCCAA	AAACTTCCAG	CGCGGTATGT	TCCTCGTCCG	GCAAAATGGAG
1651	TTCGCCCTCT	TCGATATGAT	GATTTACAGT	GAAAGCGACG	AATGCCGTCT
1701	GAAAACTGG	CAGCAGGTTT	TAGACAGCGT	GCGCAAAGAA	GTcGCCGTCA
1751	TCCAACCGCC	CGAATACAAC	CGCTTCGCCA	ACAGCTTCGG	CCacatctTC
1801	GcgggcGGCT	ATTCCGACGG	CTATTACAGC	TACGCATGGG	CCGAAGTCCt
1851	cAGCACCGAT	GCCTACGCGG	CCTTTGAAGA	AAGcGACGac	gtcGCCGCCA
1901	CAGGCAACCG	CTTCTGGCAA	GAAAtccttg	ccgtcggcgg	ctCCCCGACG
1951	gcgGCGGAAT	CCTTCAAAGC	CTTCCGCGGA	CGCGAACCGA	GCATAGACGC

2001 ACTGCTGCGC CAAagcggtT TCGACAACGC gGcttgA

This corresponds to the amino acid sequence <SEQ ID 482; ORF 128.ng>:

g128.pep

```

1 MIDNALLHLG EEPFRNQIQT EDIKPAVOTA IAEARGQIAA VKAQTHTGWA
51 NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVVHKDVR YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTQLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLKNW QQVLDsvrke VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAAPFEESDD VAATGKRWFQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR QSGFDNAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 483>:

m128.seq (partial)

```

1 ATGACTGACA ACGCACTGCT CCATTGCGG GAAGAACCCC GTTTTGATCA
51 AATCAAAACC GAAGACATCA AACCGGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCGGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTCGAC ACCCTCTCCC CCGCACAAAA AACCAACTC AACCAC
1 TACGCCAGCG AAAAACTGCG CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51 wGTCAAAAAA TAyTCCCyG TCGGCAAwGT ATTAACCGGA CTGTTGCCCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCCGTC
151 TGGCACAAG ACGTGCGCTA TTkTGAATTG CAACAAAACG GCGAAmCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CCGCCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTAKA ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAAAAT TTCGTTTGGG AATACAATGT CTGGGCACAA mTGTCAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAAA ACTTCCAAsG CCGCATGTTC yTsGTCCGGC AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAACTGGCA ACAGGTTTTA GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCCGCCCG AATACAACCG CTTCGCCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGCAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAAATCC TTCAAAGCCT TCCGCGGCCG CGAACCAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 484; ORF 128>:

m128.pep (partial)

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51 NTVEPLTGIT ERVGRIWGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH

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//

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1 YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGFTEKTPV
51 WHKDVRYXEL QONGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFSdGTL
101 QLPTAYLVCN FAPPVGGREA RLSDHEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELKDKXL
201 AAKNFQXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQQLV DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT

```

301 GKRFWQEILA VGXSRGAES FKAFRGREPS IDALLRHS GF DNAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng) from *N. gonorrhoeae*:

m128/g128

	10	20	30	40	50	60
g128.pep	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g128.pep	ERVGRIGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
g128.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
				340	350	360
g128.pep	YAGEKLREAKYAFSETEVKKYFPVGVKVLG					
m128	YASEKLREAKYAFSETXVKKYFPVGVXVLNG					
				10	20	30
	370	380	390	400	410	420
g128.pep	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
	430	440	450	460	470	480
g128.pep	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVDELGV					
m128	GRRRFSGDTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVDELGV					
	100	110	120	130	140	150
	490	500	510	520	530	540
g128.pep	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQRGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKKLAAKNFQXGMF					
	160	170	180	190	200	210
	550	560	570	580	590	600
g128.pep	LVRQMEFALFDMMIYSEDECRLKNWQQVLDVSRKEVAVIQPPEYNRFANSFGHIFAGGY					
m128	XVRQXEFALFDMMIYSEDDEGRKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
	610	620	630	640	650	660
g128.pep	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRGREPS					
	280	290	300	310	320	330

```

          670      679
g128.pep  IDALLRQSGFDNAAX
          |||||:|||||:
m128      IDALLRHSGFDNAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 485>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTGGGC GAAGAACCCC GTTTGATCA
51  AATCAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTCAC CGACACGCCC GAACTGCGCG
251 CGGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCCAGATC
401 TCGCGGATTT CGTCCTCAGC GCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCGG CCAAATTCTC
501 CAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACGCGCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCGG AAGTCAAAGC
951 CTTGCCCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAACG GACTGTTCCG
1101 CCAAAATCAA AAACCTTACG GCATCGGATT TACCGAAAAA ACCGTCGCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCGG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAT ATTTGTTTGG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCGGCCAA AAACCTTCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCGCTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCGCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CTTTGAAGA AAGCGACGAT GTCGCGGCCA
1901 CAGGCAAACG CTTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGC GC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 486; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51  NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTYG KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMDATP EQVLNFLHDL
301 ARRAKPYA EK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME

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551 FALFDMMIYS EDDEGR LKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
 601 AGGYSAGYYS YAWAEVLSAD AYA AFEESDD VAATGKRFWQ EILAVGGSRS
 651 AAESFKAFRG REPSIDALLR HSGFDNAA*

m128/a128 66.0% identity in 677 aa overlap

	10	20	30	40	50	60
m128.pep	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m128.pep	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	: :					
a128	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130					
m128.pep	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL					
	250	260	270	280	290	300
m128.pep	-----					
				140	150	
m128.pep	-----YASEKLREAKYAFSETXVKKYFPVGX					
	:					
a128	ARRAKPYAEKD LAEVKAFARES LGLADLPWD LGYAGEKLREAKYAFSETEVKKYFPVGK					
	310	320	330	340	350	360
m128.pep	160	170	180	190	200	210
	VLNGLFAQXKKLYGIGFTEKTPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWM					
	: :					
a128	VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFAFPVGGREARLSHDEILILFHETGHLHLLTQVD					
	: :					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHLHLLTQVD					
	430	440	450	460	470	480
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWD AVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
	: :					
a128	ELGVSGINGVEWD AVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540
m128.pep	340	350	360	370	380	390
	XGMFVVRQXEFALFDMMIYSEDDEGR LKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF					
	: :					
a128	RGMFLVRQMEFALFDMMIYSEDDEGR LKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF					
	550	560	570	580	590	600

368

```

      400      410      420      430      440      450
m128 .pep  AGGYSAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRG
          |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
          610      620      630      640      650      660

      460      470
m128 .pep  REPSIDALLRHSGFDNAVX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      REPSIDALLRHSGFDNAAX
          670

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 487>:

g128-1.seq (partial)

```

1  ATGATTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51  AATCAAAACC GAAGACATCA AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCGGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCTGT TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACGCGCGC
251 CCGTCTATAA CGAACTGATG CCGTAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTGACA ACGCTTTCCC CCGCACAAAA AACCAAGCTC GATCAGGACC
401 TGGCGGATTT CGTATTGAGC GCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACGCGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCGG CCAAATTCCT
501 CCAAACGCTC CTAGACGCGA CCGACGCGTT CGGCATTTC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCGCGGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCGGTTATCC AATACGCGCG CAACGCGGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAAACGCGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGCCAAA CTGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGCG GGACACGCCC GAACAGGTTT TAACTTCCT GCACGACCTC
901 GCGCGCGCGC CCAAACCTTA CGCGGAAAAA GACCTCGCCG AAGTCAAAAG
951 CTTCGCGCGC GAACACCTCG GTCTCGCCGA CCCGCGCCG TGGGACTTGA
1001 GCTACGCGCG CGAAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTTCTGGCAG GCCTGTTCCG
1101 CCAAATCAAA AACTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTGAAAT TGCAACAAA CCGCAAAACC
1201 ATCGGCGCGG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CCGGTGGATG AACGACTACA AAGGCGCGCG CCGCTTGGC GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCGCGTGGC
1351 GGCAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACC TCTTCCACGA
1401 AACCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGAC GAACTGGGCG
1451 TGTCCGGCAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 488; ORF 128-1.ng>:

g128-1.pep (partial)

```

1  MIDNALLHLG EPRFNQIKT EDIKPAVQTA IAEARGQIAA VKAQHTGWA
51  NTVERLTGIT ERVGRINGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFPVKG VLAGLFAQIK KLYGIGFAEK TVPVVHKDVR YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTQLPLTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV K

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 489>:

m128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCGGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCT AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG

```



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201 GGGCGTGGTG TCGCACCTCA ACTCCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTGAC ACCCTCTCCC CCGCACAAAA AACCAAACTC AACCAAGATC
401 TGGCGGATTT CGTCTCAGC GCGCGGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TCGCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCGCGGCAAA GCGAAAGCAA AACAGGCTAC AAAATCGGCT TGCAGATTCC
651 AACTACCTC GCGTCATCC AATACGCCGA CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCTACGTT ACCCGCGCCA GCGAACTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGCAA ACGCCCTGCA
801 AACC GCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACGCCC GAACAAGTTT TAAACTTCTT GCACGACCTC
901 GCGCGCGCGG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTGA ACCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCAG CGAAAAATG CGCGAAGCCA AATACGCGTT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTCCG
1101 CCAAATCAAA AACTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCGG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CCGCGAAACC
1201 ATAGGCGCGG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACCGCGCGG
1251 CCGGTGGATG AACGACTACA AAGGCGCGCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCTAC CTGCTGCGA ACTTCGCCCC ACCGTGCGGC
1351 GGCAGGGAAG CCCGCTGAG CCACGACGAA ATCTCATCC TCTTCCACGA
1401 AACC GGACAC GGGCTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CGTTCGAACT GCCCAGCCAG
1501 TTTATGGAAT ATTTCGTTG GGAATACAA GTCTTGCGC AAAATGTCAGC
1551 CCACGAAGAA ACCGGCGTTC CCTGCGCGAA AGAACTCTTC GACAAAAATGC
1601 TCGCGGCCAA AAACCTTCAA CGCGGCATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCGGTCT
1701 GAAAAATGG CAACAGGTTT TAGACAGCGT GCGCAAAAAA GTCGCCGTCA
1751 TCCAGCGGCC CGAATACAAC CGCTTCGCCT TGAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCGCGAGG CTATTACAGC TAGCGGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCGG CCTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAAAC CTTTGGCAG GAAATCTCG CCGTCGCGCG ATCGCGCAGC
1951 GCGGCAGAAT CCTTCAAAGC CTTCCGCGGC CGCGAACCGA GCATAGACGC
2001 ACTCTTGGC CACAGCGGTT TCGACAACGC GGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 490; ORF 128-1>:

m128-1.pep.

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51 NTVEPLTGIT ERVGRINGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251 KPDNTANIDR TLNALQTAQ LLGFKNYAEL SLATKMADTP EQVLNPLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLQF WDLGYASEKL REAKYAFSET
351 EVKKYFPVVG VLNGLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFAPPVG
451 GREARLSHDE ILILFHETGH GLHLLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLEKNW QQVLDVRKK VAVIQPPEYN RFALSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAPESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAV*

```

m128-1/g128-1 94.5% identity in 491 aa overlap

```

          10      20      30      40      50      60
g128-1.pep MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQTHTGWANTVERLTGIT
          |||
m128-1      MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQTHTGWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90      100     110     120
g128-1.pep ERVGRINGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
          |||
m128-1      ERVGRINGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90      100     110     120

```

370

	130	140	150	160	170	180
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEIAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128-1	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEIAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
	190	200	210	220	230	240
g128-1.pep	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV					
m128-1	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV					
	190	200	210	220	230	240
	250	260	270	280	290	300
g128-1.pep	TRASELSNDGKFDNTANIDRTLENALKTAKLGLGFKNYAELSLATKMADTPEQVNLFLHDL					
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLGLGFKNYAELSLATKMADTPEQVNLFLHDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
g128-1.pep	ARRAKPYAEKDIAEVKAFAREHLGLADPQWDLGYASEKLEAKYAFSETEVKKYFPVVGK					
m128-1	ARRAKPYAEKDIAEVKAFARESLNLADLPWDLGYASEKLEAKYAFSETEVKKYFPVVGK					
	310	320	330	340	350	360
	370	380	390	400	410	420
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTTGGVYMDLYAREGKRGGAWM					
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAFPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAFPVGGREARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
	490					
g128-1.pep	ELGVSGINGVK					
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 491>:

a128-1.seq

1	ATGACTGACA	ACGCACTGCT	CCATTTGGGC	GAAGAACCCC	GTTTIGATCA
51	AATCAAAACC	GAAGACATCA	AACCCGCCCT	GCAAACCGCC	ATTGCCGAAG
101	CGCGCGAACA	AATCGCCGCC	ATCAAAGCCC	AAACGCACAC	CGGCTGGGCA
151	AACACTGTGC	AACCCCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTTG
201	GGCGGTGGTG	TCGCACCTCA	ACTCCGTCA	CGACACGCCC	GAACTGCGCG
251	CGCCTACAA	TGAATTAATG	CCCGAAATTA	CCGTCTTCTT	CACCGAAATC
301	GGACAAGACA	TCGAGCTGTA	CAACCGCTTC	AAAACCATCA	AAAACCTCCC
351	CGAGTTCGAC	ACCCTCTCCC	ACGCGCAAAA	AACCAAACTC	AACCAAGATC
401	TGCGCGATTT	CGTCTCAGC	GGCGCGGAAC	TGCCGCCCGA	ACAGCAGGCA
451	GAATTGGCAA	AACTGCAAA	CGAAGGCGCG	CAACTTTCCG	CCAAATTCTC
501	CCAAACGTC	CTAGACGCGA	CCGACGCGTT	CGGCATTTAC	TTTGACGATG
551	CGCACCGCT	TGCCGGCATT	CCCGAAGACG	CGCTCGCCAT	GTTTGGCGCT
601	GCCGCGCAA	GCGAAGGCAA	AACAGGCTAC	AAAATCGGTT	TGCAGATTCC
651	GCACTACCTC	GCCGTCATCC	AATACGCCGA	CAACCGCAAA	CTGCGCGAAC
701	AAATCTACCG	CGCCTACGTT	ACCCGCGCCA	GCGAGCTTTC	AGACGACGGC
751	AAATTCGACA	ACACCGCCAA	CATCGACCGC	ACGCTCGAAA	ACGCCCTGCA
801	ACCGGCCAAA	CTGCTCGGCT	TCAAAACTA	CGCCGAATTG	TCGCTGGCAA
851	CCAAATGGC	GGACACCCCC	GAACAAGTTT	TAAACTTCCT	GCACGACCTC
901	GCCCGCGCG	CCAAACCCTA	CGCCGAAAAA	GACCTCGCCG	AAGTCAAAGC
951	CTTCGCCCC	GAAAGCCTCG	GCCTCGCCGA	TTTGCAACCG	TGGGACTTGG
1001	GCTACGCCGG	CGAAAACTG	CGCGAAGCCA	AATACGCATT	CAGCGAAACC
1051	GAAGTCAAAA	AATACTTCCC	CGTCGGCAAA	GTATTAAACG	GACTGTTTCG
1101	CCAAATCAAA	AAACTCTACG	GCATCGGATT	TACCGAAAAA	ACCGTCCCCG
1151	TCTGGCACAA	AGACGTGCGC	TATTTTGAAT	TGCAACAAAA	CGGCGAAACC
1201	ATAGCGGCG	TTTATATGGA	TTTGTACGCA	CGCGAAGCCA	AACGCGGCGG

```
1251 CCGGTGGATG AACGACTACA AAGGCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAG ATTTGCTTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCTGCGGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AACTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGCCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAGAA GTCGCCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CCTTCAAAGC CTTCCGCGGA CGGAACCGA GCATAGACGC
2001 ACTCTTGGC CACAGCGGCT TCGACAACGC GGCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 492; ORF 128-1.a>:

a128-1.pep

```
1 MTDNALLHLHG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTWA
51 NTVEPLTGIT ERVGRIGVVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVKG VLNGLFAQIK KLYGIGFTEK TVPVWHKQVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLLTQVD ELGVSGINGV EWDAVEFPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 PALFDMMIYS EDDEGRLLKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAFAESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*
```

m128-1/a128-1 97.8% identity in 677 aa overlap

	10	20	30	40	50	60
a128-1.pep	MTDNALLHLG	EEPRFDQIKT	EDIKPALQTA	IAEAREQIAA	IKAQHTGTWA	NTVEPLTGIT
m128-1	MTDNALLHLG	EEPRFDQIKT	EDIKPALQTA	IAEAREQIAA	IKAQHTGTWA	NTVEPLTGIT
	70	80	90	100	110	120
a128-1.pep	ERVGRIGVVV	SHLNSVTDTP	ELRAAYNELM	PEITVFFTEI	GQDIELYNRF	KTIKNSPEFD
m128-1	ERVGRIGVVV	SHLNSVADTP	ELRAAYNELM	PEITVFFTEI	GQDIELYNRF	KTIKNSPEFD
	130	140	150	160	170	180
a128-1.pep	TLSHAQKTKL	NHDLRDFVLS	GAELPPEQQA	ELAKLQTEGA	QLSAKFSQNV	LDATDAFGIY
m128-1	TLSPAQKTKL	NHDLRDFVLS	GAELPPEQQA	ELAKLQTEGA	QLSAKFSQNV	LDATDAFGIY
	190	200	210	220	230	240
a128-1.pep	FDDAAPLAGI	PEDALAMFAA	AAQSEGKTGY	KIGLQIPHYL	AVIQYADNRK	LREQIYRAYV
m128-1	FDDAAPLAGI	PEDALAMFAA	AAQSEGKTGY	KIGLQIPHYL	AVIQYADNRK	LREQIYRAYV
	250	260	270	280	290	300
a128-1.pep	TRASELSDDG	KFDNTANIDR	TLENALQTAK	LLGFKNYAEL	SLATKMADTP	EQVLNFLHDL
m128-1	TRASELSDDG	KFDNTANIDR	TLENALQTAK	LLGFKNYAEL	SLATKMADTP	EQVLNFLHDL
	310	320	330	340	350	360
a128-1.pep	ARRAKPYAEK	DLAEVKAFAR	ESLGLADLQP	WDLGYAGEKL	REAKYAFSET	EVKKYFPVKG

```

m128-1      ARRAKPYAEKD LAEVKAFARESLNLADLQPWD LGYASEKLREAKYAFSETEVKKYFPVGK
              310      320      330      340      350      360

              370      380      390      400      410      420
a128-1.pep  VLNGLFAQIKKLYGIGFTEKTPVWVHKDVRYPFELQQNGETIGGVYMDLYAREGKRGGAWM
              |||
m128-1      VLNGLFAQIKKLYGIGFTEKTPVWVHKDVRYPFELQQNGETIGGVYMDLYAREGKRGGAWM
              370      380      390      400      410      420

              430      440      450      460      470      480
a128-1.pep  NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHLHLLTQVD
              |||
m128-1      NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHLHLLTQVD
              430      440      450      460      470      480

              490      500      510      520      530      540
a128-1.pep  ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              |||
m128-1      ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              490      500      510      520      530      540

              550      560      570      580      590      600
a128-1.pep  RGMFLVRQMEFALFDMMIYSEDDEGRLEKNWQVLDVSRKEVAVVRPPEYNRPFANSFGHIP
              |||
m128-1      RGMFLVRQMEFALFDMMIYSEDDEGRLEKNWQVLDVSRKEVAVVRPPEYNRPFANSFGHIP
              550      560      570      580      590      600

              610      620      630      640      650      660
a128-1.pep  AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              |||
m128-1      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              610      620      630      640      650      660

              670      679
a128-1.pep  REPSIDALLRHSGFDNAAX
              |||
m128-1      REPSIDALLRHSGFDNAVX
              670

```

a128-1/ P44573

sp|P44573|OPDA_HAEIN OLIGOPEPTIDASE A >gi|1075082|pir||C64055 oligopeptidase A (prlc) homolog
- Haemophilus influenzae (strain Rd KW20)

>gi|1573174 (U32706) oligopeptidase A (prlc) [Haemophilus influenzae Rd] Length = 681

Score = 591 bits (1507), Expect = e-168

Identities = 309/677 (45%), Positives = 415/677 (60%), Gaps = 4/677 (0%)

```

Query: 4  NALLHLGEEPRFDQIKTEDIKPALQTXXXXXXXXXXXXXXXXXXTHGTWANTVEPLTGITERV 63
          N LL++ P F QIK E I+PA++ H W N + PLT +R+
Sbjct: 5  NPLLNIQGLPPFSQIKPEHIRPAVEKLIQDCRNTIEQVLKQPHTWENFILPLTETNDRL 64

Query: 64  GRIWGVVSHLNSVITDTPELRAAYNELMPEITVFFTEIGQDIELYNRFTIKNSPEFDTLS 123
          R W VSHLNSV ++ ELR AY +P ++ + T +GQ LYN + +KNS EF S
Sbjct: 65  NRAWSPVSHLNSVKNSTELREAYQTCLELLSEYSTWVGQHKGLYNAYLALKNSAEFADYS 124

Query: 124  HAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIYFDD 183
          AQK + + LRDF LSG L E+Q ++ ++L+++FS NVLDAT + ++
Sbjct: 125  IAQKKAIEENSLRDFELSGIGLSEKQORYGEIVARLSELNSQFSNNVLDATMGWEKLIEN 184

Query: 184  AAPLAGIPEDALAMFAAAQSEGKTYKIGLQIPHYLAVIQYADNRKLRQIYRAYVTRA 243
          A LAG+PE AL +A+S+G GY+ L+IP YL V+ Y +NR LRE++YRAY TRA
Sbjct: 185  EAELAGLPESALQAAQSAESKGLKGYRFTLEIPSYLPVMTYCENRALREEMYRAYATRA 244

Query: 244  SELSDD-GKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMDTPEQVLNFLHDLAR 302
          SE + GK+DN+ ++ L ++ AKLLGF Y ELSLATKMA+ P+QVL+FL LA
Sbjct: 245  SEQGPNAGKWDNSKVMEEILLRVELAKLLGPNYTYELSLATKMAENPQQVLDLFLDLAE 304

Query: 303  RAKPYAEKD LAEVKAFARESLGLADLQPWD LGYAGEKLREAKYAFSETEVKKYFPVGKVL 362
          RAKP EK+L E+K + + G+ +L PWD+G+ EK ++ YA ++ E++ YFP +V+
Sbjct: 305  RAKPQGEKELQELKGYCEKEFGVTELAPWDIGFYSEKQKQHLAYAINDEELRPYFPENRVI 364

```

Query: 363 NGLFAQIKKLYGIGFTE-KTVPVWHKDVRYFEL-QQNETIGGVYMDLYAREGKRGAWM 420
 +GLF IK+++ I E K V WHKDVR+F+L +N + G Y+DLYARE KRGAWM
 Sbjct: 365 SGLFELIKRIFNIRAVERRKGVDTWHKDVRFFDLIDENDQLRGSFYLDLYAREHKRGAWM 424

Query: 421 NDYKRRRFS DGT LQLPTAYLV CNFT PPVGGKEARLSHDEIXXXXXXXXXXXXXXXXXXQVD 480
 +D GR+R DG+++ P AY L CNF P+G K A +H+E+ Q+D
 Sbjct: 425 DDCIGRKRKLDGSIETFPVAYLTCNFPNAPIGNKPALFTHNEVTTLFHEFGHGIHMLTQID 484

Query: 481 ELGVSGINGVWD AVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAANKFQ 540
 V+GINGV WDAVELPSQFMEN+ WE LA +S H ETG PLFKE ++L AKNFQ
 Sbjct: 485 VSDVAGINGVWD AVELPSQFMENWCWEEALAFISGHYETGEPLPKEKLTQLLKAKNFQ 544

Query: 541 RGMFLVRQMEFALFDMMIYSEDDEGR LKNWQQVLD SVRKEVAVVRPPEYNRFANSFGHIF 600
 MF++RQ+EF +FD ++ D + L SV+ +VAV++ ++ R +SF HIF
 Sbjct: 545 AAMFILRQLEFGIFDFRLHHTFDAEKTNIQILD TLKSVKSQVAVIKGVWDWARAPHSFSHIP 604

Query: 601 XXXXXXXXXXXXWAEVLSADAYAAFEESDDV-AATGKRFWQEILAVGGSRSAAESPKAFR 659
 WAEVLSADAY+ FEE TKG F EIL GGS E FK FR
 Sbjct: 605 AGGYAAGYYSYLWAEVLSADAYS RFEEGIFNPITGKSFLDEILTRGGSEEPME LFKRFR 664

Query: 660 GREPSIDALLRHSGFDN 676
 GREP +DALLRH G N
 Sbjct: 665 GREPQLDALLRHKGIMN 681

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 493>:

g129.seq
 1 ATGCTTTCAC CTCCTCGGCG TAAACGGCG GCACATCAAT CAAGCCGTCT
 51 TTCATTGCG TGCGGAAAAA ATGCGGCGTG TTGCCGTGAT CAAAATCAAT
 101 ATCGTGCAGC ATCCAGCCCA AATCGCGGTT TGCCTCGCTT TCCGATAACG
 151 CCGACGGCGG CAGCGGTTCA CCCTTATCCG CGCTTTCGCC ATTTGCCCTT
 201 TCAGGCTGCG GGCATAGGGG CGGAACAGGC GCGGTCGAA TCCTGTTTCA
 251 TCCGACAAA CGCGTTGCA GTCGAAAAAT CCGGCCGGCC GTGTCAAATA
 301 ATGCGTTACT TTGGCCGGGT CTTGTCCTTT GTAAGCGCG GTCTTTTTTT
 351 GCGCGCCATC CGCATCTGTT TGGGCGCATG GCAAACGGCG GCTGCCGTAC
 401 AATCAAAATG TTTGGCGATT TCATGCAGAC AGGCATCCGG ATGCCGCCCG
 451 ACATATCGAG CCGGTTTTTG CCTATCCGAT TTGGCGCAT TTAGGCCGGT
 501 AACTGA

This corresponds to the amino acid sequence <SEQ ID 494; ORF 129.ng>:

g129.pep
 1 MLSPPRRKTA AHQSSRLSFA CGKNAACCRD QNQYRAASSP NRGLPRFPIT
 51 PTAAAVHPYP RFRHLPFQAA GIGAEQAAVE SCFIRTNALA VGKSGRPCQI
 101 MRYFGRVLSF VSGGLFLRAI RICLGAWQTA AAVQSKCLAI SCRQASGCRP
 151 TYRAGFCLSD LAAFRPVT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 495>:

m129.seq (partial)
 1 ..TATCTGCGCT TTCACTATTT GCCCTTTCAG GCTGCGGGCA TAGGGACGGA
 51 ACAGGTAGCG GTCAAATCCT GTTTCATCCA AATAAACACG TTGGTAGTCG
 101 GAAATTCGG CCGGCTGTGT CAAATAATGC GTTACTTTGG CCGGGTCTTG
 151 TTCTTTGTAA GTGGTGGTCT TTTTTCGCG GTTATCCCCA TCTGTTTGAG
 201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTTG GCGATTTCAT
 251 GCAGATAGGC ATCCGGGTGT TGCCCAACAT ATTGAGCCGG TTTTTCCTA
 301 TCCGATTGA CGGCATTTAG ACCGGTAACT TGA

This corresponds to the amino acid sequence <SEQ ID 496; ORF 129>:

m129.pep (partial)
 1 ..YLRFHYPFQ AAGIGTEQVA VKSCFIQINT LVVGKFGRLC QIMRYFGRVL
 51 FVSGGLFLR VIPICLSAXQ MVAAVQSKCL AISCRXASGC CPTYXAGFCL
 101 SDLTAFRPVT *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 129 shows 79.1% identity over a 110 aa overlap with a predicted ORF (ORF 129.ng) from *N. gonorrhoeae*:

m129/g129

						10	20	30
m129.pep						YLRFHYPFQAAGIGTEQVAVKSCFIQINT		
g129	RDQNQYRAASSPNRGLPRFPITPTAAAVHPYPRFRHL	PFQAAGIGAEQA	AVESCFIRTNA					
	30	40	50	60	70	80		
		40	50	60	70	80	90	
m129.pep	LVVGKFGRLCQIMRYFGRVLF	FFVSGGLFLRVIPICLSAXQMVA	AVQSKCLAI	SCRXASGC				
g129	LAVGKSGRPCQIMRYFGRVLSFVSGGLFLRAIRICL	GAWQTAAVQSKCLAI	SCRQASGC					
	90	100	110	120	130	140		
		100	110					
m129.pep	CPTYXAGFCLSD	LA	FRPVTX					
g129	RPTYRAGFCLSD	LA	FRPVTX					
	150	160						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 497>:

a129.seq (partial)

1	TATCTGCGCT	TTC	ACTATTT	GCCCTTTCAG	GCTGCGGGCA	TAGGGACGGA
51	ACAGGTAGCG	GTCAAATCCT	GTTTCATCCA	AATAAACACG	TTGGTAGTCG	
101	GAAATTCGG	CCAGCTGTGT	CAAATAATGC	GTTACTTTGG	CCGGGTCTTG	
151	TTCTTTGTAA	GTGGTGGTCT	TTTTTTGCGC	GTTATCCCCA	TCTGTTTGAG	
201	TGCATAGCAA	ATGGTGGCTG	CGTACAATC	AAAATGTTTG	GCGATTTCAT	
251	GCAGATAGGC	ATCCTGGTGT	TGCCCAACAT	ATTGAGCCGG	TTTTTGCTTA	
301	TCCGATTGA	CGGCATTTAG	ACCGGTAAC	TGA		

This corresponds to the amino acid sequence <SEQ ID 498; ORF 129.a>:

a129.pep (partial)

1	YLRFHYPFQ	AAGIGTEQVA	VKSCFIQINT	LVVGKFGQLC	QIMRYFGRVL
51	FFVSGGLFLR	VIPICLSA*Q	MVA	AVQSKCL	AISCR*ASWC
101	SDLTAFRPVT	*			

m129/a129 98.2% identity in 110 aa overlap

						10	20	30	40	50	60
m129.pep	YLRFHYPFQAAGIGTEQVAVKSCFIQINT	LVVGKFGRLCQIMRYFGRVLF	FFVSGGLFLR								
a129	YLRFHYPFQAAGIGTEQVAVKSCFIQINT	LVVGKFGQLCQIMRYFGRVLF	FFVSGGLFLR								
	10	20	30	40	50	60					
		70	80	90	100	110					
m129.pep	VIPICLSAXQMVA	AVQSKCLAI	SCRXASGCC	CPTYXAGFCLSD	LA	FRPVTX					
a129	VIPICLSAXQMVA	AVQSKCLAI	SCRXASWCC	CPTYXAGFCLSD	LA	FRPVTX					
	70	80	90	100	110						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 499>:

g130.seq

1	ATGAAACAAC	TCCGCGACAA	CAAAGCCCAA	GGCTCTGCAC	TGTTTACCCT
51	TGTGAGCGGT	ATCGTTATTG	TTATTGCAGT	CCTTTATTTT	CTGATTAAAGC
101	TGGCGGGCAG	TGGATCGTTC	GGCGATGTCG	ATGCCACTAC	GGAAGCGGCA
151	ACGCAGACCC	GCATCCAGCC	TGTCGGACAA	TTGACGATGG	GTGACGGCAT
201	CCCCGTGCGC	GAACGCCAAG	GCGAACAGAT	TTTCGGCAA	ATCTGTATCC

```

251 AATGCCACGC GCGGACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGGCGACT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCCTA
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGCAG
401 ACCTGACCGA TCAGGAATC AAACGGGCGA TTACCTACAT GGCAGATAAA
451 AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCCTG CCGACAATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGT GCGGCAGCCC CTGCGGTCGG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAAGTG TGCCACGGCG GTTCGATTCC
651 CGGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTGCAC AAACATGCCC TTGAAGGCTT TAACGCGATG
751 CCGGCCAAAG GCGGCAATGC AGGTTTGAGC GATGACGAAG TCAAAGCGGC
801 TGTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 500; ORF 130.ng>:

```

g130.pep
  1 MKQLRDNKAQ GSALFTLVSG IVIVIAVLYF LIKLAGSGSF GDVDATTEAA
 51 TQTRIQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVPNAPKLEH
101 NGDWAPRIAQ GFDTLFQHAL NGFNAMPAKG GAADLTQDEL KRAITYMANK
151 SGGSFNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAPAVGVVDG
201 KKVFEATCQV CHGGSIPGIP GIGKKDDWAP RIKKGKETLH KHALEGFNAM
251 PAKGGNAGLS DDEVKAADVY MANQSGAKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 501>:

```

m130.seq (partial)
  1 ..GGCGAACAGA TTTTCGGCAA AATCTGTATC CAATGCCACG CCGCGGACAG
 51 CAATGTGCCG AACGCTCCGA AACTGGAACA CAACGGCGAT TrGGCACC GC
101 GTATCGGCAA GGCTTCGATA CCTTGTTCCTA ACACGCGCTG AACGGCTTTA
151 ACGCCATGCC TGCAAAAGGC GGTGCGGCAG ACCTGACCGA TCAGGAACCTT
201 AAACGGGCGA TTACTTACAT GGCGAACAAA AGCGGCGGTT CTTTCCCGAA
251 TCCTGATGAG GCTGCGCCTG CCGACAATGC CGCTTCAGGA ACAGCTTCTG
301 CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG CGAAGGCAGA AGACAAGGGT
351 GCGGCACCCC TGCGGTCGGC GTTGACGGTA AAAAAAGTCTT CGAAGCAACC
401 TGTCAGGTGT GCCACGGCGG TTCGATTCCC GGTATTCCCG GCATAGGCAA
451 AAAAGACGAT TGGGCACCGC GTATCAAAAA AGGCAAAGAA ACCTTGACACA
501 AACACGCCCT TGAAGGCTTT AACGCGATGC CTGCCAAAG CGCAATGCA
551 GGTTTGAGCG ATGACGAAGT CAAAGCGGCT GTTGACTATA TGGCAAACCA
601 ATCCGGTGCA AAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 502; ORF 130>:

```

m130.pep (partial)
  1 ..GEQIFGKICI QCHAADSNVP NAPKLEHNGD XAPRIQGFDT LFOHALNGFN
 51 AMPAKGGAAD LTDQELKRAI TYMANKSGGS FPNPDEAAPA DNAASGTASA
101 PADSAPAEA KAEDKGAAPA VGVDGKKVFE ATCQVCHGGS IPGIPGIGKK
151 DDWAPRIKKG KETLHKHALE GFNAMPAXKG NAGLSDEVK AADVIMANQS
201 GAKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 130 shows 98.1% identity over a 206 aa overlap with a predicted ORF (ORF 130.ng) from *N. gonorrhoeae*:

```

m130/g130
                                     10      20      30
m130.pep                               GEQIFGKICIQCHAADSNVPNAPKLEHNGD
                                     |||
g130      DATTEAATQTRIQPVGQLTMDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
                                     50      60      70      80      90     100

                                     40      50      60      70      80      89
m130.pep      XAPRI-QGFDTLFOHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFPNPDEAAP
                                     |||
g130      WAPRIAQGFDTLFOHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFPNPDEAAP
                                     110     120     130     140     150     160

```

376

	90	100	110	120	130	140
m130 .pep	ADNAASGTASAPADSAAPAEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
g130	ADNAASGTASAPADSAAPAEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
	170	180	190	200	210	220
	150	160	170	180	190	200
m130 .pep	KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDDDEVKAAVDYMANQSGAKFX					
g130	KKDDWAPRIKKGKETLHKHALEGFNAMPKGGNAGLSDDDEVKAAVDYMANQSGAKFX					
	230	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 503>:

```

a130.seq
1  ATGAAACAAC TCCGCGACAA CAAAGCCCAA GGCTCTGCAC TGTTTACCCT
51  TGTGAGCGGT ATCGTTATTG TTATTGCAGT CCTTTATTTC CTGATTAAGC
101 TGGCGGGCAG CGGCTCGTTC GGCGATGTCG ATGCCACTAC GGAAGCAGCA
151 ACGCAGACCC GTATCCAGCC TGTCCGACAA TTGACGATGG GCGACGGCAT
201 CCCGTCGGC GAACGCCAAG GCGAACAGAT TTTCCGCCAA ATCTGTATCC
251 AATGCCACGC GCGGCACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGGCGATT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCCT
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGTAG
401 ACCTGACCGA TCAGGAATC AAACGGGCGA TTAATTACAT GGCGAACAA
451 AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCCTG CCGACATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGT GCGGCAGCCC CTGCGGTCGG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAGGTG TGCCACGGCG GTTCGATTCC
651 CGGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTTGAC AAACACGCC TTGAAGGCTT TAACGCGATG
751 CCTGCCAAG GCGGCAATGC AGGTTTGAGC GATGACGAAG TCAAAGCGGC
801 TGTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 504; ORF 130.a>:

```

a130.pep
1  MKQLRDNKAQ GSALFTLVSG IVIVIAVLYF LIKLAGSGSF GDVDATTEAA
51  QTTRIQQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVPNAPKLEH
101 NGDWAPRIAQ GFDTLFOHAL NGFNAMPAKG GAVDLTDQEL KRAITYMANK
151 SGGSFNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAAPAVGVDG
201 KKVFEATCQV CHGGSIPGIP GIGKKDDWAP RIKKGKETLH KHALEGFNAM
251 PAKGGNAGLS DDEVKAAVDY MANQSGAKF*

```

m130/a130 97.6% identity in 206 aa overlap

				10	20	30
m130 .pep				GEQIFGKICIQCHAADSNVPNAPKLEHNGD		
a130	DATTEAATQTRIQQPVGQLT	MDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD				
	50	60	70	80	90	100
	40	50	60	70	80	89
m130 .pep	XAPRI-QGFDTLFOHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFNPDEAAP					
a130	WAPRIAQGFDTLFOHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFNPDEAAP					
	110	120	130	140	150	160
	90	100	110	120	130	140
m130 .pep	ADNAASGTASAPADSAAPAEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
a130	ADNAASGTASAPADSAAPAEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
	170	180	190	200	210	220
	150	160	170	180	190	200
m130 .pep	KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDDDEVKAAVDYMANQSGAKFX					

g132.seq

g132.pcp

m132.seq (partial)

m132.pep (partial)

1 MEPFKTLIWI VNLISALAVF VLVLLHKGKG ADAGATFG...

m132/q132

a132.seq

a132.pap

m132/a132 92.1% identity in 38 aa overlap

	10	20	30	
m132.pep	MEPFKTLIIVNLI SALAVFVLVLLQHGKGADAGATFG			
	: :			
a132	MEAFKTLIIVNII SALAVIVLVLLQHGKGADAGATFGSGSGSAQGVFGSAGNANFLSRS			
	10	20	30	40 50 60

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 511>:

g134.seq

```

1 ATGTCCCAAG AAATCCTCGA CCAAGTGC GC CGCCGCCGCA CGTTTGCCAT
51 CATCTCCAC CCCGATGCGG GTAAACCAC GCTGACCAG AAACCTGCTGC
101 TGTTTTCGGG CGCGATTCAA AGCGCAGGCA CGGTGAAAGG TAAGAAAACC
151 GGCAAATTCG CCACCTCCGA CTGGATGGAC ATCGAGAAGC AGCGCGGCAT
201 TTCCGTGGCA TCAAGCGTGA TGCAGTTCGA CTACAAAGAC CACACCGTCA
251 ACCTCTTGA CACGCCGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CAGTGGACAG CGCCTTGATG GTCATCGACG CGGCAAAAGG
351 CGTGGAAGCG CAAACCATCA AACTCTTGAA CGTCTGCCGC CTGCGCGATA
401 CGCCGATTGT TACCTTCATG AACAAATACG ACCGCGAAGT GCGCGATTCT
451 TTGGAACCTT TGGACGAAGT GGAAGACATC CTGCAATCC GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTTCAAGGGC GTGTACCACA
551 TCCTGAACGA CGAAATCTAT CTCTTTGAAG CGGGCGGCGA ACGCCTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATAAAC AATCCCGAAT TGAACAACG
651 CTTTCCGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAATTTAAT CTCGacgaAT TTCTCGccgG CGAACTCACG
751 CCAGTGTCT TCGGCTCTGC GATTAAACAAC TTCGGCATTC AGGAAATCCT
801 CAATTCATTG ATTGACTGGG CACCCGCACC GAAACCGCGC GACGCGACCA
851 TGCGCATGGT CGGGCCGGAC GAGCCGAAAT TTTCCGATT TATCTTTAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATCG CCTTCTTGCG
951 CGTCTGCTCC GGTAAATTCG AGCGCGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTAG TAACCTTCAT GTCGCACGAC
1051 CGCGAATGG CGGAAGAAGC CTACGCCGC GACATCATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACCTG
1151 CGTTTACCGG CATCCCATTC TTCGCGCCCG AACTGTTCCG CAGCGTCCGC
1201 ATCAAAAACC CGCTGAAAAT CAAACAACTG CAAAAGGTT TGCAACAAC
1251 CGGCGAAGAA GGTGCGGTTT AAGTATTCAA ACCGATGAGC GGC CGGATT
1301 TGATTTTGGG TGC GGTGCGG GTGTTGCA GTGAAGTCGT AACCTCACG
1351 CTCGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGCGCGCG TGGGTATCGT GCGACGACAA GAAAAAACTG GCGGAATTTG
1451 AAAAAGCCAA CGCAGGCAAC CTCGCCATCG ACGCAGGCGG CAACCTCGCC
1501 TACCTCGCCC CCAACCGCGT GAATTTGGGG TTGACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCGAACA TTCGGTCAAA CTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 512; ORF 134.ng>:

g134.pep

```

1 MSQEILDQVR RRRTFAIISH PDAGKTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFATSDWMD IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDTPIVTFM NKYDREVRDS
151 LELLDEVEDI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKGIN NPELEQRFPL EIQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFPGSAINN FGIQEILNSL IDWAPAPKPR DATMRMVGPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELAEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLOFEVVTSR
451 LANEYGEAV FDSASIWSAR WVSCDDKKKL AEFEKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTOERNPDIV FHETREHSVK L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 513>:

m134.seq

```

1 ATGTCCCAAG AAATCCTCGA CCAAGTGC GC CGCCGCCGCA CGTTTGCCAT
51 CATCTCCAC CCTGACGAG GTAAAACCAC GTTGACTGAA AAACCTTGC
101 TGTTTTCGGG CGCGATTGAG AGCGCGGGTA CGGTAAAAGG CAAGAAAACC
151 GGCAAATTCG CCACTTCCGA CTGGATGGAA ATCGAGAAGC AGCGCGGCAT

```

```

201  TTCGGTGGCA  TCAAGTGTGA  TGCAGTTCGA  TTACAAAGAC  CACACCGTCA
251  ACCTCTTGGA  CACGCCGGGA  CACCAAGACT  TCTCCGAAGA  CACCTACCGC
301  GTTTTAACCG  CCGTGGACAG  CGCATTAAATG  GTCATCGACG  CGGCAAAAGG
351  CGTGAAGCG  CAAACCATCA  AGCTCTTAAA  CGTCTGCCGC  CTGCGCGATA
401  CACCGATTGT  TACGTTTATG  AACAAATACG  ACCGCGAAGT  GCGCGATTCC
451  CTGGAACTTT  TGGACGAAGT  GGAAAACATT  TTAATAATCC  GCTGCGCGCC
501  CGTTACCTGG  CCGATCGGTA  TGGGCAAAA  CTTCAAGGGC  GTGTACCACA
551  TCCTGAACGA  TGAAATTTAT  CTCTTTGAAG  CTGGCGGCGA  ACGCCTGCCG
601  CACGAGTTCG  ACATCATCAA  AGGCATCGAT  AATCCTGAAT  TGGAACAACG
651  CTTTCCGTTG  GAAATCCAGC  AGTTGCGCGA  CGAAATCGAA  TTGGTGCAGG
701  CGGCTTCCAA  CGAGTTTAAT  CTCGACGAAT  TCCTCGCCGG  CGAACTCAGC
751  CCCGTATTCT  TCGGCTCTGC  GATTAACAAC  TTCGGTATTG  AGGAAATCCT
801  CAATTCAATG  ATTGACTGGG  CGCCCGCGCC  GAAACCGCGC  GACGCGACCG
851  TACGTATGGT  CGAGCCGGAC  GAGCCGAAGT  TTTCCGGATT  TATCTTCAAA
901  ATCCAAGCCA  ATATGGACCC  GAAACACCGC  GACCGTATTG  CTTTCTTGCG
951  CGTCTGCTCC  GGCAAATTCG  AGCGCGGCAT  GAAGATGAAA  CACCTGCGTA
1001  TCAACCGCGA  AATCGCGGCC  TCCAGCGTGG  TTACCTTCAT  GTCGCGACG
1051  CGCGAGCTGG  TTGAAGAAGC  CTACGCCGGC  GACATTATCG  GCATCCCGAA
1101  CCACGGCAAC  ATCCAAATCG  GCGACAGCTT  CTCCGAAGGC  GAACAACCTG
1151  CGTTCACCGG  CATCCCATTC  TTCGACCCG  AACTGTTCCG  CAGCGTACGC
1201  ATCAAAAACC  CGCTGAAAAT  CAAACAACCTG  CAAAAGGCT  TGCAACAGCT
1251  CGGCGAAGAA  GCGCGGGTGC  AGGTGTTCAA  ACCGATGAGC  GGCGCGGATT
1301  TGATTTTGGG  CGCGGTCGGC  GTGTTGCAGT  TTGAAGTCGT  TACCTCGCGC
1351  CTCGCCAACG  AATACGGCGT  AGAAGCCGTG  TTCGACAGCG  CATCCATCTG
1401  GTCGCGCGCG  TGGGTATCGT  GCGACGACAA  GAAAAAAGT  GCTGAATTG
1451  AAAAAGCCAA  CGCGGGCAAC  CTCGCCATCG  ACGCAGGCGG  CAACCTCGCC
1501  TACCTCGCCC  CCAACCGCGT  GAATTTGGGA  CTCACGCAAG  AACGTTGCC
1551  GGACATCGTG  TTCCAGGAAA  CACGCGAACA  TTCGGTCAA  CTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 514; ORF 134>:

```

m134 . pep
1  MSQEILDQVR  RRRRTFAIISH  PDAGKTTLTE  KLLLFSGAIQ  SAGTVKGKKT
51  GKFATSDWME  IEKQRGISVA  SSVMQFDYKD  HTVNLLDTPG  HQDFSEDYR
101  VLTAVDSALM  VIDAAGVEA  QTIKLLNVCR  LRDTPIVTFM  NKYDREVRDS
151  LELLDEVENI  LKIRCAPVTW  PIGMGKNFKG  VYHILNDEIY  LFEAGGERLP
201  HEFDIIKGID  NPELEQRFPL  EIQLRDEIE  LVQAASNEFN  LDEFLAGELT
251  PVFFGSAINN  FGIQEILNSL  IDWAPAPKPR  DATVRMVEPD  EPKFSGFIFK
301  IQANMDPKHR  DRIAFLRVCS  GKFERGMKMK  HLRINREIAA  SSVVTFMSHD
351  RELVEEAYAG  DIIGIPNHGN  IQIGDSFSEG  EQLAFTGIPF  FAPELFRSVR
401  IKNPLKIKQL  QKGLQQLGEE  GAVQVFKPMS  GADLILGAVG  VLQFEVVTSR
451  LANEYGVEAV  FDSASIWSAR  WVSCDDKKKL  AEFKANAGN  LAIDAGGNLA
501  YLAPNRVNLG  LTQERWPDIV  FHETREHSVK  L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 134 shows 98.7% identity over a 531 aa overlap with a predicted ORF (ORF 134.ng) from *N. gonorrhoeae*:

m134/g134

```

               10      20      30      40      50      60
m134 . pep  MSQEILDQVRRRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME
              |||||
g134        MSQEILDQVRRRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD
              |||||
               10      20      30      40      50      60

               70      80      90     100     110     120
m134 . pep  IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDLSALMVIDAAGVEA
              |||||
g134        IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDLSALMVIDAAGVEA
              |||||
               70      80      90     100     110     120

               130     140     150     160     170     180

```

380

m134 . pep	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLLDEVENILKIRCAPVTWPIMGKNFKG
g134	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLLDEVEDILQIRCAPVTWPIMGKNFKG
	130 140 150 160 170 180
m134 . pep	VYHILNDEIYLF EAGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN
g134	VYHILNDEIYLF EAGGERLPHEFDIIKGINNPELEQRFPLEIQQLRDEIELVQAASNEFN
	190 200 210 220 230 240
m134 . pep	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATVRMVEPDEPKFSGFIFK
g134	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATMRMVGPDPEPKFSGFIFK
	250 260 270 280 290 300
m134 . pep	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFM SHDRELVEEAYAG
g134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFM SHDRELAEAYAG
	310 320 330 340 350 360
m134 . pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIQQLQKGLQQLGEE
g134	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIQQLQKGLQQLGEE
	370 380 390 400 410 420
m134 . pep	GAVQVFKPMMSGADLILGAVGVQLQFEVVT SRLANEYGV EAVFDSASIWSARWVSCDDKKKL
g134	GAVQVFKPMMSGADLILGAVGVQLQFEVVT SRLANEYGV EAVFDSASIWSARWVSCDDKKKL
	430 440 450 460 470 480
m134 . pep	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
g134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
	490 500 510 520 530

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 515>:

```

a134 . seq
1  ATGTCCCAAG AATCCTCGA CCAAGTGCGC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC  CCTGACGCAG GTAAAACCAC GTTGACTGAA AAACCTCTGC
101 TGTTTTCAGG TGCATTCAA AGCGCGGGTA CGGTAAAAGG CAAGAAAACC
151 GGCAAATTCG CCACCTCCGA CTGGATGGAC ATCGAGAAGC AGCGCGGCAT
201 TTCCGTGGCA TCAAGCGTGA TGCAGTTCGA CTATAAAGAC CACACCGTCA
251 ACCTTTTGGA CACGCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTGACCG CCGTCGATAG TGCCTTGATG GTCATCGACG CGGCAAAAGG
351 CGTGGAAGCG CAAACCATCA AACTCTTGAA CGTCTGCCGC CTGCGCAATA
401 CGCCGATTGT TACGTTTCATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAATTGC TGGACGAAGT GGAAAACATC CTGCAAATCC GCTGCGCGCC
501 CGTAACCTGG CCGATCGGCA TGGGCAAAAA CTCAAAGGC GTGTACCACA
551 TCCTGAACGA CGAAATCTAT CTCTTTGAAG CGGGCGGCGA ACGCTTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATCGAT AATCCCGAAT TGAACAACG
651 CTTTCCGTTA GAAATACAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAGTTCAAT CTCGACGAAT TCCTCGCCGG CGAACTCAGC
751 CCCGTATTCT TCGGCTCTGC GATTAAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTCATTG ATTGAATGGG CGCCCGCGCC GAAACCACGC GATGCGACCG
851 TCGGTATGGT CGAGCCGGAC GAGCCGAAGT TTCCCGGATT TATCTTCAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CCTTCTTGCG

```

```

951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAAATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TAACCTTCAT GTCCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GTATCCCAAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACTGA
1151 CGTTTACCGG CATCCCATTG TTCGCGCCCG AACTGTTCCG CAGCGTTCGC
1201 ATCAAAAACC CGCTGAAAAT CAAGCAACTG CAAAAGGTT TGCAACAGCT
1251 TGGCGAAGAA GGTGCGGTGC AGGTGTCAA ACCAATGAGC GGC GCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCAGT TTGAAGTCGT TACCTCGCGC
1351 CTTGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAACG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAACTG GCGGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCGGGCGG CAACCTCGCC
1501 TACCTCGCCC CTAACCGCGT GAATCTGGA CTCACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCGAGCA TTCGGTCAA CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 516; ORF 134.a>:

```

a134.pep
  1 MSQEILDQVR RRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
 51 GKFATSDWMD IEKQGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCRLRNTPIVTFM NKYDREVRDS
151 LELLDEVENI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKGID NPELEQRFPL EIQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IEWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIIGIPNHGN IQIGDSFSEG EQLTFTGIPI FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGEAV FDNASIWSAR WVSCDDKKKL AEFEKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

m134/a134 98.9% identity in 531 aa overlap

```

          10      20      30      40      50      60
m134.pep  MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME
          10      20      30      40      50      60
a134      MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD

          70      80      90      100     110     120
m134.pep  IEKQGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAGVEA
          70      80      90      100     110     120
a134      IEKQGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAGVEA

          130     140     150     160     170     180
m134.pep  QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVENILKIRCAPVTWPIGMGKNFKG
          130     140     150     160     170     180
a134      QTIKLLNVCRLRNTPIVTFMKNKYDREVRDSLELLDEVENILQIRCAPVTWPIGMGKNFKG

          190     200     210     220     230     240
m134.pep  VYHILNDEIYLF EAGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN
          190     200     210     220     230     240
a134      VYHILNDEIYLF EAGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN

          250     260     270     280     290     300
m134.pep  LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATVRMVEPD EPKFSGFIFK
          250     260     270     280     290     300
a134      LDEFLAGELTPVFFGSAINNFGIQEILNSLIEWAPAPKPRDATVRMVEPD EPKFSGFIFK

          310     320     330     340     350     360
m134.pep  IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSSVVTFMSHDRELVEEAYAG
          310     320     330     340     350     360
a134      IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSSVVTFMSHDRELVEEAYAG

```

382

	370	380	390	400	410	420
m134 .pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
a134	DIIGIPNHGNIQIGDSFSEGEQLTFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m134 .pep	GAVQVFKPMSGADLILGAVGVQLQFEVVT SRLANEYGV EAVFDSASIWSARWVSCDDKKKL					
a134	GAVQVFKPMSGADLILGAVGVQLQFEVVT SRLANEYGV EAVFDNASIWSARWVSCDDKKKL					
	430	440	450	460	470	480
	490	500	510	520	530	
m134 .pep	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
a134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 517>:

g135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCG
51  TTCGGACgGC AGCCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCTG CAGGGTTCGG CGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CCGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GTGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCGATTCCC ATCATCAATG
401 AAAACGACAC GGTTCGGTT GAGGAGTTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTTCGGC AAACGGCACG GGCGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCACTCAA ACCCGATTCA TTGGCCGAAG CCGCCGAACA TCAGGCGGAC
751 GGCTCGTTT TCGTcccCcg tgCCAAAGGT TTGCGGACAC AGAAGCAATG
801 GctggCGTTC TATTcggaaa gcgggGgcag cgtttAtgtg gacgaaagtg
851 cggaaacacgc tTgtccgaa caagggaaaag cctgCTGA

```

This corresponds to the amino acid sequence <SEQ ID 518; ORF 135.ng>:

g135.pep

```

1  MKYKRIVFKV GTSSITRSDG SLRSGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQORRAIP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHNHEIIEM
201 AGGSGSANGT GGMLTKIKAA TIAAESGVPV YICSSLKPDs LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESGGSVYV DESAEHALSE QGKAC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 519>:

m135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCTGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CCGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCGCAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGGTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT

```

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501 GACCGACATA GACGGTCTTT ACACGGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCAGC GCGGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTTGCCGAAG CTGCCGAACA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 GCTGGCGTTC TATTCGAAA GCCGGGGCAG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGGAAAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATT TTCCCGTATG GACACCGTAA CCGTGTACAG
951 CAAGGCAACC AAACAGCCCC TGGGCAAAGG GCGCGTCCTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATCGCGTA AGGCGAAAGG CGTGTTTCATC
1051 CATCGGGACG ACTGGATTTC CATCACGCCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 520; ORF 135>:

```

m135.pep
  1 MKYKRIVFKV GTSSITHSDG SLSRGKIQTI TCQLAALHHA GHELVLVSSG
 51 AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAPV IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGPNPS NPDAVRLDKI EHHINHEIEM
201 AGSGSGSANGT GGMLTKIKAA TIAESGVPV YICSSLKPDA LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESRSVYV DEGAEHALSE QGKSLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAAEDLL KSRKAKGVFI
351 HRDDWISITP EIRLLLTEF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 135 shows 97.6% identity over a 294 aa overlap with a predicted ORF (ORF 135.ng) from *N. gonorrhoeae*:

m135/g135

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLSRGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
g135	MKYKRIVFKVGTSSITRSDGSLSRGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQIILSRADFADKRRYQNAGGAL					
g135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQIILSRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
m135.pep	SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNPS					
g135	SVLLQRRAPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNPS					
	130	140	150	160	170	180
m135.pep	NPDAVRLDKIEHHINHEIEMAGSGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPDA					
g135	NPDAVRLDKIEHHINHEIEMAGSGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPD					
	190	200	210	220	230	240
m135.pep	LAEAAEHQADGSGFFVPRAKGLRTQKQWLAFYSESRSVYVDEGAEHALSEQGKSLMSGI					
g135	LAEAAEHQADGSGFFVPRAKGLRTQKQWLAFYSESRSVYVDEGAEHALSEQKACX					
	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSGFFVPRAKGLRTQKQWLAFYSESRSVYVDEGAEHALSEQGKSLMSGI					
g135	LAEAAEHQADGSGFFVPRAKGLRTQKQWLAFYSESRSVYVDEGAEHALSEQKACX					
	310	320	330	340	350	360

m135.pep

AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFGSAAEDLLKSRKAKGVFIHRDDWISITP

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 521>:

a135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCCGCGT CGGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCGG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGCGT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCACA GCGGGTATGC TGACTAAAT
651 CAAAGCGGCG ACGATTGCGA CCGAGTCCGG CGTACCGGTC TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTGCGGAAG CGGCAGATAA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 GCTGGCGTTC TATTCGAAA GCAGGGGCGG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGAAAAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATT TTTCCGTATG GACACCGTAA CCGTGTACAG
951 CAAGGCAACC AAACAGCCTT TGGGCAAAGG GCGAGTCCTG TTCGGCTCTG
1001 CCGCCGCGCA AGACCTGCTC AAATTGCGTA AGGCGAAAGG CGTGTTCATC
1051 CATCGGGACG ACTGGATTTC CATCACGCCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 522; ORF 135.a>:

a135.pep

```

1  MKYKRIVFKV GTSSITHSDG SLSRGIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAVP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHHINHEIEM
201 AGSGSANGT GGMLTKIKAA TIATESGVFV YICSSLKPPA LAEADNQAD
251 GSFFVPRAKG LRTQKQWLAF YSESRGGVYV DEGAERHALSE QGKSLLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAEDLL KLRKAKGVFI
351 HRDDWISITP EIRLLLTEF*

```

m135/a135 98.4% identity in 369 aa overlap

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLSRGIQTIITQLAALHHAGHELVLVSSGAVAAGFGALG					
a135	MKYKRIVFKVGTSSITHSDGSLSRGIQTIITQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
a135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m135.pep	SVLLQRRAVPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
a135	SVLLQRRAVPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m135.pep	NPDAVRLDKIEHHINHEIEMAGSGSANGTGGMLTKIKAATIAESGVFVYICSSLKPPA					
a135	NPDAVRLDKIEHHINHEIEMAGSGSANGTGGMLTKIKAATIAESGVFVYICSSLKPPA					
	190	200	210	220	230	240

385

	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESRGVSYYVDEGAEHALSEQKSLMSGI					
a135	LAEAADNQADGSFFVPRAKGLRTQKQWLAFYSESRGGVYVDEGAEHALSEQKSLMSGI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m135.pep	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFGSAAEDLLKSRKAKGVFIHRDDWISITP					
a135	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFGSAAEDLLKLRKAKGVFIHRDDWISITP					
	310	320	330	340	350	360
	370					
m135.pep	EIRLLLTEFX					
a135	EIRLLLTEFX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 523>:

g136.seq

1	ATGGAAATCC	GGTTTCAGAC	AGCATTTT	CGTTTGGTTC	AGatgaAAAC
51	AAACGCTtca	aTTCTtaccg	caACACGCCT	TGTATTTCCCT	GccgCTGCCG
101	CACGGACAGG	GATCGTTCCT	GCCGgtTTTT	TCCCCTTCCC	TGCGGACGGT
151	TTGCGGTTTG	TTGATGACCG	CCTGCCAGTA	GCGGTAGATG	Tctgccagcg
201	cgTAAGGcag	tTCGGAcgca	agttccgcca	gctcgccttc	ggTGAATTGC
251	AGgcccataa	cgccgtttTC	CTCTCGTCg	taaatgccgc	ccactgccat
301	cacgGGGTAA	AACAGCTCTT	CAAACGCTTC	ATCATCGGCG	GCTTCAAACC
351	AATCGGTCGG	CACAATGTCC	AAACCGTAAA	GATAGGCGTT	GCACCAAGTG
401	TAAAAATCGC	TGCCGCCCTC	GCCGTCGTCG	TAGAGCCACA	AATCGGGCAG
451	CTTTTATCC	GACATCGCGG	CGTTTGTTC	CATCGCCATT	GCCAAAACCA
501	GCCGTTGAT	TTCGGAACGT	TCGGCGGCGG	TAAATTGCGA	TTCTGCGCCC
551	AACACTTCGG	GCAGCCAGTC	GAGCGGTGCC	AATTTGTCCG	GCCCCGCTCAA
601	CAGCGCCGTC	ATAAACCTT	GAACCTCGTC	GCAACGCATC	GTGTTGCCTT
651	GTTTCGCTTT	GGCATCCAAT	AA		

This corresponds to the amino acid sequence <SEQ ID 524; ORF 136.ng>:

g136.pep

1	MEIRFQTAFL	RLVQMKTNAS	ILTATRLVFP	AAAARTGIVP	AGFFPPPADG
51	LRFVDDRLPV	AVDVCQVRVQ	FGRKFRQLAF	GELQADNAVF	LFVVNAAHCH
101	HGVKQLFKRF	IIGGFKPIGR	HNVTQVKIGV	APSVKIAAAL	AVVVEPQIGQ
151	LFIRHRGGCF	HRHCQNQPF	FGTFGGGKLR	FVAQHFGQPV	ERCQFVRPAQ
201	QRRHKTNLV	ATHRVALFAF	GIQ*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 525>:

m136.seq

1	ATGGAAACAA	ACGCTTCAAT	TCTTACCGCA	ACACGCCTTG	TATTTTCTGC
51	CGTGCCGCA	CGGACAGGGA	TCGTTCCCTGC	CTGTTTTTTC	GCCTTCCCTG
101	CGGACGGTTT	GCGGTTTGT	GATGACTGCC	TGCCAGTAGC	GGTAGATATC
151	CGCCAATGCA	TAAGGCAACT	CGGATTCCAG	TCCGCCAGC	TGCCTTCTG
201	TGAATTGCAG	ACGGATAGCG	CCGTTTTCCT	CTTCGTCGTA	AATACCGCCC
251	AATGCCATGA	TGGGATAAAA	CAACTCTTCA	AACGCTTCAT	CATCGACGGC
301	TTCAAACCAA	TCGGTCGGCA	CAATATCCAA	ACCGTAAAGA	TAAGCATTGC
351	ACCATGTGTA	AAAATCGCTG	CCGCCGTCTT	CGTTTTTCATA	CAGCCACAAA
401	TCGGGCAGTT	TTTTATCCGA	CATCGCGGCG	GTTGTTTCCA	TCGCCATTGC
451	CAAAACCAGC	CGTTCGATT	CGGAACGTT	GGCGGCGGTA	AATTGCGATT
501	CGTCGCCCAA	CACCTTCGGC	AGCCAGTCGA	GCGGTGTCAA	TTTGTCCGGC
551	CCGCTCAACA	GCGCCGTCAT	AAAACCTTGA	ACCTCGTCGC	AACGCATCGT
601	GTTGCCTTGT	TCGCTTTTGG	CATCCAACAA	TTGCTCAAC	CGCCGTTTGG
651	ATGCTTCGGT	AAATTTTCGG	GAATCCATCA	TTTTCTTTT	CAAATGGGTT
701	TTGCGCCCTA	TTATCGCCGC	AATGCCGTCT	GA	

This corresponds to the amino acid sequence <SEQ ID 526; ORF 136>:

386

m136.pep
 1 METNASILTA TRLVFSAAAA RTGIVPACFF AFPADGLRFV DDCLPVAVDI
 51 RQCIRQLGFQ FRQLAFCELQ TDSAVFLFVV NTAQCHDGIK QLFKRFIIDG
 101 FKPIGRHNIQ TVKISIAPCV KIAAAVFVFI QPQIGQFFIR HRGGCFHRHC
 151 QNQPFDPGTF GGGKLRFVAQ HFGQPVERCQ FVRPAQQRH KTLNLVATHR
 201 VALFAFGIQQ FAQPPFGCFG KFSGIHHFPF QMGFAPYYRR NAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 136 shows 85.6% identity over a 209 aa overlap with a predicted ORF (ORF 136.ng) from *N. gonorrhoeae*:

m136/g136

	10	20	30	40
m136.pep	METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPV			
g136	MEIRFQTAFRLRLVQMKTNASILTATRLVFPAAAARTGIVPAGFFFPADGLRFVDDRLPV			
	10	20	30	40
	50	60	70	80
m136.pep	AVDIRQCIRQLGFQFRQLAFCELQTD SAVFLFVVNTAQCHDGIKQLFKRFIIDGFKPIGR			
g136	AVDVCQRVRQFGRKFRQLAFGELQADNAVFLFVVNAACHHGKQLFKRFIIGGFKPIGR			
	70	80	90	100
	110	120	130	140
m136.pep	HNIQTVKISIAPCVKIAAAVFVFIQ P QIGQFFIRHRGGCFHRHCQNQPFDFGTFGGGKLR			
g136	HNVQTVKIGVAPSVKIAAALAVVVEPQIGOLFIRHRGGCFHRHCQNQPFDFGTFGGGKLR			
	130	140	150	160
	170	180	190	200
m136.pep	FVAQHFGQPVERCQFVRPAQQRHKT LNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIH			
g136	FVAQHFGQPVERCQFVRPAQQRHKT LNLVATHRVALFAFGIQX			
	190	200	210	220
	230	240		
m136.pep	HFPFQMGFAPYYRRNAVX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 527>:

a136.seq

1 ATGGAACAA ACGCTTCAAT TCTTACCGCA ACACGCCTTG TATTTTCTGC
 51 CGTGCCGCA CGGACAGGGA TCGTTCCTGC CTGTTTTCCT GCCTTCCCTG
 101 CGGACGGTTT GCGGCTTGTT GATGACCGCC TGCCAGTAGC GGTAGATATC
 151 CGCCAATGCA TAAGGCAACT CGGATTCCAG TTCCGCCAGC TCGCCTTCTG
 201 TGAATTGCAG ACGGATAGTG CCGTTGTCCT CTTGTCGTA AATACGCCCC
 251 AATGCCATGA TGGGATAAAA CAACTCTTCA AACGCTTCAT CATCGACGGC
 301 TTCAAACCAA TCGGTCGGCA CAATATCCAA ACCGTAAAGA TAAGCATTGC
 351 ACCATGTGTA AAAATCGCTG CCGCCGTCTT CGTTTTTATA CAGCCACAAA
 401 TCGGGCAGTT TTTTATCCGA CATCGCGGCG GTTGTTTCCA TCGCCATTGC
 451 CAAAACCAGC CGTTCGATT TCGGAACGTT GCGGCGGTA AATTGCGATT
 501 CGTCGCCCAA CACTTCGGGC AGCCAGTCGA GCGGTGTCAA TTTGTCCGGC
 551 CCGCTCAACA GCGCCGTCAT AAAACCTTGA ACCTCGTCGC AACGCATCGT
 601 GTTGCCTTGT TCGCTTTTGG CATCCAACAA TTCGCTCAAC CGCGTTTGG
 651 ATGCTTCGGT AAATTTTCGG GAATCCATCA TTTCTCTTT CCAATGGGTT
 701 TTGCGCCCTA TTATAGTGA TTAATTTAA ATCAGGACAA GGCGACGAAG
 751 CCGCAGACAG TACAAATAGT ACGGCAAGGC GAGGCAACGC CGTACTGGTT
 801 TAAATTTAAT CCACTATATC GCCGCAATGC CGTCTGA

This corresponds to the amino acid sequence <SEQ ID 528; ORF 136.a>:

a136.pep

```

1  METNASILTA  TRLVFSAAAA  RTGIVPACFF  AFPADGLRLV  DDRLPVAVDI
51  RQCIRQLGFQ  FRQLAFCELO  TDSAVVLFV  NTAQCHDGIK  QLFKRFIIDG
101 FKPIGRHNIQ  TVKISIAPCV  KIAAAVFVFI  QPQIGQFFIR  HRGGCFHRHC
151 QNQPFDGTF  GGGKLRFVAQ  HFGQPVERCQ  FVRPAQORRH  KTLNLVATHR
201 VALFAFGIQQ  FAQPPFGCFG  KFSGIHHFPF  PMGFAPYYS  LNLNQDKATK
251 PQTQIVRQG  EATPYWFKFN  PLYRRNAV*

```

m136/a136 98.3% identity in 238 aa overlap

```

          10      20      30      40      50      60
m136.pep  METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPVAVDIRQCIRQLGFQ
          |||
a136      METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRLVDDRLLPVAVDIRQCIRQLGFQ
          10      20      30      40      50      60

          70      80      90     100     110     120
m136.pep  FRQLAFCELOTD SAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV
          |||
a136      FRQLAFCELOTD SAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV
          70      80      90     100     110     120

          130     140     150     160     170     180
m136.pep  KIAAAVFVFIQ P QIGQFFIRHRGGCFHRHCQNQPFDFGTGGGKLRFVAQHFGQPVERCQ
          |||
a136      KIAAAVFVFIQ P QIGQFFIRHRGGCFHRHCQNQPFDFGTGGGKLRFVAQHFGQPVERCQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m136.pep  FVRPAQORRHKT LNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPFQMGFAPYYRR
          |||
a136      FVRPAQORRHKT LNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPFPMGFAPYYSG
          190     200     210     220     230     240

m136.pep  NAVX
a136      LNLNQDKATKPQTQIVRQGEATPYWFKFNPLYRRNAVX
          250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 529>:

g137.seq

```

1  ATGATTATCC  ATCACcaATT  CGATCCCGTC  CTCATCAGTA  TCGGCCCGCT
51  TGCCGTCCGC  TGGTATGCCT  TAAGCTACAT  CCTCGGATTT  ATTCTTTTTA
101 CCTTCTCGG  CAGAAGGCGC  ATCGCGCAAG  GCTGTCCGT  TTTTACCAA
151 GAATCGCTCG  ACGACTTCCT  GACATGGGGC  ATTTGGGCG  TGATTTTGGG
201 CGGACGCTTG  GGCTATGTCC  TGTTTTACAA  ATTCTCCGAC  TACCTCGCCC
251 ATCCGCTTGA  TATTTTCAAG  GTATGGGAAG  GCGGAATGTC  GTTCCACGGC
301 GGCTTTTGG  GTGTAGTTAT  TGCCATATGG  TTGTTAGCC  GCAAGCACGG
351 CATCGGCTTC  CTCAAACCTGA  TGGACACGGT  CGCGCCGCTC  GTTCCGCTGG
401 GTCTCGCTTC  GGGACGTATC  GGCAACTTTA  TCAACGGCGA  ACTTTGGGGA
451 CGCATTACCG  ACATTAAACGC  ATTTTGGGCA  ATGGGCTTCC  CGCAAGCCCA
501 TTACGAAGAT  GCCGAAGCCG  CCGCGCACAA  TCCGCTTTGG  GCAGAATGGC
551 TGCAACAATA  CGGTATGCTG  CCGCGTCATC  CCTCGCAGCT  TTATCAGTTT
601 GCCCTTGAAG  GCATCTGCCT  GTTCGCCGTC  GTTTGGCTGT  TTTCCAAAAA
651 ACCGCGCCCG  ACCGGGCAGA  CTGCCGCGCT  TTTTCTCGGC  GGCTACGGCG
701 TGTTCGCTT  TATTGCGGAA  TTTGCGCGCC  AACCCGACGA  CTATCTCGGG
751 CTGCTGACCT  TGGGGCTGTC  GATGGGGCAA  TGGTTGAGCG  TCCCAGATGAT
801 TGTTTTGGGT  ATCGTCGGCT  TTGTCCGGTT  CGGCATGAAA  AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 530; ORF 137.ng>:

g137.pep

```

1  MIIHHQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSY YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIW LFSRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINGELWG
151 RITDINAFWA MGFPQAHYED AEAHAHNPLW AEWLQOYGML PRHPSQLYQF
201 ALEGICLFAV VWLFSKKPRP TGQTAALFLG GYGVFRFIAE FARQPDYDLG
251 LLTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 531>:

m137.seq

```

1  ATGATTACCC ATCCCAATT CGATCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTCCGC TGGTATGCCC TAAGCTACAT CCTCGGATT ATTCTTTTAA
101 CCTTCTCCG CAGAAAGCGC ATCGCGCAAG GCTTGTCCGT TTTTACCAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TAATTTTGGG
201 CGGGCGTTTG GGTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTGG GTGTAGTTAT TGCCATACGG TTGTTCGGCC GCAAACACGG
351 CATCGGCTTC CTCAAACTGA TGGATACGGT CGCACCGCTC GTTCCGCTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAT CCGGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTACCGTTC ATTTGGCTGT TCTCTAAAAA
651 ACAGCGGTCG ACCGGACAAG TCGCCTCGCT CTTCTCGGC GGCTACGGCA
701 TATTCCGCTT CATTGCCGAA TTCGCACGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 532; ORF 137>:

m137.pep

```

1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSY YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIR LFRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINGELWG
151 RVTDINAFWA MGFPQARYED AEAHAHNPLW AEWLQOYGML PRHPSQLYQF
201 ALEGICLFTV IWLFSKKQRS TGQVASLFLG GYGVFRFIAE FARQPDYDLG
251 LLTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 137 shows 95.4% identity over a 283 aa overlap with a predicted ORF (ORF 137.ng) from *N. gonorrhoeae*:

m137/g137

	10	20	30	40	50	60
m137.pep	MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW					
g137	MIIHHQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m137.pep	ILGVILGGRLGYVLFYKFSYLAHPLDIFKVWEGGMSFHGGFLGVVIAIRLFRKHGIGF					
g137	ILGVILGGRLGYVLFYKFSYLAHPLDIFKVWEGGMSFHGGFLGVVIAIWLFSRKHGIGF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m137.pep	LKLMDTVAPLVPLGLASGRIGNFINGELWGRVTDINAFWAMGFPQARYEDAEAAAHNPLW					
g137	LKLMDTVAPLVPLGLASGRIGNFINGELWGRITDINAFWAMGFPQAHYEDAEAAAHNPLW					
	130	140	150	160	170	180
	190	200	210	220	230	240
m137.pep	AEWLQOYGMLPRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGVFRFIAE					

```

a137.seq
1  ATGATTACCC ATCCCCAATT CGACCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTTCGC TGGTATGCCC TAAGCTACAT CCTCGGATTT ATTCTTTTTT
101 CCTTTCTCCG CAGAAGCGCG ATCGCGCAAG CTTGTGCTGT TTTTACCAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC APTTTGGGCG TAATTTTGGG
201 CGGGCGTTTG GGTTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG CGGGAATGTC GTTCCACGGC
301 GGCTTTTTCG GTGTAGTTAT TGCCATATGG TTGTTCCGTC GCAAACACGG
351 CATCGGCTTC CTCAACTGA TGGACACGGT CGCACCCTGC GTTCCACTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAC CTCGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT TTTCCGCGTC GTTGGCTGT TCTCTAAAAA
651 ACAGCGGGCG ACCGGACAAG TCGCCTCACT CTTCTCGGCT GGCTACGGCA
701 TATTCCGCTT CATTCGGGAA TTTGCACGCC AACCCGACGA CTATCTCGGG
751 TGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851  GA

```

a137.pep

1	MITHPQFDPV	LISIGPLAVR	WYALSYILGF	ILFTFLGRRR	IAQGLSVFTK
51	ESLDDFLTWG	ILGVILGGRL	GYVLFYKFS	YLAHPLDIFK	VWEGGMSFHK
101	<u>GFLGVVIAIW</u>	<u>LFGRKHGIGF</u>	LKLMDTVAPL	VELGLASGRI	GNFINGELWG
151	RVTDINAFWA	MGFPQARYED	LEAAAHNPLW	AEWLQQYQML	PRHPSQLYQF
201	<u>ALEGICLFAV</u>	<u>WLVFSKKQRP</u>	TQGVASLFLG	GYGIFRFAIE	FARQPDDYLG
251	LTLGLSMGQ	WLSFPMIVLG	IGVFVRFGMK	KOH*	

	10	20	30	40	50	60
m137.pep	MITHPQFDPVLISIGPLAVRWYALS	YILGFILETFLGRRRIAQGLSVETKESLDDFLT	WG			
a137	MITHPQFDPVLISIGPLAVRWYALS	YILGFILETFLGRRRIAQGLSVETKESLDDFLT	WG			
	10	20	30	40	50	60
	70	80	90	100	110	120
m137.pep	ILGVILGGRLGYVLFYKFS	DYLAHPLDIFKVVWEGGMSFHGGFLGVVIAIRL	FGRKHGIGF			
a137	ILGVILGGRLGYVLFYKFS	DYLAHPLDIFKVVWEGGMSFHGGFLGVVIAIWLF	FGRKHGIGF			
	70	80	90	100	110	120
	130	140	150	160	170	180
m137.pep	LKLMDTVAPLVPPLGLASGRIGNFINGELWGRVTDINAFWAMGF	PQARYEDAEAAAHNPLW				
a137	LKLMDTVAPLVPPLGLASGRIGNFINGELWGRVTDINAFWAMGF	PQARYEDLEAAAHNPLW				
	130	140	150	160	170	180
	190	200	210	220	230	240
m137.pep	AEWLQQYGMLPRHPSQLYQFALEGICLFTVIWLF	SKKQIRSTGOVASLFLGGYGIFRFIAE				
a137	AEWLQQYGMLPRHPSQLYQFALEGICLFAVWLF	SKKQIRPTGOVASLFLGGYGIFRFIAE				

	190	200	210	220	230	240
	250	260	270	280		
m137 . pep	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQHX					
a137						
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 535>:

```

g138.seq
1   ATGGAGTTTG AAAACATTAT TTCCGCCGCC gaCAAGGCGC GTATCCTTGC
51  CGAAGCACTG CCTTACatcc gccgGTTTTC CGGTTCCGTC GCCGTCATCA
101 AGTATGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GCGAATTTGT CCAAGGAATG CGCGTTACCG ACAAAGAGAC GATGGATATT
301 GTCGAAATGG TATTGGGCGG GCACGTCAAC AAGGAAATCG TGTCGATGAT
351 TAACACATAT GGAGGGCACG CGGTCGGCGT GAGCGGGCGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGGTCGATA CGCCGAACA GAATAGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGCGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 TTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT GGCAGGCAAA
601 TTGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAAtatcgc
651 cgGTGTGATG GACAAAACGG GCAATCTGCT GACCAAATC acgCCGAAAC
701 GGATTGATGG GCTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCcgccgtc aACGGTGTGA AAGCCACGCA
801 CATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGGTCGATG ATTTTAGGCA GAGGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 536; ORF 138.ng>:

```

g138.pep
1   MEFENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKETMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LVDTPEQNSV
151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDGLIA DGTLYGGMLP
251 KIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGRGEDA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 537>:

```

m138.seq
1   ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51  CGAAGCGCTG CCTTACATCC GCCGGTTTTC CGGTTCCGTC GCCGTCATCA
101 AATACGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAAGAGGC GATGGATATT
301 GTCGAAATGG TGTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GGCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGATCGATA CGCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGTGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 TTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT AGCAGGCAAA
601 TTGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CGGTGTGATG GACAAAACGG GCAATCTGCT GACCAAATC ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCCGCGTTC AACGGTGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGTTTCGATG ATTTTGGGCG GTGGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 538; ORF 138>:

```

m138.pep
1   MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA

```

51 RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAMD
 101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
 151 DIGQVGTVES IDTGLVKGLI ERGCIPVVP VGVGEKGEAF NINADLVAGK
 201 LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
 251 KIASAVEAAV NGVKATHIID GRPLNALLLE IFTDAGIGSM ILGGGEDA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 138 shows 98.0% identity over a 298 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

m138/g138

	10	20	30	40	50	60
m138.pep	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVLLKLVG					
g138	MEFENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKVGGKGEFVQGM RVTDKAMDIVEMVLGGHVNKEIVSMINTY					
g138	IHPVIVHGGGPQINAMLEKVGGKGEFVQGM RVTDKETMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKKLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVVP					
g138	GGHAVGVSGRDDHFIKAKKLIDTPEQNSVDIGQVGTVESIDTGLVKGLIERGCIPVVP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
g138	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDGLIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRPLNALLLEIFTDAGIGSMILGGGEDAX					
g138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRPLNALLLEIFTDAGIGSMILGRGEDAX					
	250	260	270	280	290	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 539>:

a138.seq

1	ATGGAGTCTG	AAAACATTAT	TCCGCCGCC	GACAAGGCGC	GTATCCTTGC
51	CGAAGCGCTG	CCTTACATCC	GCCGGTTTTC	CGGTTCCGGTC	GCCGTCATCA
101	AATACGCGCG	CAACGCGATG	ACCGAACCTG	CCTTGAAAGA	AGGGTTTGCC
151	CGCGATGTCG	TGCTGCTGAA	GCTGGTCGGC	ATCATCCCG	TCATCGTTCA
201	CGGCGGCGGG	CCGCAGATCA	ATGCGATGCT	TGAAAAAGTC	GGCAAAAAGG
251	GTGAGTTTGT	CCAAGGAATG	CGCGTTACCG	ACAAAGAGGC	GATGGATATT
301	GTCGAAATGG	TGTTGGGCGG	GCATGTCAAT	AAAGAAATCG	TGTCGATGAT
351	TAACACATAT	GGCGGACACG	CGGTCGGCGT	AAGCGGACGC	GACGACCATT
401	TCATTAAGGC	GAAGAACTT	TTGATCGATA	CGCCGAACA	GAATGGCGTG
451	GACATCGGAC	AGGTCGGTAC	GGTGGAAAGC	ATCGATACCG	GTTTGGTTAA
501	AGGGCTGATA	GAACGTGGCT	GCATTCCCGT	CGTCGCCCCC	GTCGGCGTAG
551	GTGAAAAAGG	CGAAGCGTTC	AACATCAACG	CCGATTGGT	AGCAGGCAAA
601	TTGGCGGAAG	AATTGAACGC	CGAAAACTC	TTGATGATGA	CGAATATCGC
651	CGGTGTGATG	GACAAAACGG	GCAATCTGCT	GACCAAACTC	ACGCCGAAAC
701	GGATTGATGA	ACTGATTGCC	GACGGCACGC	TGTATGGCGG	TATGCTGCCG
751	AAAATCGCTT	CTGCGGTGCA	AGCCGCCGTC	AACGGCGTGA	AAGCCACGCA
801	TATCATCGAC	GGCAGGGTGC	CCAACGCGCT	TTTGCTGGAA	ATCTTTACCG
851	ATGCCGGTAT	CGGTTTCGATG	ATTTTGGGCG	GTGGGAAGA	TGCCTGA

This corresponds to the amino acid sequence <SEQ ID 540; ORF 138.a>:

```
a138.pep
  1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
 51  RDVVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDEAMDI
101  VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
151  DIGQVGTVES IDTGLVKGLI ERGCIPVVAP VGVGEKGEAF NINADLVAGK
201  LAEELNAEKL LMTNIAAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
251  KIASAVEAAV NGVKATHIID GRVPNALLLE IFTDAGIGSM ILGGGEDA*
```

m138/a138 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m138.pep	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
a138	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKVGGKGEFVQGM RVTDEAMDIVEMVLGGHVNKEIVSMINTY					
a138	IHPVIVHGGGPQINAMLEKVGGKGEFVQGM RVTDEAMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVVAP					
a138	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAAGVMDKTGNLLTKLTPKRIDELIA					
a138	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAAGVMDKTGNLLTKLTPKRIDELIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGGGEDAX					
a138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRVPNALLLEIFTDAGIGSMILGGGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 541>:

```
g139.seq
  1  ATGCGAACCA CCTCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
 51  GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAggc ggcggcggag
101  gcGGCACTTC TGCTCCCGAC TTTAATGCAG GCGGCACCGG TATCGGCAGC
151  AACAGCAGGG CAACGATAGC GGAATCAGCA GCAGTATCTT ACGCCGGTAT
201  AAAAAACGAA ATGTGCAAG ACAGAAGCAT GCTCTGTGCC GGTCCGGATG
251  ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAAAGCCCC CCGAATCTGC
301  ATACCGGAGA CTTTTCAAAC CCAAATGACC AATATTAAGA ATATGATCAA
351  CCTCAAACCT GCAATTGAAG CAGGCTATAC AGGACGCGGG GTAGAGGTAG
401  GTATCGTCGA TACAGGCGAA TCCGTCGGCA GCATATCCTT TCCGAACTG
451  TATGGCAGAA AAGAACACGG CTATAACGAA AATTACAAAA ACAAAATTACA
501  AAAACTATAC GCGGTATATG CGGAAGGAAG CGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 542; ORF 138.ng>:

```
g139.pep
  1  MRTTSTFPTK TFKPAAMALA VATTLSACLG GGGGTSAPD FNAGGTGIGS
 51  NSRATIAESA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKIKAPRIC
101  IPETFQTQMT NIKNMINLKP AIEAGYTGRG VEVGIVDTGE SVGSISFPPEL
151  YGRKEHGYNE NYKNKLQKLY GVYAEGSA*
```


The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 543>:

```
m139.seq
1  ATGCGAACGA CCCCAACCTT CCCTACAAAA ACTTTCAAAC CGACTGCCAT
51  GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAGGC GGCGGCGGAG
101 GCGGCACTTC TGCGCCCGAC TTCAATGCAG GCGGTACCGG TATCGGCAGC
151 AACAGCAGAG CAACAACAGC GAAATCAGCA GCAGTATCTT ACGCCGGTAT
201 CAAGAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTGCGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAATGCCCC CCCCCGAATC
301 TGCATACCGG AGACTTTCCA AACCCAAATG ACGCATLACA AGAATTTGAT
351 CAACCTCAAA CCTGCAATTG AAGCAGGCTA TACAGGACGC GGGGTAGAGG
401 TAGGTATCGT CGACACAGGC GAATCCGTCG GCAGCATATC CTTTCCCGAA
451 CTGTATGGCA GAAAAGAACA CGGCTATAAC GAAAATTACG AAAAATAATA
501 CGGCGTATAT GCGGAAGGAA GCGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 544; ORF 138>:

```
m139.pep
1  MRTTPTFPTK TFKPTAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS
51  NSRATTAKSA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
101 CIPETFTQTM THYKNLINLK PAIEAGYTGR GVEVGIVDTG ESVGSI SFPE
151 LYGRKEHGYN ENYEKLYGVY AEGSA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 138 shows 92.2% identity over a 179 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

```
m139/g139
10      20      30      40      50      60
m139.pep MRTTPTFPTKTFKPTAMALAVATTLSACLGGGGGTSAPDFNAGGTGIGSNSRATTAKSA
g139      MRTTSTFPTKTFKPAAMALAVATTLSACLGGGGGTSAPDFNAGGTGIGSNSRATIAESA
10      20      30      40      50      60
70      80      90      100     110     120
m139.pep AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETFTQTMTHYKNLINLK
g139      AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKIKAP-RICIPETFTQMTNINKMINLK
70      80      90      100     110
130     140     150     160     170
m139.pep PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENY----EKLYGVYAEGSAX
g139      PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENYKNKLQKLYGVYAEGSAX
120     130     140     150     160     170
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 545>:

```
a139.seq
1  ATGCGAACGA CCCCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
51  GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAGGC GGCGGCGGAG
101 GCGGCACTTC TGCGCCCGAC TTCAATGCAG GCGGCACCGG TATCGGCAGC
151 AACAGCAGGG CAACAACAGC GAAATCAGCA GCAATATCTT ACGCCGGTAT
201 CAAGAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTGCGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAATGCCCC CCCCCGAATC
301 TGCATACCGG AGACTTTACA AACCCAAATG ACGCAT.ACA AGAATTTGAT
351 CAACCTCAAA CCTGCAATTG AAGCAGGCTA TACAGGACGC GGGGTAGAGG
401 TAGGTATCGT CGACACAGGC GAATCCGTCG GCAGCATATC CTTTCCCGAA
451 CTGTATGGCA GAAAAGAACA CGGCTATAAC GAAAATTAC. AAAAATAATA
501 CGGCGTATAT GCGGAAGGAA GCGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 546; ORF 139.a>:

```
a139.pep
1  MRTTPTFPTK TFKPAAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS
```

51 NSRATTAKSA AISYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
 101 CIPETLQTOM THXKNLINLK PAIEAGYTGR GVEVGIVDTG ESVGSISFPE
 151 LYGRKEHGYN ENYXKLYGVY AEGSA*

m139/a139 97.1% identity in 175 aa overlap

	10	20	30	40	50	60
m139.pep	MRTTPTFPKTKFKPTAMALAVATTLTSLACLGSGGGGTSAPDFNAGGTGIGSNSRATTAKSA					
a139	MRTTPTFPKTKFKPAAMALAVATTLTSLACLGSGGGGTSAPDFNAGGTGIGSNSRATTAKSA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m139.pep	AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETFTQTMTHXKNLINLK					
a139	AISYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETLQTQTMTHXKNLINLK					
	70	80	90	100	110	120
	130	140	150	160	170	
m139.pep	PAIEAGYTGRGVEVGIVDTGESVGSISFPELYGRKEHGYNENYEKLYGVYAEGSAX					
a139	PAIEAGYTGRGVEVGIVDTGESVGSISFPELYGRKEHGYNENYXKLYGVYAEGSAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 547>:

g140.seq

1	Atgtcggcac	gCGGCAAGGG	GGCAGgctat	ctcAACAGTA	CCGGACGACa
51	TGTTCCCTTC	CTGAGTGCCG	CCAAAATCGG	GCAGGATTAT	TCTTTCTTCA
101	AAAATATCAA	AACCGACGGC	GGTCTGCTGG	CTTCCCTCGA	CAGCGTCGAA
151	AAAACAGCGG	GCAGTGAAGG	CGACACGCCG	TCCTATTATG	TCCGTCGCGG
201	CAATGCGGCA	CGGACTGCTT	CGGCAGCGGC	ACATTCCGCG	CCCGCCGGTC
251	TGAAACACGC	CGTAGAACAG	GGCGGCAGCA	ATCTGGAATA	CCTGATGGTC
301	GAGCTGGATG	CCTCCGAATC	ATCCGCAACA	CCCGAGACGG	TTGAACTGTC
351	GGTCGCGGAC	CGCACAGATA	TGCCGGGCAT	CCGCCTACGG	CGCACAACTT
401	TCCGCACAGC	GGCAGCCGTA	CAGCATGCGA	ATACCGCCGA	CGGCGTACGc
451	aTCTTcaaCA	GTCTCGCCGC	TAccgTCTAt	GccgACAGTG	CCGCCGCCCA
501	TGccgATATG	CAGGGACGCC	GCCTGAAAGC	CGTATCGGAC	GGGTTGGACC
551	ACAACGGTAC	GGGTCTGCGC	GTCATCGCGC	AAACCCAACA	GGACGGTGGA
601	ACGTGGGAAC	AGGCGGGTGT	CGAAGGCAAA	ATGCGCGGCA	GTACCCAAAC
651	TATCGGCATT	GCCGCGAAAA	CCGCGAAAAA	TACGACAGCA	GCCGCCACAC
701	TGGGCATAGG	ACGCAGCACA	TGGAGCGAAA	ACAGTGCAAA	TGCAAAAACC
751	GACAGCATTa	GTCTGTTTGC	AGGCATACGG	CACGATGTGG	GCGATATCGG
801	CTATCTCAAA	GGCCTGTTCT	CctaCGGACG	CTACAAAAAC	AGCATCAGCC
851	GCAGCACC GG	TGCGGATGAA	TATGCGGAAG	GCAGCGTCAA	CGGCACGCTG
901	ATGCAGCTGG	GCGCACTGGG	TGGTGTCAAC	GTTCCGTTTG	CCGCAACGGG
951	AGATTTGACG	GTTGAAGGCG	GTCTGCGCCA	CGACCTGCTC	AAACAGGATG
1001	CATTTCGCCGA	AAAAGGCagt	GCTTTGGGCT	GGAGCGGCAA	CAGCCTCACT
1051	GAAGGCACAC	TGGTCGGACT	CGCGGGTCTG	AAACTGTGCG	AACCTTGAG
1101	CGATAAAGCC	GTCCTGTCTG	CGACGGCGGG	CGTGAACGC	GACCTGAACG
1151	GACGCGACTA	CGCGGTAACG	GGCGGCTTTA	CCGGCGCGGC	TGCAGCAACC
1201	GGCAAGACGG	GTGCACGCAA	TATGCCGCAC	ACCGCGCGGG	TTGCCGGTCT
1251	GGGGGTGGAT	GTCAATTTCG	GCAACGGCTG	GAACGGCTTG	GCACGTTACA
1301	GCTACACCGG	TTCCAAACAG	TACGGCAACC	ACAGCGGACA	AATCGGCGTA
1351	GGCTACCGGT	TCTGA			

This corresponds to the amino acid sequence <SEQ ID 548; ORF 140.ng>:

g140.pep

1	MSARGKGAGY	LNSTGRHVPF	LSAAKIGQDY	SFFKNIKTDG	GLLASLDSVE
51	KTAGEGSDTP	SYVVRGNAA	RTASAAAHSA	PAGLKHAVEQ	GGSNLENLMV
101	ELDASESSAT	PETVETAVAD	RTDMPGIRLR	RTTFRATAAV	QHANTADGVR
151	IFNSLAATVY	ADSAAAHADM	QGRRLKAVSD	GLDHNGTGLR	VIAQTQDGG
201	TWEQGGVEGK	MRGSTQTIGI	AAKTGENTTA	AATLGIGRST	WSENSANAKT

251 DSISLFAGIR HDVGDIGYLK GLFSYGRYKN SISRSTGADE YAEGSVNGTL
 301 MQLGALGGVN VPFAATGDLT VEGGLRHDLL KQDAFAEKGS ALGWSGNSLT
 351 EGTIVGLAGL KLSQPLSDKA VLSATAGVER DLNGRDYAVT GGFTGAAAT
 401 GKTGARNMPH TRRVAGLGVD VEFNGWNGL ARYSYTGSKQ YGNHSGQIGV
 451 GYRF*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 549>:

m140.seq
 1 ATGTCGGCAC GCGGCAAGGG GGCAGGCTAT CTCAACAGTA CCGGACGACG
 51 TGTTCCCTTC CTGAGTCCCG CCAAAATCGG GCAGGATTAT TCTTCTTCA
 101 CAAACATCGA AACCGACGGC GGCCTGCTGG CTTCCCTCGA CAGCGTCGAA
 151 AAAACAGCGG GCAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
 201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCGGGTC
 251 TGAAACACGC CGTAGAACAG GGCGGCAGCA ATCTGAAAAA CCTGATGGTC
 301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
 351 GGCAGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCCTAC GGCGCAACTT
 401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCGA CGGTGTACGC
 451 ATCTTCAACA GTCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
 501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
 551 ACAACGGCAC GGGTCTGCGC GTCATCGCGC AAACCCAAACA GGACGGTGGA
 601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAAC
 651 CGTCGGCATT GCCGCGAAAA CCGGCGAAAA TACGACAGCA GCCGCCACAC
 701 TGGGCATGGG ACGCAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
 751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
 801 CTATCTCAAA GGCTGTCTCT CCTACGGACG CTACAAAAAC AGCATCAGCC
 851 GCAGCACCGG TGCGGACGAA CATGCGGAAG GCAGCGTCAA CGGCACGCTG
 901 ATGCAGCTGG GCGCACTGGG CGGTGTCAAC GTTCCGTTTG CCGCAACGGG
 951 AGATTTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
 1001 CATTGCGCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCCTCACT
 1051 GAAGGCACGC TGGTCGGACT CGCGGTCTG AAGCTGTGCG AACCTTGAG
 1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGGAACGC GACCTGAACG
 1151 GACGCGACTA CACGGTAACG GGCGGCTTTA CCGGCGCGAC TGCAGCAACC
 1201 GGCAAGACGG GGGCACGCAA TATGCCGCAC ACCCGTCTGG TTGCCGGCCT
 1251 GGGCGCGGAT GTCGAATTCG GCAACGGCTG GAACGGCTTG GCACGTTACA
 1301 GCTACGCCGG TTCCAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
 1351 GGCTACCGGT TCTGA

This corresponds to the amino acid sequence <SEQ ID 550; ORF 140>:

m140.pep
 1 MSARGKGAGY INSTGRRVPF LSAKIGQDY SFFTNIETDG GLLASLDSVE
 51 KTAGSEGDITL SYVVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
 101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAAV QHANAADGVR
 151 IFNSLAATVY ADSTAAHADM QGRLKAVSD GLDHNGTGLR VIAQTQDDGG
 201 TWEQGVVEGK MRGSTQTVGI AAKTGENTTA AATLGMORST WSENSANAKT
 251 DSISLFAGIR HDAGDIGYLK GLFSYGRYKN SISRSTGADE HAEGSVNGTL
 301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSLT
 351 EGTIVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
 401 GKTGARNMPH TRRVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
 451 GYRF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 140 shows 94.5% identity over a 454 aa overlap with a predicted ORF (ORF 140.ng) from *N. gonorrhoeae*:

m140/g140

	10	20	30	40	50	60
m140.pep	MSARGKGAGYLNSTGRRVPFLSAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDITL					
g140	MSARGKGAGYLNSTGRHVPFLSAKIGQDYSFFKNIKTDGGLASLDSVEKTAGSEGDTP					
	10	20	30	40	50	60
	70	80	90	100	110	120

m140 . pep	SYVVRGNAARTASAAAHSAPAGLKHAVEQGGSNLENLMVELDASESSATPETVETAAAD
g140	SYVVRGNAARTASAAAHSAPAGLKHAVEQGGSNLENLMVELDASESSATPETVETAVAD
	70 80 90 100 110 120
m140 . pep	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNLSLAATVYADSTAAHADMQGRRLLKAVSD
g140	RTDMPGIRLRRRTTFRATAAVQHANTADGVRIFNLSLAATVYADSAAAHADMQGRRLLKAVSD
	130 140 150 160 170 180
m140 . pep	GLDHNGTGLRVIAQTQQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST
g140	GLDHNGTGLRVIAQTQQDGGTWEQGGVEGKMRGSTQTIGIAAKTGENTTAAATLIGRST
	190 200 210 220 230 240
m140 . pep	WSENSANAKTDSISLFAIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL
g140	WSENSANAKTDSISLFAIRHDVGDIGYLKGLFSYGRYKNSISRSTGADEYAEGSVNGTL
	250 260 270 280 290 300
m140 . pep	MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSLTGECTLVGLAGL
g140	MQLGALGGVNVFPAATGDLTVEGGLRHDLLKQDAFAEKGSALGWSGNSLTGECTLVGLAGL
	310 320 330 340 350 360
m140 . pep	KLSQPLSDKAVL FATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD
g140	KLSQPLSDKAVLSATAGVERDLNGRDYAVTGGFTGAAAATGKTGARNMPHTRRVAGLGVD
	370 380 390 400 410 420
m140 . pep	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX
g140	VEFGNGWNLARYSYTGSKQYGNHSGQIGVGYRFX
	430 440 450

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 551>:

```

a140 . seq
1  ATGTCGGCAG GCGGTAAGGG GGCAGGCTAT CTCAACCGTA CCGGACAACG
51  TGTTCCTTC CTGAGTGCCG CCAAATCGG GCGGGATTAT TCTTCTTCA
101 CAAACATCGA AACCGACGGC GGTCTGCTGG CTTCCTCGA CAGCGTCGAA
151 AAAACAGCGG GTAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCCGGTC
251 TGAAACACGC CGTAGAACAG GCGGCGAGCA ATCTGAAAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGCCGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCTAC GGCGCAACTT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCG CCGTGTACGC
451 ATCTTCAACA ATCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGCTAC GGGCTGCGC GTCATCGCGC AAACCCAACA GGACGGTGA
601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAAC
651 CGTCGGCATT GCCGCGAAAA CCGGCGAAAA TACGACAGCA GCCGCCACAC
701 TGGGCATGGG ACACAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CCTACGGACG CTACAAAAAC AGCATCAGCC
851 GCAGCACCGG TCGGACGAA CATGCGGAAG GCAGCGTCAA CGGCACGCTG
901 ATGCAGCTGG GCGCACTGGG CCGTGTCAAC GTTCCGTTTG CCGCAACGGG

```

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951 AGATTTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
1001 CATTGCGCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCATCACT
1051 GAAGGCACAC TGGTCGGACT CGCGGGTCTG AAGCTGTCGC AACCCCTGAG
1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGGAACGC GACCTGAACG
1151 GACGCGACTA CACGGTAACG GCGGGCTTTA CCGGCGCGAC TGCAGCAACC
1201 GGCAAGACGG GGGCAGGCAA TATGCCGCAC ACCCGCCTGG TTGCCGGTCT
1251 GGGCGCGGAT GTCGAATTCG GCAACGGCTG GAACGGCTTG GCACGTTACA
1301 GCTACGCCGG TTCCAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 552; ORF 140.a>:

a140.pep

```

1 MSAGGKGAGY LNRTGQRPVF LSAAKIGRDY SFFTNIETDG GLLASLDSVE
51 KTAGSEGDTL SYVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
151 IFNNLAATVY ADSTAAHADM QGRRLLKAVSD GLDHNATGLR VIAQTQDGG
201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGHST WSENSANAKT
251 DSISLFAIR HDAGDIGYK GLFSYGRYKN SISRSTGADE HAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL QDAFAEKGS ALGWSGNSIT
351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
451 GYRF*

```

m140/a140 98.2% identity in 454 aa overlap

m140.pep	10	20	30	40	50	60
	MSARGKGAGYLNSTGRRVPFLSAAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDTL					
a140	MSAGGKGAGYLNRTGQRPVFLLSAAKIGRDYSFFTNIETDGGLLASLDSVEKTAGSEGDTL					
	10	20	30	40	50	60
m140.pep	70	80	90	100	110	120
	SYVRRGNAAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
a140	SYVRRGNAAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
	70	80	90	100	110	120
m140.pep	130	140	150	160	170	180
	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNSLAATVYADSTAAHADMQGRRLLKAVSD					
a140	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNNLAATVYADSTAAHADMQGRRLLKAVSD					
	130	140	150	160	170	180
m140.pep	190	200	210	220	230	240
	GLDHNATGLRVIAQTQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST					
a140	GLDHNATGLRVIAQTQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGHST					
	190	200	210	220	230	240
m140.pep	250	260	270	280	290	300
	WSENSANAKTDSISLFAIRHDAGDIGYKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
a140	WSENSANAKTDSISLFAIRHDAGDIGYKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
	250	260	270	280	290	300
m140.pep	310	320	330	340	350	360
	MQLGALGGVNVFPFAATGDLTVEGGLRYDLLQDAFAEKGSALGWSGNSITEGTLVGLAGL					
a140	MQLGALGGVNVFPFAATGDLTVEGGLRYDLLQDAFAEKGSALGWSGNSITEGTLVGLAGL					
	310	320	330	340	350	360
m140.pep	370	380	390	400	410	420
	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					
a140	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					

398

	370	380	390	400	410	420
	430	440	450			
m140 . pep	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX					
a140	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX					
	430	440	450			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 553>:

g141.seq

```

1  atgagcttca aAaccgATGC CGAAACCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAGCTG
151 CCGCAAAAC AAGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GGC GGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGTGTTTCG GCGTGAAGG CGGCGCGGCA GCGCGCGGCT ACGCGCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGCGGAC TTCCACGCCA
401 TCGTGCGGCG GAATAACCTC CTCGCGGCCA TGCTCGACAA CCATATCTAC
451 CAAGGTAACG AGTTGAACAT CGACCCCAAA CGCGTGCTGT GCGGCGCGCT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGTATGGGCA
551 AGCCTGTtga cggCGTGATG CGtcccGACG GCTTCGACAT CACCGTCGCC
601 TCCGAAGTGa tggcgGTATT CTGCCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTt t gGCAATATTC TCGTCGCCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTTGAAG GCACACGGCG CGATGGCGGC ATTGCTAAAA
751 GATGCGATTA AGCCCAATTT GGTGCAAACC ATCGAAGGCA CTCCGGCCTT
801 TGTACACGGC GGCCCGTTCG CCAACATCGC CCACGGCTGC AACTCCGTTA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG TCGGGA AAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCAGT CGTCGTGGCG ACTGTCCGCG
1001 CCCTGAAATA CAACGGCGGC GTGGAACGCG CCAACCTTGG TGAAGAAAC
1051 CTCGAAGCCT TGGCAAAAGG TTTGCCCAAC CTGTTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTTCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GCGGCGCGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA TGCCATCGAC AACCAACCTA
1301 ATAACCTTCG TTTCCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAGT GTACGGCGCG GAAGATGTCG ATTTAGCGC
1401 GGAAGCGTCT GCCGAAATCG CCTCGCTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATATT CATTGAGCGA CAACGCCAAA
1501 CTCTTGGGCT GCCCCGAAGG CTTCCGCATC GCCGTACGCG GTATCACTGT
1551 TTCCGCGGCG GCGGGCTTCA TCGTTGCGTT GTGCGGCAAT ATGATGAAAA
1601 TGCCGCGGCT GCCGAAAGT CCGGCTGCCG AGAAAATCGA TGTGACGAA
1651 CACGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 554; ORF 141.ng>:

g141.pep

```

1  MSFKTDAETA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFGVKGGAA GGGYAQVLPM EDINLHFTGD FHAIGAANNL LAAMLDNHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKPDGDM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERF GNILVAYAKD GSPVYAKDLK AHGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LEALAKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDSDAE LAMIEKACAE
401 HGVEVSLTEV WGKGGAGGAD LARKVNAID NQPNNFGFAY DVELGIKDKI
451 RAIQAQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TOYSLSDNAK
501 LLGCPGEGFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDE
551 HGVHGLF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 555>:

m141.seq

```

1   ATGAGCTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGCGGAA ATTGCGGCCA AGCTTGGTCT GAATGCCGAC AACATTGAGC
101 CTTACGGTCA TTACAAGGCG AAAATCAATC CTGCCGAAGC GTTCAAAGCT
151 CCGCAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GCGCGGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCGTTGC
251 GCCACATCGG CAAAGATGCC GTGATTGCCC TGCGCGAACC TTCTCTGGGG
301 CCGGTGTTTC GCGTGAAAGG CGGCGCGGCA GCGGCGGCT ATGCCCAAGT
351 TTTGCGCATG GAAGACATCA ACCTGCACCT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GGCGGCGCGT
501 GGTCGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGTA
551 AACCCTGTTG CCGCGTGTAT CGTCCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCATTGTGAA
651 AGAGCGTTTG GGCAACATCC TTGTCGCCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAACC ATCGAAGGCA CGCCGCGCTT
801 CGTACACGGC GGCCCGTTTC CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAT
1051 TTAGACGCTT TGGAAAAAGG TTTGCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTGCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCGACGCG CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACTTCGG TTTCCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGGCATTG CCCAAAAGT GTACGGCGCG GAAGATGTTG ATTTCAGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCCGAAGA CTTCCGCATC GCCGTGCGCG GCATCACCGT
1551 TTCCGCAGGC GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCCT GCCCAAAGTT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 556; ORF 141>:

m141.pep

```

1   MSFKTDAEIA QSSTMRPIGE IAAKLGLNAD NIEPYGHYKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDA VIALREPSLG
101 PVFVGKGGAA GGGYAQVLPM EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKFPVDGM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDADAE LAMIEKACAE
401 HGVEVSLTEV WGKGGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIKDKI
451 RAIAQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TOYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVIHGLF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 141 shows 97.5% identity over a 558 aa overlap with a predicted ORF (ORF 141.ng) from *N. gonorrhoeae*:

m141/g141

```

          10      20      30      40      50      60
m141.pep  MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKL PQKQGRLLIV
          |||||  |||||  |||||  |||||  |||||  |||||
g141      MSFKTDAETAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKL PQKQGRLLIV
          10      20      30      40      50      60

```

400

	70	80	90	100	110	120
m141.pep	TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGAAGGGYAQVLPM					
g141	TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGAAGGGYAQVLPM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m141.pep	EDINLHFTGDFHAIGAANNLLAAMLNDNHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID					
g141	EDINLHFTGDFHAIGAANNLLAAMLNDNHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID					
	130	140	150	160	170	180
	190	200	210	220	230	240
m141.pep	GMGKPVDPGVMRDPGFDITVASEVMAVFLAKDISDLKERLGNILVAYAKDGSFVYAKDLK					
g141	GMGKPVDPGVMRDPGFDITVASEVMAVFLAKDISDLKERFGNILVAYAKDGSFVYAKDLK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m141.pep	ANGAMAALLKDAIKPNLVQTIETGPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
g141	AHGAMAALLKDAIKPNLVQTIETGPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m141.pep	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
g141	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLEALAKGLPN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m141.pep	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEGHGEVSLTEVWGKGGAGGAD					
g141	LLKHISNLKNVFGLPVVVALNRFVSDSDAELAMIEKACAEGHGEVSLTEVWGKGGAGGAD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m141.pep	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
g141	LARKVVNAIDNQNNFGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m141.pep	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
g141	LDKMPICMAKTQYSLSDNAKLLGCPGEGFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
	550	559				
m141.pep	PAAEKIDVDAEGVIHGLFX					
g141	PAAEKIDVDEHGVHGLFX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 557>:

a141.seq

```

1  ATGAGTTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAACCTG
151 CCGCAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC

```



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201 GCGGGGCGAA GGTA AACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGGTGTTCG GCGTGAAAGG CGGCGCGGCA GCGGGCGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAAA CGCGTGCTGT GCGGCGCGCT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGCA
551 AGCCTGTTGA CGGCGTGATG CGTCCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTTGAA
651 AGAGCGTTTG GGCAACATCC TTGTCGCCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAAAC ATCGAAGGCA CGCCCGCCTT
801 CGTACACGGC GGCCCGTTTC CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAT
1051 TTAGACGCTT TGGAAAAAGG TTTGCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTGCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCGGAATC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACCTCGG TTTGCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCAAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCCGCATC GCCGTGCGCG GCATCACCGT
1551 TTCCGCAGGC GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCCT GCCCAAAGT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 558; ORF 141.a>:

a141.pep

```

1 MSFKTDAEIA QSSTMRPIGE IAAKGLNVD NIEPYGHYKA KINPAEAFKL
51 PQKQGRLLV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFVGKGGAA GGYAQVLP EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVDM NDRQLRNIID GMGKPDVGM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NREVSDDAE LAMIEKACAE
401 HGVEVSLTEV WKGKGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIKDKI
451 RAIAQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAEKIDVDA
551 EGVHGLF*

```

m141/a141 99.5% identity in 558 aa overlap

```

          10      20      30      40      50      60
m141.pep MSFKTDAEIAQSSTMRPIGEIAAKGLNADNIEPYGHYKAKINPAEAFKL PQKQGRLLV
|||||
a141 MSFKTDAEIAQSSTMRPIGEIAAKGLNVDNIEPYGHYKAKINPAEAFKL PQKQGRLLV
          10      20      30      40      50      60

          70      80      90      100     110     120
m141.pep TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFVGKGAAGGGYQVLP
|||||
a141 TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFVGKGAAGGGYQVLP
          70      80      90      100     110     120

          130     140     150     160     170     180
m141.pep EDINLHFTGDFHAIGAANLLAAMLNDHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID
|||||
a141 EDINLHFTGDFHAIGAANLLAAMLNDHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID
          130     140     150     160     170     180

```

402

m141.pep	190	200	210	220	230	240
	GMGKPVGDGVMRPDGFDTIVASEVMAVFLAKDISDLKERLGNILVAYAKDGSPPVYAKDLK					
a141	GMGKPVGDGVMRPDGFDTIVASEVMAVFLAKDISDLKERLGNILVAYAKDGSPPVYAKDLK					
	190	200	210	220	230	240
m141.pep	250	260	270	280	290	300
	ANGAMAALLKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
a141	ANGAMAALLKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
m141.pep	310	320	330	340	350	360
	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
a141	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
	310	320	330	340	350	360
m141.pep	370	380	390	400	410	420
	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEHGVEVSLTEVWKGKGAGGAD					
a141	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEHGVEVSLTEVWKGKGAGGAD					
	370	380	390	400	410	420
m141.pep	430	440	450	460	470	480
	LARKVVNAIESQTNNFGFAYDVELGIKDKIRALAQKVYGAEDVDFSAEASAEIASLEKLG					
a141	LARKVVNAIESQTNNFGFAYDVELGIKDKIRALAQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
m141.pep	490	500	510	520	530	540
	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
a141	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
m141.pep	550	559				
	PAAEKIDVDAEGVIHGLFX					
a141	PAAEKIDVDAEGVIHGLFX					
	550					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 559>:

```

g142.seq
1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCCGTGC AGGTGCGCCA
51  ACGCGCCTTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAAATATGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAATGTTC
151 GGCAACATCC TGATGTTTCGT CCGCCAGCAT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATcggaATG AttcgCGCAC TCCGGTTTAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCGGT AACC GGCGCA ACCGCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCAC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC CGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCC ATGTGCAGCA GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 560; ORF 142.ng>:

```

g142.pep
1  MRADFMFADN MPVQVRQRAF YFKLSRFAAM PNMVGKPLFG RQAGQPGKMF
51  GNILMFVRQH IDAEAAVFRQ DRNDSRTVPY AQHHGRRLVG NRRNRRHCNA
101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN RPLYKNAAHK
151 ASPHVQQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 561>:

```
m142.seq
1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
51  ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTC
151 GGCAACATCC TGATGTTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTTCGCGCAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCGGT AACCGGCGCG ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
351 AAGATGCCAT CGCATCACGG AACGAAGTTT GAAAATTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC TGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCCc ATGTGCAGCA GTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 562; ORF 142>:

```
m142.pep
1  MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
51  GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLVG NRRDRRHCA
101 VTPCRTVCRD DMNACRARCH RITERSLKIF LQIRHFSPLN CPLYKNAAHK
151 ASPHVQQF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 142 shows 93.7% identity over a 158 aa overlap with a predicted ORF (ORF 142.ng) from *N. gonorrhoeae*:

```
m142/g142
10      20      30      40      50      60
m142.pep MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFNGNILMFVRQR
g142      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
10      20      30      40      50      60
m142.pep MRADFMFADNMPVQVRQAFYFKLSRFAAMPNMVGKPLFGRQAGQPGKMFNGNILMFVRQH
g142      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
70      80      90      100     110     120
m142.pep IDAEAAVFRQDRNDSRTPVDAQHHGRRLVGNRRDRRHCAVTPCRTVCRDDMNACRARCH
g142      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
70      80      90      100     110     120
m142.pep IDAEAAVFRQDRNDSRTPVYAQHHGRRLVGNRRDRRHCAVTPCRTVCRDDMNACRTGCH
g142      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
130     140     150     159
m142.pep RITERSLKIFLQIRHFSPLNCPPLYKNAAHKASPHVQQFX
g142      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
130     140     150
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 563>:

```
a142.seq
1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
51  ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTC
151 GGCAACATCC TGATGTTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTTCGCGCAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCGGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC TGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCACCCCCCA TGTGCAGCAG TTCTGATTCA AAAAGCCGTC GGTCCGACAT
501 TTCCGCGCGT TACGGCGTAT TACGAGTTCA ACGCATCCTC GATTTTGGCA
551 AGTTCTGCCA ACAGGTCTTT AAGCAGCAGC ATTTTCTCGC GGCCAGCAC
601 TTCCTCGATA GCGTCGTAAC GCTCGTCCAC TTCTTCGCCG ATTTCTCAT
651 ACAGCTTCTC GCCCTCGGCA GTCAGCTTCA GAAAACACG TCGTTGGTCG
701 TTGGAAAGTT TCAGGCGGAC AACCAAACCC GCTTTTCAA GGCGGGTCAG
751 GATACCGGTC AGGCTGGGGC GCAAAATGCA CGCCTGATTC GCCAAATCTT
```

801 GAAAGTCCAG CGTGCCGTTT TCCGCCAAAA GACGGATAAT CCGCCATTGC
 851 TGATCGGTAA TATTCGCCTG ATTCAGAATA GGCCTGAATT GGGTCATCAG
 901 GGCTTCCCTT GCCTGTATCA GACCGATATT GATAGACGCA TGTTTTGA

This corresponds to the amino acid sequence <SEQ ID 564; ORF 142.a>:

a142.pep
 1 MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG ROAGQPGKMF
 51 GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLLVR NRRNRRHCNA
 101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN CPLYKNAAHK
 151 APPMCSSSDS KSRRSDISAR YGVLVRQRI LDFGKFCQV FQKQHFLLAAQH
 201 FLDSVVTLVH FFADFLIQLL ALGSOLQKNT SLVVGRFQAD NQTRFFKAGQ
 251 DTGOAGAONA RLIRQILKVQ RAVFRQKTDN PPLLIGNIRL IQNRPGLGHQ
 301 GFPCLYQTDI DRRMF*

m142/a142 96.1% identity in 153 aa overlap

	10	20	30	40	50	60
m142.pep	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMF	GNILMFVRQR				
a142	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMF	GNILMFVRQR				
	70	80	90	100	110	120
m142.pep	IDAEAAVFRQDRNDSRTPVDAQHHGRRLLVGNRRDRRHCNAVTPCRTVCRDDMNACRARCH					
a142	IDAEAAVFRQDRNDSRTPVDAQHHGRRLLVNRNRRRHCNAVTPCRTVCRDDMNACRTGCH					
	130	140	150	159		
m142.pep	RITERSLKIFLQIRHFSPLNCPPLYKNAAHKASPHVQQFX					
a142	RITERSLKSFQIRHFSPLNCPPLYKNAAHKAPPMCSSSDSKSRRSDISARYGVLVRQRI					
	130	140	150	160	170	180
a142	DFGKFCQVQKQHFLLAAQHFLDSVVTLVHFFADFLIQLLALGSOLQKNTSLVVGRFQAD					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 565>:

g143.seq
 1 ATGTTGAGCT TCGGCTATCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG
 51 CTCGCAGATG AGCCGCATT TTTCAAACGCT AGGCGCAGAC CCGCACAAAT
 101 TGGGCTGGTT TTTTCATCTG CCGCCGCTGG CGGGGATGCT GGTTCAGCCG
 151 ATAGTGgGCT ACTACTCAGA CCGCACTTGG AAGCCGCGCT TGGGCGGCGC
 201 CCGCCTGCCG TATCTGCTTT ACGGCACGCT GATTGCGGTC ATCGTGATGA
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
 301 GCCTTGTCGT TCGGCGCGCT GATGATTGCG CTGTTGGACG TGTCGTCGAA
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGATATG GTCAACGAGG
 401 AGCAGAAAAG CTACGCCTAC GGGATTCAAA GTTTCTTAGC GAATACGGAC
 451 GCGGTTGTGG CAGCGATTCT GCCGTTTGTG TTcgcgata TCGGTTTGGC
 501 GAACACTGCC GAGAAAGGCG TTGTGCCACA AACCGTGGTC GTAGCATTCT
 551 ATGTGGGTGC GCGGTTACTG ATTATTACCA GTGCGTTCAC AATCTCCAAA
 601 GTCAAAGAAT ACGACCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGTT CGAACTCTTA AAAACCGCGC
 701 CTAAAGTGT TTTGGACGGT ACTCCGGTAC AGTTTTCTCG CTGTTTCGCC
 751 TTCCGGTATA TGTGGACTTA CTCGGCAGGC GCGATTGCAG AAAACGTCTG
 801 GCACACTACC GATGCGTCTT CCGTAGGCCA TCAGGAGGCG GGCAACCGGT
 851 ACGGCGTTTT GCGGCGGGTG TAGTCGGTTG CGGCGGTGAT TTGTTGCTTT
 901 ATTCTGGCAA AAGTACCGAA TAAATACCAT AAGGCGGGTT ATTTGCGCTG
 951 TTTGGCTTTG GCGGCGCTCG GTTCTTCTC TATCTTCTTC ATCTACAATC
 1001 AATACGCACT CATCCTGTCT TATATCTTAA TCGGCATCGC TTGGGCGGGC
 1051 ATTATCACTT ATCCGCTGAC GATTGTGGCC AACGCTTGT CGGGCAAACA
 1101 CATGGATACT TATTTGGGCC TGTTtaacgg ctctgtCTGT ATGCcgcaaa
 1151 tcgTcgctTC GctgttagAG TTCGTGCTTT TCCCGATGCT GGGCGGCCAT

405

1201 CAGGCAACCA TGTTCCTGGT TGCAGGCGCA GTCTTGCTGC TGGGAGCCTT
 1251 CTCAGTCTGT CTGATTAAAG AGATCCACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 566; ORF 143.ng>:

g143.pep

1 MLSFGYLGVO TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
 51 IVGYYSDRTW KPRLGRRRLP YLLYGTLIAV IVMILMPNSG SFGFGYASLA
 101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDV VNEEQKSYAY GIQSFLANTD
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL IITSAFTISK
 201 VKEYDPETYA RYHGIDVAAN QEKANWFELL KTAPKVFMTV TPVQFFCWFA
 251 FRYMWTSYAG AIAENVWHTT DASSVGHQEA GNRYGVLAAY *SVAAVICSF
 301 ILAKVPNKYH KAGYFGCLAL GALGFFSIFV IYNOYALILS YILIGIAWAG
 351 IITYPLTIVA NALSGKHMMDT YLGLFNGSVC MPQIVASLLS FVLFPMLGGH
 401 QATMFLVAGA VLLLGAFSVC LIKEIHGGV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 567>:

m143.seq

1 ATGCTCAGTT TCGGCTTTCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG
 51 CTCGCAAATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAATT
 101 TGGGCTGGTT TTTCATCCTG CCGCCGCTGG CGGGGATGCT GGTGCAAGCCG
 151 ATTGTCGGCC ATTACTCCGA CCGCACTTGG AAGCCGCGTT TGGGCGGCCG
 201 CCGTCTGCCG TATCTGCTTT ATGGCACGCT GATTGCGGTT ATTGTGATGA
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
 301 GCTTTGTGCT TCGGCGCGCT GATGATTGCG CTGTTAGACG TGTCGTCAAA
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGACATG GTCAACGAGG
 401 AGCAGAAAGG CTACGCCTAC GGGATTCAAA GTTTCTTAGC AAATACGGGC
 451 GCGGTCGTGG CCGCGATTCT GCCGTTTGTG TTTGCGTATA TCGGTTTGCG
 501 GAACACCGCC GAGAAAGGCG TTGTGCCGCA GACCGTGGTC GTGGCGTTTT
 551 ATGTGGGTGC GGCCTTGCTG GTGATTACCA GCGCGTTCAC GATTTTCAAA
 601 GTGAAGGAAT ACGATCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGAT CGAACTCTTG AAAACCGCCG
 701 CTAAGGCGTT TTGGACGGTT ACTTTGGTGC AATTCTTCTG CTGGTTCGCC
 751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCTG
 801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACGTGT
 851 ACGGCGTTTT GCGCGCGGTG CAGTCGGTTG CCGCGGTGAT TTGTTCTGTT
 901 GTATTGGCGA AAGTCCGGA TAAATACCAT AAGGCGGGTT ATTTCGGCTG
 951 TTTGGCTTTG GCGCGCTCG GCTTTTTCTC CGTTTTCTTC ATCGGCAACC
 1001 AATACGCGCT GGTGTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
 1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CCGGCAAGCA
 1101 TATGGGCACT TACTTGGGCT TGTTTAACGG CTCTATCTGT ATGCCTCAA
 1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
 1201 CAGGCCACTA TGTCTTGGT AGGGGGCGTC GTCCTGCTGC TGGGCGCGTT
 1251 TTCCGTGTTT CTGATTAAAG AAACACACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 568; ORF 143>:

m143.pep

1 MLSFGFLGVO TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
 51 IVGHYSDRTW KPRLGRRRLP YLLYGTLIAV IVMILMPNSG SFGFGYASLA
 101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDV VNEEQKGYAY GIQSFLANTG
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
 201 VKEYDPETYA RYHGIDVAAN QEKANWIELL KTAPKAFMTV TLVQFFCWFA
 251 FQYMWTSYAG AIAENVWHTT DASSVGYQEA GNWYGVLAAY QSVAAVICSF
 301 VLAKVPNKYH KAGYFGCLAL GALGFFSVFF IGNOYALVLS YTLIGIAWAG
 351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPQIVASLLS FVLFPMLGGH
 401 QATMFLVGGV VLLLGAFSVF LIKEIHGGV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m143 / g143 93.9% identity in 429 aa overlap

10 20 30 40 50 60

406

m143.pep	MLSFGFLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW
g143	MLSFGYLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGYSDRTW
	10 20 30 40 50 60
m143.pep	70 80 90 100 110 120
m143.pep	KPRLGGRRLPYLLYGTLLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
g143	KPRLGGRRLPYLLYGTLLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
	70 80 90 100 110 120
m143.pep	130 140 150 160 170 180
m143.pep	QPFKMMVGDVNEEQKGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGVVPQTVV
g143	QPFKMMVGDVNEEQKSYAYGIQSFLANTDAVVAAILPFVFAYIGLANTAEGVVPQTVV
	130 140 150 160 170 180
m143.pep	190 200 210 220 230 240
m143.pep	VAFYVGAALLVITSFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV
g143	VAFYVGAALLIITSFTISKVKEYDPETYARYHGIDVAANQEKANWFELLKTAPKVEWTV
	190 200 210 220 230 240
m143.pep	250 260 270 280 290 300
m143.pep	TLVQFFCWFAFYMWYTSAGAIENVWHTTDASSVGYQEAGNRYGVLAQVSVAAVICSF
g143	TPVQFFCWFAFRYMWYTSAGAIENVWHTTDASSVGHQEAGNRYGVLAQVXSVAAVICSF
	250 260 270 280 290 300
m143.pep	310 320 330 340 350 360
m143.pep	VLAQVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIIVT
g143	ILAKVPNKYHKAGYFGCLALGALGFFSIFFIYNOYALILSYILIGIAWAGIITYPLTIIVA
	310 320 330 340 350 360
m143.pep	370 380 390 400 410 420
m143.pep	NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLPMLGGLQATMFLVGGVLLLGAFSVC
g143	NALSGKHMDTYLGLFNGSVCMPQIVASLLSFVLPMLGGHQATMFLVAGAVLLLGAFSVC
	370 380 390 400 410 420
m143.pep	430
m143.pep	LIKETHGGVX
g143	LIKEIHGGVX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 569>:

```

a143.seq
1  ATGCTCAGTT TCGGCTTTCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG
51  CTCGCAGATG AGCCGCATCT TCCAGACGCT CGGTGCCGAT CCGCACAGCC
101 TCGGCTGGTT CTTTATCCTG CCGCCGCTGG CGGGGATGCT GGTGCAGCCG
151 ATTGTCGGCC ATTACTCCGA CCGCACTTGG AAGCCGCGTT TGGGCGGCCG
201 CCGTCTGCCG TATCTGCTTT ATGGCACGCT GATTGCGGTT ATTGTGATGA
251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
301 GCTTTGTCTG TCGGCGCGCT GATGATTGCG CTGTTAGACG TGTCGTCAAA
351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGACATG GTCAACGAGG
401 AGCAGAAAGG CTACGCCCTAC GGGATTCAAA GTTTCTTAGC GAATACGGGC
451 GCGGTCGTGG CGGCGATTCT GCCGTTTG TGTTGCGTATA TCGGTTTGGC
501 GAACACCGCC GAGAAAGGCG TTGTGCCGCA GACCGTGCTC GTGGCGTTT
551 ATGTGGGTGC GCGTTTGCTG GTGATTACCA GCGCGTTCAC GATTTTCAAA
601 GTGAAGGAAT ACAATCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
651 CGCCGCGAAT CAGGAAAAAG CCAACTGGAT CGAACTCTTG AAAACCGGCC
701 CTAAGCGGTT TTGACGGTT ACTTTGGTGC AATTCTTCTG CTGTTTCGCC

```

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751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCTG
801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACGTGT
851 ACGGCGTTTT GCGGCGGGTG CAGTCGGTTG CCGGCGTGAT TTGTTCTGTT
901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGGCGGGTT ATTTCTGGCTG
951 TTTGGCTTTG GCGCGGCTCG GCTTTTCTC CGTTTTCTTC ATCGGCAACC
1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
1101 TATGGGCACT TACTTGGGCC TGTTAACGG CTCTATCTGT ATGCCGCAA
1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
1201 CAGGCCACTA TGTTCTTGGT AGGGGGCGTC GTCCTGCTGC TGGGCGCGTT
1251 TTCCGTGTTT CTGATTAAAG AAACACACGG CGGGGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 570; ORF 143.a>:

```

a143.pep
1  MLSFGLGVQ TAFTLQSSQM SRIFQTLGAD PHSLGWFFIL PPLAGMLVQP
51  IVGHYSDRTW KPRLGRRRLP YLLYGTIAIV IVMILMPNSG SFGFGYASLA
101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKYAY GIQSFLANTG
151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
201 VKEYNPETYA RYHGIDVAAN QEKANWIELL KTA PKAFWTV TLVQFFCWFA
251 FOYMWYSAG AIAENVWHTT DASSVGQEA GNWYGVLAAV QSVAAVICSF
301 VLAKVPNKYH KAGYFGCLAL GALGFFSVFF IGNOYALVLS YTLIGIAWAG
351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPOIVASLLS FVLFPMLGGL
401 QATMFLVGGV VLLGAFSVF LIKETHGGV*

```

m143/a143 99.5% identity in 429 aa overlap

	10	20	30	40	50	60
m143.pep	MLSFGLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW					
a143	MLSFGLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW					
	10	20	30	40	50	60
m143.pep	KPRLGRRRLPYLLYGTIAIVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
a143	KPRLGRRRLPYLLYGTIAIVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
	70	80	90	100	110	120
m143.pep	KPRLGRRRLPYLLYGTIAIVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
a143	KPRLGRRRLPYLLYGTIAIVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
	70	80	90	100	110	120
m143.pep	QPFKMMVGDMVNEEQKYAYGIQSFLANTGAVVAAILPFVFAYIGLANTA EKGVPQTVV					
a143	QPFKMMVGDMVNEEQKYAYGIQSFLANTGAVVAAILPFVFAYIGLANTA EKGVPQTVV					
	130	140	150	160	170	180
m143.pep	QPFKMMVGDMVNEEQKYAYGIQSFLANTGAVVAAILPFVFAYIGLANTA EKGVPQTVV					
a143	QPFKMMVGDMVNEEQKYAYGIQSFLANTGAVVAAILPFVFAYIGLANTA EKGVPQTVV					
	130	140	150	160	170	180
m143.pep	VAFYVGAALLVITSAFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
a143	VAFYVGAALLVITSAFTIFKVKEYNPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
	190	200	210	220	230	240
m143.pep	VAFYVGAALLVITSAFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
a143	VAFYVGAALLVITSAFTIFKVKEYNPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
	190	200	210	220	230	240
m143.pep	TLVQFFCWFAFOYMWYSAG AIAENVWHTT DASSVGQEA GNWYGVLAAVQSVAAVICSF					
a143	TLVQFFCWFAFOYMWYSAG AIAENVWHTT DASSVGQEA GNWYGVLAAVQSVAAVICSF					
	250	260	270	280	290	300
m143.pep	TLVQFFCWFAFOYMWYSAG AIAENVWHTT DASSVGQEA GNWYGVLAAVQSVAAVICSF					
a143	TLVQFFCWFAFOYMWYSAG AIAENVWHTT DASSVGQEA GNWYGVLAAVQSVAAVICSF					
	250	260	270	280	290	300
m143.pep	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNOYALVLSYTLIGIAWAGIITYPLTIVT					
a143	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNOYALVLSYTLIGIAWAGIITYPLTIVT					
	310	320	330	340	350	360
m143.pep	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNOYALVLSYTLIGIAWAGIITYPLTIVT					
a143	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNOYALVLSYTLIGIAWAGIITYPLTIVT					
	310	320	330	340	350	360
m143.pep	NALSGKHMGT YLGLFNGSIC MPOIVASLLS FVLFPMLGGLQATMFLVGGV VLLGAFSVF					
a143	NALSGKHMGT YLGLFNGSIC MPOIVASLLS FVLFPMLGGLQATMFLVGGV VLLGAFSVF					
	370	380	390	400	410	420
m143.pep	NALSGKHMGT YLGLFNGSIC MPOIVASLLS FVLFPMLGGLQATMFLVGGV VLLGAFSVF					
a143	NALSGKHMGT YLGLFNGSIC MPOIVASLLS FVLFPMLGGLQATMFLVGGV VLLGAFSVF					

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a143      |||||
          NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLFPMGLGLQATMFLVGGVVLLLGAFSVF
          370      380      390      400      410      420

          430
m143.pep  LIKETHGGVX
          |||||
a143      LIKETHGGVX
          430

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 571>:

```

g144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGGGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGTGC GTCTTCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC CCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGTAGGACTT ACCGCGTGA GGCACACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTCGCAC GGGCTGGCCG TTACCGgtTT
351 CAACGCGGTG GCGGCAGACG GccgacggTt atCCCAACGA TTtGGatatT
401 TCctaccgCT TGGACGAGGA CGGCCGGCTT ACCGttaccT ATCGCGCCAC
451 CGCgctCGGC GACACGGTGT TCGACCCGAC GCTGCACATT TACTGGCGGC
501 TGGACGCGGG CCTGCACGAT GCGGTTCTGC ATATTCCGCA GGGCGGACAT
551 ATTCCGGCCG ATGCCGAAAA ACTGCCCGTC TTAACGGTTT CAGACGGCCT
601 CGAAGTATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 572; ORF 144.ng>:

```

g144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTC VFVLDLGGIV QEFVSLADGV
51  RENPVVSFDD AASYADNPFFQ INKQIGRVAG RIRGAAFDIN GRTRYVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRRLSQR FGyFLPLGRG RPAYRYLSRH
151 RARRHGVRPD AAHLAAGRG PARCSAYSAY GRYSGRCRK TARLNGFRRP
201 RSI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 573>:

```

m144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGTCTGATCG ACGGGCGGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTC GTTCGATGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGA GGCACACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTCGCAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTCCGT GGTGCTGCGC AGCCGCCTGg
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGG ATATTTCCTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TAaCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTTCGAC CCGACGCTGC ACATTTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATGCC
601 GGCCGATGCC GAAAACTGC CCGTCTCAAC GGTTTCAGAC GACCTCGAAG
651 TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 574; ORF 144>:

```

m144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFVSLADGV
51  RENLVVSFDD AASYADNPFFQ INKQIGRVAG RIRGAAFDIN GRTRYVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLATVGRRL SQRFGGYFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAAHLL AAGRGPARCG SAYSAGRTYA
201 GRCRK TARLN GFRRPRSI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m144 / g144 91.3% identity in 218 aa overlap

	10	20	30	40	50	60
m144.pep	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFVSLADGVRENLVVSFDD					
g144	MSDTPATRDFGLIDGRAVTGYVLSNRRGTCVFVLDLGGIVQEFVSLADGVRENPFVVSFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m144.pep	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					
g144	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m144.pep	AADGRSVVLRSLATVGRRLSQRFGFYFLPLGRGRPAYRYLSRHRARRHGVRPDAAHLL					
g144	AAD-----GRRLSQRFG--YFLPLGRGRPAYRYLSRHRARRHGVRPDAAHLL					
		130	140	150	160	
	190	200	210	219		
m144.pep	AAGRGPARGSAYSAGRTYAGRCRKRTARLNGFRRPRSIX					
g144	AAGRGPARGSAYSAGRTYSGRCRKRTARLNGFRRPRSIX					
	170	180	190	200		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 575>:

a144.seq

1	ATGAGCGATA	CCCCCGCTAC	CCGCGATTTC	GGCCTGATCG	ACGGGCGTGC
51	CGTAACCGGC	TATGTGCTGT	CCAACCGGCG	TGGTACGCGT	GTCTGCGTGC
101	TGGACTTGGG	CGGGATTGTG	CAGGAATTTT	CCGTTTGGC	AGACGGCGTG
151	CGCGAAAACC	TCGTGGTGTC	GTTCGACGAT	GCGGCTTCCT	ATGCGGACAA
201	TCCGTTTCAG	ATTAACAAGC	AGATAGGGCG	CGTGGCCGGA	CGCATCCGCG
251	GTGCGGCGTT	CGACATCAAC	GGCAGGACTT	ACCGCGTGGA	GGCCAACGAA
301	GGCAGGAACG	CGCTGCACGG	CGGTTCCGAC	GGGCTGGCCG	TTACCCGTTT
351	CAACGCGGTG	GCGGCAGACG	GCCGTTCCGT	GGTGTGCGC	AGCCGCGCTG.
401	CAACAGTCGG	CCGACGGTTA	TCCCAACGAT	TTGGATTG	ATATTTCTTA
451	CCGCTTGGAC	GAGGACGACC	GGCTTACCGT	TACCTATCGC	GCCACCGCGC
501	TCGGCGACAC	GGTGTTCGAC	CCGACGCTGC	ACATTACTG	GCGGCTGGAC
551	GCGGGCCTGC	ACGATGCGGT	TCTGCATATT	CCGCAGGGCG	GACATATTCC
601	GGCCGATGCC	GAAAACTGC	CCGTCTCAAC	GGTTTCAGAC	GACCTCGAAG
651	TATTTGA				

This corresponds to the amino acid sequence <SEQ ID 576; ORF 144.a>:

a144.pep

1	MSDTPATRDF	GLIDGRAVTG	YVLSNRRGTR	VCVLDLGGIV	QEFVSLADGV
51	RENLVVSFDD	AASYADNPFQ	INKQIGRVAG	RIRGAADFID	GRTYRVEANE
101	GRNALHGGSH	GLAVTRFNAV	AADGRSVVLR	SRLXTVGRRL	SQRFGFGYFL
151	PLGRGRPAYR	YLSRHRARRH	GVRPDAHLL	AAGRGPARGC	SAYSAGRTYS
201	GRCKRTARLN	GFRRPRSI*			

m144/a144 99.1% identity in 218 aa overlap

	10	20	30	40	50	60
m144.pep	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFVSLADGVRENLVVSFDD					
a144	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFVSLADGVRENLVVSFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m144.pep	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					

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|||||
a144      AASYADNPFQINKQIGRVAGRIrgAAFDINGRTYrVEANEGRNALHGGSHGLAVTRFNAV
              70          80          90          100          110          120

              130          140          150          160          170          180
m144.pep  AADGRSVVLRSLATVGRRLSQRFGFGYFLPLGRGRPAYRyLSRHRARRHGVRPDAAHLL
|||||
a144      AADGRSVVLRSLXTVGRRLSQRFGFGYFLPLGRGRPAYRyLSRHRARRHGVRPDAAHLL
              130          140          150          160          170          180

              190          200          210          219
m144.pep  AAGRGPARGCSAYSAGRTYAGRCrKTARLNGFRRPRsIX
|||||
a144      AAGRGPARGCSAYSAGRTYSGRCrKTARLNGFRRPRsIX
              190          200          210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 577>:

```

g146.seq
1  ATGAAGCAAA TCCCCCTCCG CCTTCTCCAG GTCGTCATTG ACCACGACAA
51  AGTCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAa ctTCCCGACT GTCCGTCCCG CGCctTTGA GCGCGCGGC
151 AAGCACGTCG AAAGAAGGCG GCAGGATAAA GATACCGACA GCTTCCGGCA
201 GCGCGTTGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCAG
251 TCATAGCCTG CCGCCGCCAA CGCATTCACG CCCTCCGTGC TTGTGCCGTA
301 ATAGTTGCCG AATACGTCTG CGTATTCCAA AAAAGCCTCC TGC GCGATAA
351 GCGATTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGGCG CGTCGTATGC GACACGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAA CCGATTGTAT CACAACGGAC ACCCTATTTT
601 ATATTGCGG ATGCCCATAT TTTGCCGCTA TTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 578; ORF 146.ng>:

```

g146.pep
1  MKQIPLRLLO VVIDHDKVEQ YGLDFMPCL RQPPLDNFPT VRPAPFEARG
51  KHVERRRQDK DTDsFRQrVA NLRRALNVDF QNHVIACRRQ RIHALRACAV
101 IVAEYVCVFQ KSLLRDKREK LFFGNKVIMY AVCFAFTRRA RRMRHGNAQT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPYF
201 IFADAHILPL LF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 579>:

```

m146.seq
1  ATGGCGCAAA TCCTCCTCCG CTCGCGCCAA GTCGTCATTG ACCACGACAA
51  AGTCAAACAA TACGGACTGC TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAA CTTCCCGACT GTCCGTCCCG CGTCCGTGA GCGCGCGGC
151 AAGTACGTCG AAAGAAGGCG GCAGGATAAA GATGCCGACG GCTTCCGGCA
201 GCGCGTCGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCAG
251 TCATAGCCTG CCGCCGCCAA CGCATTCACA CCCTCCGCGC CTGTGCCGTA
301 ATAGTTGCCA AATACGTCTG CGTATTCCAA AAAAGCCTCC TGC GCGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGGCG CGTCGTGTGC GACACGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAATGGAC ACCCAGTTTC
601 CTATTGCGG ATGCCCATAT TTTGCCGCTA TTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 580; ORF 146>:

```

m146.pep
1  MAQILLRSRQ VVIDHDKVKQ YGLLDFMPCL RQPPLDNFPT VRPASVEARG
51  KYVERRRQDK DADGFGQrVA NLRRALNVDF QNHVIACRRQ RIHTLRACAV
101 IVAKYVGVFQ KSFLRDKRLK LFFGNKVIMY AVCFAFTRRA RRVRHGNAQT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQWTPSF
201 LFADAHILPL LF*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m146 / g146 90.1% identity in 212 aa overlap

m146.pep	10	20	30	40	50	60
	MAQILLRSRQVVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRQDK					
g146	MKQIPLRLQVVVIDHDKVEQYGLFDFMPCLRQPPLDNFPTVRPAPFEARGKHVERRRQDK					
	10	20	30	40	50	60
m146.pep	70	80	90	100	110	120
	DADGFGQVRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFLRDKRLK					
g146	DTDSFRQVRVANLRRALNVDFQNHVIACRRQRIHALRACAVIVA EYVCVFQKSLLRDKRFK					
	70	80	90	100	110	120
m146.pep	130	140	150	160	170	180
	LFFGNKVIMYAVCFAFTRRRVRHGNNAQTMVVCQPPRHQRFARAGSGRNDKDVAFSIS					
g146	LFFGNKVIMYAVCFAFTRRRVRHGNNAQTMVVCQPPRHQRFARAGSGRNDKDVAFSIS					
	130	140	150	160	170	180
m146.pep	190	200	210			
	GHIFYLYIFQPIVSQWTPSFLFADAHILPLLFX					
g146	GHIFYLYIFQPIVSQRTPYFIFADAHILPLLFX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 581>:

```
a146.seq
1  ATGGCGCAAA TCCTCCTCCG CCCGCGCCAA GTCATCATTG ACCACGACAA
51  AATCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAA CTTCCCGACT GTCCGTCCCG CGTCCGTGTA GACGCGCAGC
151 AAGCACATCG AAAGACGGCG GCAGGATAAA GATGCCGACG GCTTCGGGCA
201 GCGCATCTCG AACCTGAGCC GCGCCCTGAA CGTCGATTTC CAAAATCAGC
251 TCATAACCTG CCGCCGCCAA CGCATTACCA CCCTCCGCGC TTGTGCCGTA
301 ATAGTTGCCG AACACGTCCG CGTATTCCAA AAAAGCCTCC TGCGCGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGACG CGTCGTGTGC GACACGGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAACGGAC ACCCGGTTTC
601 CTATTTGCCG ATGCCCATAT TTGCGCGCTA TTGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 582; ORF 146.a>:

```
a146.pep
1  MAQILLRPRQ VIIDHDKIEQ YGLDFMPCL RQPPLDNFPT VRPASVETR
51  KHIERRRQDK DADGFGQRIS NLSRALNVDF QNHVITCRRQ RIHTLRACAV
101 IVAEHVRVFQ KSLLRDKRLK LFFGNKVIMY AVCFAFTRRT RRVRHGNAQT
151 VMVCQPPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPGF
201 LFADAHILPL LF*
```

m146/a146 90.6% identity in 212 aa overlap

m146.pep	10	20	30	40	50	60
	MAQILLRSRQVVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRQDK					
a146	MAQILLRPRQVIIDHDKIEQYGLDFMPCLRQPPLDNFPTVRPASVETRSKHIERRRQDK					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m146.pep      DADGFGQRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFLRDKRLK
                |||||:::| | |||||:::| | |||||:::| | |||||:::| | |||||:::|
a146          DADGFGQRI SNLSRALNVDFQNHVITCRRQRIHTLRACAVIVA EHVRFQKSLLRDKRLK
                70          80          90          100         110         120

                130         140         150         160         170         180
m146.pep      LFFGNKVIMYAVCFATRRRRVRHGN AQTVMVCQPRHQRGFARAGSGRNDKDVAFSIS
                |||||:::| | |||||:::| | |||||:::| | |||||:::| | |||||:::|
a146          LFFGNKVIMYAVCFATRRRRVRHGN AQTVMVCQPRHQRGFARAGSGRNDKDVAFSIS
                130         140         150         160         170         180

                190         200         210
m146.pep      GHIFYLYIFQPIVSQWTPSELFADAHILPLLEFX
                |||||:::| | |||||:::| | |||||:::| | |||||:::|
a146          GHIFYLYIFQPIVSQRTPGFLFADAHILPLLEFX
                190         200         210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 583>:

```

g147.seq (partial)
1  ..ATGCGACGAG AAGCCAAAAT GGCACAAATC ACACTCAAAC CCATTGTTTT
51 ATCAATTCTT TTAATCAACA CACCCCTCCT CGCCCAAGCG CATGAAACTG
101 AGCAATCGGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCCG
151 CGCGCGACTT CGGGCTGCT GCACACTTCG ACCGCCTCCG ACAAATCAT
201 CTCCGGCGAT ACTTTGCGCC AAAAAGCCGT CAACTTGGGC GACGCTTGG
251 ACGGCGTACC GGGCATCCAC GCTTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC GGGCAGACGG ATTAAAGTAT TGAACCATCA
351 CGGCGAAACG GCGGATATGG CGGACTTTTC TCCGATCAC GCCATTATGG
401 TAGATACCGC CTTGTCGCAA CAGGTTGAAA TCCTGCGCGG GCCGGTTACG
451 CTCTTGTA CA GCTCGGgcaa tgtggccgGG GCTGGtcaat gttgccgatg
501 gAAAAAtccc caaaaAAtg cc..

```

This corresponds to the amino acid sequence <SEQ ID 584; ORF 147.ng>:

```

g147.pep (partial)
1  ..MRREAKMAQI TLKPIVLSIL LINTPLLAQA HETEQSVGLE TVSVVGKSRP
51 RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFSPDH AIMVDTALSQ QVEILRGPVT
151 LLYSSGNVAG AGQCCRWNKP PKNA..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 585>:

```

m147.seq (partial)
1  ..CCGCATAAAA CTGAGCAATC GGTGGATTG GAAACGGTCA GCGTCGTCGG
51 CAAAAGCCGT CCGCGCGCCA CGTCGGGGCT GTTGCACT TCGACCGCT
101 CCGACAAAT CATCTCCGGC GATACCTTGC GCCAAAAGC CGTCAACTTG
151 GGCGACGCTT TAGACGGCGT ACCGGGCATC CACGCTTCG AATACGGCGG
201 CGGCGCGTCT GCTCCCGTCA TTCGCGGTCA AACAGGCAGG CGGATTAAAG
251 TGTTGAACCA TCACGGCGAA ACAGGCGATA TGGCGGATT TCGCCCGAT
301 CACGCCATTA TGGTAGATAC CGCCTTGTCG CAACAGGTCG AAATCCTGCG
351 CGGGCCGGTT ACGCTCTTGT ACAGCTCGGG CAATGTGGCG GGGCTGGTCG
401 ATGTTGCCGA TGGCAAAATC CCCGAAAAA TGCTGAAAA CGGCGTATCG
451 GCGGAAC TCG GATTGCGTTT GAGCAGCGGC AATCTGGA AACTCACGTC
501 CGGCGGCATC AATATCGGTT TGGGCAAAA CTTTGATTG CACACGGAAG
551 GGCTGTACCG CAAATCGGGG GATTACGCCG TACCGGTTA CCGCAATCTG
601 AAACGCCTGC CCGACAGCCA CGCCGATTG CAAACGGGCA GCATCGGGCT
651 GTCTTGGGTT GGCGAAAAAG GTTTTATCGG CGTAGCGTAC AGCGACCGTC
701 GCGACCAATA TGGTCTGCCT GCCACAGCC ACGAATACGA TGATTGCCAC
751 GCCGACATCA TCTGGCAAAA GAGCTTGATT AACAAACGCT ATTTACAGCT
801 TTATCCGCAG CTGTTGACCG AAGAAGACAT CGATTACGAC AATCCGGGCT
851 TGAGCTGCAG CTTCCACGAC GACGATAATG CACACGCACA CACCCACAGC
901 GGCAGACCGT GGATAGACCT GCGCAACAAA CGTACGAAC TCCGTGCCGA
951 ATGAAGCAA CCGTTCCCGG GTTTTGAAGC CCTGCGCGTA CACCTGAACC
1001 GCAACGACTA CCGCCACGAC GAAAAAGCAG GCGATGCAGT CGAAAACCTT
1051 TTTAACAACC AAACGCAAAA CGCCGCGCAT GAGTTGCGCC ACCAACCCAT

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1101 AGGTCGTCTG AAAGGCAGCT GGGGCGTGCA ATATTTACAA CAAAATCCA
1151 GTGCTTTATC TGCCATATCC GAAGCGGTTA AACACCGGAT GCTGCTTGAC
1201 AACAAAGTGC AACATTACAG CTTTTTCGGT GTAGAACAGG CAAACTGGGA
1251 CAACTTCACG CTTGAAGGAG GCGTACGCGT GGAAAAACAA AAAGCCTCCA
1301 TTCAGTACGA CAAAGCATTG ATTGATCGGG AAAACTACTA CAACCACCCC
1351 CTGCCCGACC TCGGCGCGCA CCGCCAAACC GCCCGCTCAT TCGCACTTTC
1401 GGGCAACTGG TATTTACAGC CACAACACAA ACTCAGCCTG ACCGCCTCCC
1451 ATCAGGAACG CCTGCCGTCA ACGCAAGAGC TGTACGCACA CGGCAAACAC
1501 GTCGCCACCA ACACCTTTGA AGTCGGCAAC AAACACCTCA ACAAAGAGCG
1551 TTCCAACAAT ATCGAACTCG CGCTGGGCTA CGAAGGCGAC CGCTGGCAAT
1601 ACAATCTGGC ACTCTACCGC AACCGCTTCG GTAACATACAT TTACGCCCAA
1651 ACCTTAAACG ACGGACGCGG CCCCAAATCC ATCGAAGACG ACAGCGAAAT
1701 GAAGCTCGTG CGCTACAACC AATCCGGCGC CGACTTCTAC GCGCGGGAAG
1751 GCGAAATCTA CTTCAAACCG ACACCGCGCT ACCGCATCGG CGTTTCCGGC
1801 GACTATGTAC GAGGCGGTCT GAAAAACCTG CCTTCCCTAC CCGGCAGAGA
1851 AGATGCCTAC GGCAACCGTC CTTTCATCGC ACAGGACGAC CAAAATGCCC
1901 CCCGTGTTCC GGCTGCGCGC CTCGGCTTCC ACCTGAAAGC CTCGCTGACC
1951 GACCGTATCG ATGCCAATTT GGACTACTAC CGCGTGTTCC CCCAAACAA
2001 ACTCGCCCGC TACGAAACGC GCACGCCCGG ACACCATATG CTCACCTCG
2051 GCGCAAACCTA CCGCCGCAAT ACGCGCTATG GCGAGTGGAA TTGGTACGTC
2101 AAAGCCGACA ACCTGCTCAA CCAATCCGTT TACGCCACA GCAGCTTTCT
2151 CTCTGATACG CCGCAAATGG GCCGCAGCTT TACCGCGCGC GTGAACGTGA
2201 AGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 586; ORF 147>:

```

m147.pep (partial)
1 ..PHKTEQSVDL ETVSVVGKSR PRATSGLLHT STASDKIISG DTLRQKAVNL
51 GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGE TGDMAFSPD
101 HAIMVDTALS QQVEILRGPV TLLYSSGNVA GLVDVADGKI PEKMPENGVS
151 GELGLRLSSG NLEKLTSGGI NIGLGKNEVL HTEGLYRKSG DYAVPRYRNL
201 KRLPDSHADS QTSIGLSWV GEKGFIVGAY SDRRDQYGLP AHSHEYDDCH
251 ADIIWQKSLI NKRYLQLYPH LLTEEDIDYD NPGLSCGFHD DDNAHAHTHS
301 GRPWIDLRNK RYELRAEWKQ PFPGFALRV HLNRRNDYRH EKAGDAVENF
351 FNNQTQNAI ELRHQPIGRL KGSWGVQYLQ QKSSALS AIS EAVKQPMLLD
401 NKVQHYSEFFG VEQANWDNFT LEGGVRVEKQ KASIQYDKAL IDRENYNHP
451 LPDLGAHRQT ARSFALSGNW YFTPOHKLSL TASHQERLPS TOELYAHGKH
501 VATNTFEVGN KHLNKERSNN IELALGYEGD RWQYNLALYR NRGNYIY AQ
551 TLNDGRGPKS IEDDSEMKLV RYNQSGADFY GAEGEIYFKP TPRYRIGVSG
601 DYVRGRKLNK PSLPGREDAY GNRPFIAQDD QNAPRVPAAR LGFHLKASLT
651 DRIDANLDYY RVFAQNKLAR YETRTPGHHM LNLGANYRRN TRYGEWNWYV
701 KADNLLNQSV YAHSSFLSDT PQMGRSFTGG VNVKF*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m147 / g147 92.3% identity in 142 aa overlap

```

m147.pep          10      20      30
                  PHKTEQSVDL ETVSVVGKSR PRATSGLLHTS
g147              MRREAKMAQITLKP IVLSILLINTPLLAQAHETE QSVGLETVSVVGKSR PRATSGLLHTS
                  10      20      30      40      50      60
m147.pep          40      50      60      70      80      90
                  TASDKIISGDTLRQKAVNLGDALDGVPGI HASQYGGGASAPVIRGQTGRRIKVLNHHGET
g147              TASDKIISGDTLRQKAVNLGDALDGVPGI HASQYGGGASAPVIRGQTGRRIKVLNHHGET
                  70      80      90      100     110     120
m147.pep          100     110     120     130     140     150
                  GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGLVDVADGKIPEKMPENGVS
g147              GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGAGQCCRWNPKNA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 587>:

a147.seq

```

1   ATGCGACGAG AAGCCAAAAT GGCACAAACT ACAC TCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CTCCCAAGCG CATGGAAC TG
101 AGCAATCAGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTC CG
151 CGCGCCACTT CGGGGCTGCT GCACACTTCT ACCGCTCCG ACAAATCAT
201 CAGCGGCGAC ACCTTGGGAC AAAAAGCCGT CAACTTGGGT GATGCTTTAG
251 ACGGCGTACC GGGCATT CAT GCCTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC AGGCAGACGG ATTAAAGTGT TGAACCATCA
351 CGGCGAAACG GGCACATGG CGGACTTCTC TCCAGACCAT GCAATCATGG
401 TGGACAGCGC CTTGTGCGAA CAGGTCGAAA TCCTGCGCGG TCCGGTTACG
451 CTCTTGTA CA GCTCGGGCAA TGTGGCGGGG CTGGTCGATG TTGCCGATGG
501 CAAAATCCCC GAAAAATG C TGAAAACGG CGTATCGGGC GAACTCGGAT
551 TGGCTTTGAG CAGCGCAAT CTGGAAAAAC TCACGTCCGG CGGCATCAAT
601 ATCGGTTTGG GCAAAAAC TTGATTGCAC ACGGAAGGGC TGTACCGCAA
651 ATCGGGGGAT TACGCCGTAC CGCGTTACCG CAATCTGAAA CGCCTGCCCG
701 ACAGCCACGC CGATTGCAA ACGGGCAGCA TCGGGCTGTC TTGGGTTGGC
751 GAAAAAGGCT TTATCGGCGC AGCATACAGC GACCGTCGCG ACCAATATGG
801 TCTGCCTGCC CACAGCCACG AATACGATGA TTGCCACGCC GACATCATCT
851 GGC AAAAGAG TTTGATTAA C AAACGCTATT TGCAGCTTTA TCCGCACCTG
901 TTGACCGAAG AAGACATCGA TTACGACAAT CCGGGCTTGA GCTGCGGCTT
951 TCACGACGAC GATGATGCAC ACGCCCATGC CCACAACGGC AAACCTTGGA
1001 TAGACCTGCG CAACAAACGC TACGAACTCC GCGCCGAATG GAAGCAACCG
1051 TTCCCCGGTT TTGAAGCCCT GCGCGTACAC CTGAACCGCA ACGACTACCG
1101 CCACGACGAA AAAGCAGGCG ATGCAGTAGA AAAC TTTTTT AACAACCAA
1151 CGCAAAACGC CCGTATCGAG TTGCGCCACC AACC CATAGG CCGTCTGAAA
1201 GGCAGCTGGG GCGTGCAATA TTTGGGACAA AAATCCAGTG CTTTATCTGC
1251 CACATCCGAA GCGGTCAAAC AACCGATGCT GCTTGACAAT AAAGTGCAAC
1301 ATTACAGCTT TTTCGGTGTA GAACAGGCAA ACTGGGACAA CTTACGCTT
1351 GAAGGCGGCG TACGCGTGA AAAACAAAAA GCCTCCATCC GCTACGACAA
1401 AGCATTGATT GATCGGGAAA ACTACTACAA CCATCCCCTG CCCGACCTCG
1451 GCGCGCACCG CCAAACCGCC CGCTCATTCG CACTTTCGGG CAACTGGTAT
1501 TTCACGCCAC AACACAACT CAGCCTGACC GCCTCCATC AGGAACGCCT
1551 CCCGTCAACG CAAGAGCTGT ACGCACACGG CAACACGTC GCCACCAAC
1601 CCTTTGAAGT CGGCAACAAA CACCTCAACA AAGAGCGTTC CAACAATATC
1651 GAACTCGGCG TGGGCTACGA AGGCGACCGC TGGCAATACA ATCTGGCACT
1701 CTACCGCAAC CGCTTCGGCA ACTACATTTA CGCCCAAACC TTAAACGACG
1751 GACGCGGCCC CAAATCCATC GAAGACGACA GCGAAATGAA GCTCGTGCGC
1801 TACAACCAAT CCGGTGCGGA CTTCTACGGC GCGGAAGGCG AAATCTACTT
1851 CAAACCGACA CGCGCTACC GCATCGGCGT TTCCGCGGAC TATGTACGAG
1901 GCCGTCTGAA AAACCTGCCT TCCCTACCCG GCAGGGAAGA CGCCTACGGC
1951 AACC GCCCAC TCATTGCCCA AGCCGACCAA AACGCCCTC GCCTTCCGGC
2001 TCGCGCGCTC GCGGTCCACC TGAAGCCTC GCTGACCGAC CGCATCGATG
2051 CCAATTGGA CTACTACGCG GTGTTGCGCC AAAACAACT CGCCCGTAC
2101 GAAACGCGCA CGCCCGGACA CCATATGCTC AACCTCGGCG CAAACTACCG
2151 CCGCAATACG CGCTATGGCG AGTGAATTG GTACGTCAA GCGGACAACC
2201 TGCTCAACCA ATCCGTTTAC GCCCACAGCA GCTTCCTCTC TGATACGCCG
2251 CAAATGGGCC GCAGCTTTAC CGGCGGCGTG AACGTGAAGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 588; ORF 147.a>:

a147.pep

```

1   MRREAKMAQT TLKPIVLSIL LINTPLLSQA HGTEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFSPDH AIMVDSALSQ QVEILRGFVT
151 LLYSSGNVAG LVDVADGKIP EKMPENGVS G ELGLRLSSGN LEKLTSGGIN
201 IGLGKNFVLH TEGLYRKSGD YAVPRYRNK RLPDSHADSQ TSGISLSWVG
251 EKGFIGAAYS DRRDQYGLPA HSHEYDDCHA DIIWQKSLIN KRYLQLYPHL
301 LTEEDIDYDN PGLSCGFHDD DDAHAHAHNG KPWIDLNRKR YELRAEWKQP
351 FPGFEALRVH LNRNDYRHE KAGDAVENFF NNQTONARIE LRHQPIGRLL
401 GSWGVOYLQ KSSALSATSE AVKQPMLLDN KVQHYSFEGV EQANWDNFTL
451 EGGVRVEKQK ASIRYDKALI DRENYYNHPL PDLGAHQRTA RSFALSGNWY
501 FTPQHKLSLT ASHQERLPST QELYAHGKHV ATNTFEVGNK HLNKERSNNI
551 ELALGYEGDR WQYNLALYRN RFGNYIYAQT LNDGRGPKSI EDDSEMKLVR

```

601 YNQSADFYG AEGEIYFKPT PRYRIGVSGD YVRGLKNLP SLPGREDAYG
651 NRPLIAQADQ NAPRVFAARL GVHLKASLTD RIDANLDYYR VFAQNKLARY
701 ETRTPGHML NLGANYRNT RYGEWNWYVK ADNLLNOSVY AHSSFLSDTP
751 QMGRSFTGGV NVKF*

m147/a147 98.1% identity in 734 aa overlap

m147.pep				10	20	30
				PHKTEQSV	DET	TVSVVGKSRPRATSGLLHTS
a147	MRREAKMAQTTLKPIVLSILLINTPLLSQA	HGT	QSV	GL	ET	TVSVVGKSRPRATSGLLHTS
	10	20	30	40	50	60
m147.pep	40	50	60	70	80	90
	TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGET				
a147	TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGET				
	70	80	90	100	110	120
m147.pep	100	110	120	130	140	150
	GDMADFS	PDHAIMVDTALSQQVEILRG	PVTLLYSSGNVAGLVDVADGKIPEKMPENGVS			
a147	GDMADFS	PDHAIMVDSALSQQVEILRG	PVTLLYSSGNVAGLVDVADGKIPEKMPENGVS			
	130	140	150	160	170	180
m147.pep	160	170	180	190	200	210
	ELGLRLSSGNLEKLTSGGINIGLGNFV	LHTEGLYRKSGDYAVPRYRNLKRLPDSHADSQ				
a147	ELGLRLSSGNLEKLTSGGINIGLGNFV	LHTEGLYRKSGDYAVPRYRNLKRLPDSHADSQ				
	190	200	210	220	230	240
m147.pep	220	230	240	250	260	270
	TGSIGLSWVGEKGFIGVAYS	DRRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHL				
a147	TGSIGLSWVGEKGFIGAAYS	DRRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHL				
	250	260	270	280	290	300
m147.pep	280	290	300	310	320	330
	LTEEDIDYDNPG	LSCGFHDDDNAHAH	THSGRPWIDLRNKRYELRAEWKQPFPGFEALRVH			
a147	LTEEDIDYDNPG	LSCGFHDDDAHAH	ANGKRPWIDLRNKRYELRAEWKQPFPGFEALRVH			
	310	320	330	340	350	360
m147.pep	340	350	360	370	380	390
	LNRNDYRHDEKAGDAVENFF	NNQTQNARIELRHQPIGRLKGSWG	VQYLGQKSSALSATSE			
a147	LNRNDYRHDEKAGDAVENFF	NNQTQNARIELRHQPIGRLKGSWG	VQYLGQKSSALSATSE			
	370	380	390	400	410	420
m147.pep	400	410	420	430	440	450
	AVKQPM	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIQYDKALIDRENYNHPL				
a147	AVKQPM	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPL				
	430	440	450	460	470	480
m147.pep	460	470	480	490	500	510
	PDLGAHRQTARSFALSGN	WYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
a147	PDLGAHRQTARSFALSGN	WYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
	490	500	510	520	530	540
m147.pep	520	530	540	550	560	570
	HLNKERSNNIELALGYEG	DRWQYNLALYRNRF	GNIIYAQTLNDGRGPKSIEDDSEMKLVR			
a147	HLNKERSNNIELALGYEG	DRWQYNLALYRNRF	GNIIYAQTLNDGRGPKSIEDDSEMKLVR			

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	550	560	570	580	590	600
	580	590	600	610	620	630
m147 . pep	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFI AQDDQ					
a147	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFI AQADQ					
	610	620	630	640	650	660
	640	650	660	670	680	690
m147 . pep	NAPRVPAARLGFHLKASLTDRIDANLDYYRVFAQNK LARYETRTPGHHMLNLGANYRRNT					
a147	NAPRVPAARLGVHLKASLTDRIDANLDYYRVFAQNK LARYETRTPGHHMLNLGANYRRNT					
	670	680	690	700	710	720
	700	710	720	730		
m147 . pep	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
a147	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750	760		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 589>:

```

g148 . seq
1  ATGGCGTTAA AAACATCAAA CTTGGAACAC GCAATGctgg ttcaTCCCGA
51  AgctATgagt gtcggcgCGC TTGccgAcaa AATCCGCAAA AtcgaAAact
101 gGCCGCAAAA AGgcaTCTTA TTCCACGACA TCACGCCCGT CCTGCAAAGT
151 GCGGAATACT TCCGCCTTTT GGTGCGATTG CTGGTTTACC GCTATATGGA
201 TCAGAAAATC GACATCGTTG CCGGCTTGGA CGCGCGCGGC TTCATTATCG
251 GCGCGGCACT CGCCTACCAG CTCaACGtcg gctTCGTCCC CATCCGCAAA
301 AAAGGCAAGC TGCCTTTTGA AACCGTATCG CAAAGCTAcg cgcTCGAATA
351 CGGGGAAGCT GCGGTGGAAA TCCACACCGa tgccgTCAAA CCGGTTTCGC
401 GCGTCCTGCT GGTGCGATGAT TTGGTTGCCA CGGGCGGCAC AATGCTTGCC
451 GGGCTGGAAC TGATCCGCAA ACTCGGCGGG GAAATTGTGCG AAgccgcccG
501 CATTTTGGAA TTTACCGACC TTCAAGCGCG CAAGAATATC CGCGCAAGTG
551 GCGCGCCCTT ATTTACCCTG CTTCAAAACG AAGGCTGCAT GAAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 590; ORF 148.ng>:

```

g148 . pep
1  MALKTSNLEH AMLVHPEAMS VGALADKIRK IENWPQKIL FHDITPVLQS
51  AEYFRLLVDL LVYRYMDQKI DIVAGLDARG FIIGAALAYQ LNVGFVPiRK
101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK PGRVLLVDD LVATGGTMLA
151 GLELIRKLGG EIVEAAAIL EFDLQGGKNI RASGAPLFTL LQNEGCMKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 591>:

```

m148 . seq
1  ATGGCGTTAA AAACATCAAA CTTGGAACAC GCAATGCTGG TTCATCCCGA
51  AGCTATGAGT GTCGGCGCGC TTGCCGACAA AATCCGCAAA ATCGAAAAC
101 GGCCGCAAAA AGGCATCTTA TTCCACGACA TCACGCCCGT CCTTCAAAGC
151 GCGGAATACT TCCGCCTTTT GGTGATTGTA TTGGTTTACC GCTATATGGA
201 TCAGAAAATC GACATCGTTG CCGGTTTGGA CGCGCGCGGC TTCATTATCG
251 GCGCGGCACT CGCCTACCAG CTCaACGTCG GTTTCGTCCC CATCCGCAAA
301 AAAGGCAAGC TGCCTTTTGA AACCGTATCG CAAAGCTACG CGCTCGAATA
351 CGGGGAAGCT GCGGTGGAAA TCCACACCGA TGCCGTCAAA CTCGGTTTCGC
401 GCGTCCTGCT GGTGCGATGAT TTGATTGCCA CGGGCGGCAC GATGCTTGCC
451 GGAAGGCAAC TGATCCGCAA ACTCGGCGGA GAAATTGTGCG AAGCCGCGCG
501 CATTTTGGAA TTTACCGACC TTCAAGGCGG CAAGAATATC CGTGCAAGCG
551 GCGCGCCCTT ATTTACCCTG CTTCAAAACG AAGGCTGTAT GAAGGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 592; ORF 148>:

```

m148 . pep
1  MALKTSNLEH AMLVHPEAMS VGALADKIRK IENWPQKIL FHDITPVLQS
51  AEYFRLLVDL LVYRYMDQKI DIVAGLDARG FIIGAALAYQ LNVGFVPiRK

```


101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK LGSRVLLVDD LIATGGTMLA
 151 GLELIRKLGG EIVEAAAILE FTDLQGGKNI RASGAPLFTL LQNEGCMKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m148 / g148 99.0% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
g148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m148.pep	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
g148	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m148.pep	AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
g148	AVEIHTDAVKPGSRVLLVDDLVATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
	130	140	150	160	170	180
	190	200				
m148.pep	RASGAPLFTLLQNEGCMKGX					
g148	RASGAPLFTLLQNEGCMKGX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 593>:

a148.seq

1	ATGGCGTTAA	AAACATCAAA	CTTGGAACAC	GCAATGCTGG	TTCATCCCGA
51	AGCTATGAGT	GTCGGTGCGC	TTGCCGACAA	AATCCGCAAA	ATCGAAAAC
101	GGCCGCAAAA	AGGCATCTTA	TTCCACGACA	TCACGCCCGT	CCTGCAAAGC
151	GCGGAATACT	TCCGACTTTT	GGTTGATTTA	TTGGTTTACC	GCTATATGGA
201	TCAGAAAATC	GACATCGTTG	CCGGTTTGGA	CGCGCGCGGC	TTCATTATCG
251	GCGCGGCACT	CGCCTACCAG	CTCAACGTCG	GTTTCGTCCC	CATCCGCAAA
301	AAAGGCAAGC	TGCCTTTTGA	AACCGTATCG	CAAAGCTACG	CGCTCGAATA
351	CGGGGAAGCT	GCGGTGGAAA	TCCACACCGA	TGCCGTCAAA	CTCGGTTTCG
401	GCGTGCTGCT	GGTCGATGAT	TTGGTTGCCA	CGGGCGGCAC	GATGCTTGCC
451	GGAATGGAGC	TGATCCGCAA	ACTCGGCGGG	GAAATTGTCG	AAGCCGCCGC
501	CATTTTGGA	TTTACCGACC	TTCAAGGCGG	CAAGAATATC	CGTGCAAGCG
551	GCGCGCCCTT	ATTTACCCTG	CTTCAAAACG	AAGGCTGTAT	GAAGGGCTGA

This corresponds to the amino acid sequence <SEQ ID 594; ORF 148.a>:

a148.pep

1	MALKTSNLEH	AMLVHPEAMS	VGALADKIRK	IENWPQKGIL	FHDITPVLQS
51	AEYFRLLVDL	LVYRYMDQKI	DIVAGLDARG	FIIGAALAYQ	LNVG FVPIRK
101	KGKLPFETVS	QSYALEYGEA	AVEIHTDAVK	LGSRVLLVDD	LVATGGTMLA
151	GLELIRKLGG	EIVEAAAILE	FTDLQGGKNI	RASGAPLFTL	LQNEGCMKG*

m148/a148 99.5% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
a148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m148.pep  LVYRYMDQKIDIVAGLDARGFTIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
|||||
a148      LVYRYMDQKIDIVAGLDARGFTIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
              70      80      90      100     110     120

              130      140      150      160      170      180
m148.pep  AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
|||||
a148      AVEIHTDAVKLGSRVLLVDDLVATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
              130      140      150      160      170      180

              190      200
m148.pep  RASGAPLFTLLQNEGCMKGX
|||||
a148      RASGAPLFTLLQNEGCMKGX
              190      200

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 595>:

```

g149.seq
1   ATGTTGATTG ACAACAATGT CCGCCATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
101 AAAAAAGCCTC CATCCGGTAC GACAAAGCAT TGATTGATCG AGAAAACTAC
151 TACAACCAGC CCCTGCCCCG CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 GTTCGCACTT TCGGGCAACT GGTATTTTAC GCCACACCAC AAATCAGCC
251 TGACCGCCTC CCATCAGGAa cgCCTGCCGT CAACGCaaga actGtACgca
301 cacggcAAGC ACGtcgccac CAACACCTTT GAagtcgga acaaACACCT
351 CAACAAAGaG CgttccaacA atatcgaACT CGCGCTGGgc tAcaaaggcg
401 accGCTGGCA ATACAATCTG GCAGCTTACC GCAACCGaTt CGGCAACTAC
451 ATTTACGCCC AAACCTTAaa cgacggacgC GGCCCCAAAT CCATCgaaga
501 cgacagcgaa ATGaagcTCG TCGCTACAA CCAATCCGGT GCCGACTTCT
551 ACgGcgcgga aggcgaaatc tACTTcaaaC CGAcACCGCG CTACCGCATC
601 GGTGTTTCCG GCGACTatgt acgaggcgT CTGAAAAACC TGCCGTCCCT
651 ACCCGGCAGG gaagatccCT AcggcAAACG TCccttcaTC GCACAAGCCG
701 ACCAAACGC CCCCCGCATT ccggctGCGC GCCTCGGCTT CCACCTGAAA
751 ACCTCGCTAA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCCGGTGTT
801 CGCCCAAAAC AAATCGCCC GCTACGAAAC GCGTACGCCC GGACACCATA
851 TGCTCAACCT CGGTGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGTTACG TCAAAGCCGA CAACCTGTct aACcaatCcg tTTACGCCCa
951 cAGCAGCTTC CTCTCTGATA CGCCGCAAat gGGCCGcAGC TTTgcccGcG
1001 gcgtaAACGT GaAGTTttaA

```

This corresponds to the amino acid sequence <SEQ ID 596; ORF 149.ng>:

```

g149.pep
1   MLIDNNVRHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51  YNQPLPDLGA HRQTARSFAL SGNWYFTPHH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YKDRWQYNL AAYRNRFGNY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVSGDYVRGR LKNLPSLPGR EDPYGKRPFi AQADQNAPRI PAARLGfHLK
251 TSLTDRIDAN LDYRVFAQN KLARYETRTP GHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FAGGVNVKf*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 597>:

```

m149.seq
1   ATGCTGCTTG ACAACAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATGCG GACAACTTCA CGCTTGAAGG AGGCGTACGC GTGGAAAAAC
101 AAAAAAGCCTC CATTCACTAC GACAAAGCAT TGATTGATCG GGAAAACTAC
151 TACAACCACC CCCTGCCCCG CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 ATTCGCACTT TCGGGCAACT GGTATTTTAC GCCACAACAC AAATCAGCC
251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
301 CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAAACACCT
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGTAACTAC

```

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451  ATTTACGCCC AAACCTTAAA CGACGGACGC GGCCCCAAAT CCATCGAAGA
501  CGACAGCGAA ATGAAGCTCG TCGCTACAA CCAATCCGGC GCCGACTTCT
551  ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC
601  GCGGTTTCCG GCGACTATGT ACGAGGCGGT CTGAAAAACC TGCCTTCCCT
651  ACCCGGCAGA GAAGATGCCT ACGGCAACCG TCCTTTCATC GCACAGGACG
701  ACCAAAATGC CCCCCGTGTT CCGGCTGCGC GCCTCGGCTT CCACCTGAAA
751  GCCTCGCTGA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
801  CGCCCAAAAC AAACCTCGCCC GCTACGAAAC GCGCACGCCC GGACACCATA
851  TGCTCAACCT CGGCGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901  AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCAATCCG TTTACGCCCA
951  CAGCAGCTTT CTCTCTGATA CGCCGCAAAT GGGCCGCGAG TTTACCGGCG
1001 GCGTGAAAGT GAAGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 598; ORF 149>:

m149.pep

```

1  MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIQY DKALIDRENY
51  YNHPLPDLGA HRQTARFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFNGY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQS GADFYGAEGEI YFKPTPRYRI
201 GVSGDYVRGR LKNLPSLPGR EDAYGNRPFI AQDDQONAPRV PAARLGFHLK
251 ASLTDRIDAN LDYRVFAQN KLARYETRTP GHHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKFX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 149 shows 95.9% identity over a 339 aa overlap with a predicted ORF (ORF 149.ng) from *N. gonorrhoeae*:

m149/g149

m149.pep	10	20	30	40	50	60
	MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIQYDKALIDRENY NHPLPDLGA					
g149	MLIDNNVRHYSFFGVEQANW DNFTLEGGVR VEKQKASIRYDKALIDRENY NQPLPDLGA					
	10	20	30	40	50	60
m149.pep	70	80	90	100	110	120
	HRQTARFALSGNWYFTPQH KLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
g149	HRQTARFALSGNWYFTP HHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
m149.pep	130	140	150	160	170	180
	RSNNIELALGYEGDRWQYNLALYRNRFNGYIYAQTLNDGRGPKSIEDDSEM KLVRYNQS					
g149	RSNNIELALGYKDRWQYNLAAYRNRFNGYIYAQTLNDGRGPKSIEDDSEM KLVRYNQS					
	130	140	150	160	170	180
m149.pep	190	200	210	220	230	240
	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGR LKNLPSLPGRE DAYGNRPFI AQDDQONAPRV					
g149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGR LKNLPSLPGRE DPYGRPFIAQADQONAPRI					
	190	200	210	220	230	240
m149.pep	250	260	270	280	290	300
	PAARLGFHLKASLTDRIDANLDYRVFAQNKLARYETRTPGH HMLNLGAN YRRNTRYGEW					
g149	PAARLGFHLKTSLTDRIDANLDYRVFAQNKLARYETRTPGH HMLNLGAN YRRNTRYGEW					
	250	260	270	280	290	300
m149.pep	310	320	330	340		
	NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					

g149 NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFAGGVNVKFX
310 320 330 340

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 599>:

a149.seq
1 ATGCTGCTTG ACAATAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA
51 GGCAAAGCTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATCCGCTAC GACAAAGCAT TGATTGATCG GGAAACTAC
151 TACAACCATC CCCTGCCGGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 ATTCGCACTT TCGGGCAACT GGTATTTTAC GCCACAACAC AAATCAGCC
251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
301 CACGCGAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAAACACCT
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGCGC
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGCAACTAC
451 ATTTACGCCC AAACCTTAAA CGACGGACGC GGCCCCAAAT CCATCGAAGA
501 CGACAGCGAA ATGAAGCTCG TGCCTACAA CCAATCCGGT GCGGACTTCT
551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC
601 GCGCTTTCG GCGACTATGT ACGAGGCCGT CTGAAAAACC TGCCTTCCCT
651 ACCCGGCAGG GAAGACGCCT ACGGCAACCG CCCACTCATT GCCCAAGCCG
701 ACCAAAACGC CCCTCGCGTT CCGCTGCGC GCCTCGCGCT CCACCTGAAA
751 GCCTCGCTGA CCGACCGCAT CGATGCCAAT TTGGACTACT ACCGCGTGT
801 CGCCCAAAC AAACCTGCCC GCTACGAAAC GCGCAGGCC GGACACATA
851 TGCTCAACCT CGGCGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCAATCCG TTTACGCCCA
951 CAGCAGCTTC CTCTCTGATA CGCGCAAAT GGGCCGCAGC TTTACCGCGC
1001 GCGTGAACGT GAAGTTTAA

This corresponds to the amino acid sequence <SEQ ID 600; ORF 149.a>:

a149.pep
1 MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51 YNHPLPDLGA HRQTARSFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFGNY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVSGDYVRGR LKNLPSLPGR EDAYGNRPLI AQADQNAPRV PAARLGVHLK
251 ASLTDRIAN LDYYRVFAQN KLARYETRTP GHMMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF*

m149/a149 98.8% identity in 339 aa overlap

m149.pep	10	20	30	40	50	60
	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIYQYDKALIDRENYYNHPLPDLGA					
a149	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYYNHPLPDLGA					
	10	20	30	40	50	60
m149.pep	70	80	90	100	110	120
	HRQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
a149	HRQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
m149.pep	130	140	150	160	170	180
	RSNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMKLVRYNQSG					
a149	RSNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMKLVRYNQSG					
	130	140	150	160	170	180
m149.pep	190	200	210	220	230	240
	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGR LKNLPSLPGREDAYGNRPPIAQDDQNAPRV					
a149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGR LKNLPSLPGREDAYGNRPPIAQADQNAPRV					
	190	200	210	220	230	240
m149.pep	250	260	270	280	290	300
	PAARLGFHLKASLTDRIANLDYYRVFAQNKLARYETRTPGHMMLNLGAN YRRNTRYGEW					

g149-1.seq

1	ATGGCACAAA	TCACACTCAA	ACCCATTGTT	TTATCAATTC	TTTTAATCAA
51	CACACCCCTC	CTCGGCCAAG	CGCATGAAAC	TGAGCAATCG	GTGGGCTTGG
101	AAACGGTCA	CGCTGTCGGC	AAAAGCGCTC	CGCGCGCGAC	TTCCGGGGCTG
151	CTGCACACTT	CGACGCGCTC	CGACAAAATC	ATCTCCGGCG	ATACCTTTGCG
201	CCAAAAAGCC	GTCAACTTGG	GCACGCTTT	GGACGCGCTA	CCGGGCTATCC
251	ACGCTTCCGA	ATACGGCTGG	GGCGCATCCG	CTCCGGTTAT	CGCGCGTCAAT
301	ACGGGCAGAC	GGATTAAAGT	ATTGAACCAT	CACGGCGAAA	TGGCGGTATAT
351	GCGGACTTTT	TCTCCCGATC	ACGCCATTAT	GGTAGATACC	GCCTTGTCGC
401	AAACAGTTGA	AATCTCGTGC	GGGCGGTTCT	CGCTCTTGTA	CAGCTCCGGT
451	AATGTGGCGG	GGCTGGTCCG	TGTTGGCGAT	GGAAAAATCC	CGGAAAAAAT
501	GCTTGAAAAC	GGCGTATCGG	GCgaagccgG	ATTGCGTTTG	AGCAGCGGCA
551	ATTTGAAAAA	ACTGACATCC	GCAGGCATCA	ATATCGGACT	GGGCAAAAAC
601	TTCGTGTGTC	ATACCGAAGT	CTTGATCCGC	AAATCGGGCG	ATTACGCCGT
651	ACCGCGTTAC	CGCAATCTGA	AACGCGTGCC	CGACAGCCAT	CGCGATTTCG
701	AAACGGGCGC	CATCGGGCTG	CTTGTGGGTG	GCGAAAAAGG	CTTTATCGGC
751	GAGCATACAG	GCGACCGTCG	CGACCCTAC	GGCCTGCGCT	CCCAACGCCA
801	CGAATACGAT	GATTGCCACG	CGCATCTCAT	CTGGCAAAAG	AGTTTGATCA
851	ACAAACGCTA	TTTGACGCTT	TATCCGCACT	TGTTGACCGA	AGAAGACATC
901	GATTACGACA	ATCCGGGCTT	GAGCTGCGGC	TTCACCGAGC	GCGACGGTGC
951	ACACGCACAC	ACCCACAACG	GCAAAACGTG	GATAGACCTG	CGCAACAAAC
1001	GCTACGAACT	CCGCGCCGAA	TGGAAGCAGC	CATTCCCCGG	TTTTGAAGCC
1051	CTCGCGGTAC	ATCTGAACCC	CAATGACTAC	CACCACGACG	AAAAAGCAGG
1101	CGATGCAGTA	GAAAATCTCT	TCAACAACAA	AACACAACAAC	GCGCGTATCG
1151	AGTTGCGCCA	CCAACCCATA	GGCCGTCTGA	AAGGCAGCTG	GGGCGTGCAA
1201	TATTTGGGAC	AAAAATCCAG	CGCGCTTTCC	GCCATTCCCG	AAACCGTGCA
1251	ACAACCGATG	TTGATTGACA	ACAATGTCCG	CCATTACAGC	TTTTTCGGTG
1301	TAGAACAGGC	AAATTGGGAC	AACTTCACGC	TTGAAGGCGG	CGTAGCGGTG
1351	GAAAAACAAA	AAGCCTCCAT	CCGGTACGAC	AAAGCATTTA	TTGATCGAGA
1401	AAACTACTAC	AACACAGCCC	TGCCCGACCT	CGGCGCGCAC	CGCCAAACCG
1451	CCCGCTCGTT	CGCATCTTCG	GGCAACTGGT	ATTTCACGCC	ACACCAACAA
1501	CTCAGCTCAG	CCGCTCCCA	TACGAAAGCA	CTGCGGTCAA	CGCAAGAACT
1551	GTAGCCACAG	GGCAAGCAGC	TCGCCACCAA	CACCTTTGAA	GCTGCGCAACA
1601	AAACACTCAA	CAAGAGCGGT	TTCAACAAATA	TCAAGCTCGC	GTGCGGCTAC
1651	GAAGGCGACC	GCTGGCAATA	CAATCTGGCA	GCCTACCGCA	ACCGATTTCG
1701	CAACTACATT	TACGCGCAAA	CCTTAAACGA	CGGACGCGCG	CCCAAAATCCA
1751	TCGAAGACGA	CAGCGAAATG	AAGCTCGTGC	GCTACAAACCA	ATCCGGTGGC
1801	GACTTCTACG	GCGCGGAAGG	CGAAATCTAC	TTCAAACCGA	CACCGCGCTA
1851	CCGCTACGGT	GTTTCGGGCG	ACTATGTACG	AGGCCGTCTG	AAAAACCTGC
1901	CGTCCCTACC	CGGGAGGGAA	GATCCCTACG	GCAAAAGTCC	CTTCATCGCA
1951	CAAGCCGACC	AAAACGCCCC	CCGCATTCCG	GCTGCGCGCC	TTCGCTTCCA
2001	CCTGAAAAAC	TCGCTAACCG	ACCGTATCGA	TGCCAATTTG	GACTACTACC
2051	GCGTGTTCCG	CCAAAACCAA	CTGCCCCGCT	ACGAAAACGG	TACGCGCCGA
2101	CACCATATGC	TCAAACCTCG	TGCAAACTAC	CGCGCGAATA	CGCGCTATGG
2151	CGAGTGGAA	TGGTAGCTCA	AAGCGACCAA	CCTGCTCAAC	CAATCCGTTT
2201	ACGCGCCACG	CAGCTTCTCT	TCGTGATACG	CGCAAAATGG	CCGCAGCTTT
2251	ACCGCGGGCG	TAAACGTGAA	GTTTTAA		

q149-1.pap

1	MAQITLKPIV	LSILLINTPL	LAQAHETEQS	VGLETVSVVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRQKA	VNLGDALDGV	PGIHASQYGG	GASAPVLYRG
101	TGRRIKVNLN	HGETGDMADF	SPDHAIMVDT	ALSQQVEILR	GPVTLLYSSQ
151	NVAGLVVDVAD	GKTIPEKMPEN	GVSGEAGLRL	SSNGLEKLTs	AGINIGLGKN
201	FVLHTEGLRY	KSGDYAVPRY	RNLKRLPDSh	ADsQTGSIGL	SWVGKEGFTG
251	AAYSDNDRDRY	GLPAHSHEYD	DCHADIIWQK	SILINKRYLQL	YQPHLLTEEDI
301	YDYNPGLSCG	FHDGDGAHAH	THNGKPIWDL	RNKRYELRAE	WKPFPGPEFA

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351 LRVHLNRNDY HHDEKAGDAV ENFFNNKTHN ARIELRHQPI GRLKGSWGVQ
401 YLGQKSSALS AIPETVQQPM LIDNNVRHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NQPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA AYRNRFNGYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSLPGRE DPYGKRPFIA
651 QADQNAPIRI AARLGPHLKT SLTDRIDANL DYYRVFAONK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 603>:

m149-1.seq

```

1 ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTTAATCAA
51 CACACCCCTC CTCGCCCAAG CGCATGAAAC TGAGCAATCG GTGGATTGCG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGGCCAC GTCGGGGCTG
151 TTGCACACTT CGACCGCCTC CGACAAAATC ATCTCCGGCG ATACCTTGCG
201 CCAAAAAGCC GTCAACTTGG GCGACGCTTT AGACGGCGTA CCGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GCGCGCTCTG CTCCCGTCAT TCGCGGTCAA
301 ACAGGCAGGC GGATTAAAGT GTTGAACCAT CACGGCGAAA CAGGCGATAT
351 GCGCGATTTT TCGCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTCGC
401 AACAGGTCGA AATCCTGCGC GGGCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCTGA TGTGCGCAT GGCAAAATCC GCGAAAAAAT
501 GCCTGAAAAC GCGGTATCGG GCGAACTCGG ATTGCGTTTG AGCAGCGGCA
551 ATCTGAAAAA ACTCACGTCC GCGCGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCGCGTTCC CGCAATCTGA AACGCCGTCC CGACAGCCAC CCGGATTTCG
701 AAACGGGCGA CATCGGGCTG TCTTGGGTG GCGAAAAGG TTTTATCGGC
751 GTAGCGTACA GCGACCGTCG CGACCAATAT GGTCTGCCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGCTTGATTA
851 ACAAACGCTA TTTACAGCTT TATCCGCACC TGTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTCCACGACG ACGATAATGC
951 ACACGCACAC ACCCACAGCG GCAGACCGTG GATAGACCTG CGCAACAAC
1001 GCTAGCAACT CCGTGCCGAA TGGAAACAAAC CGTTCCCGCG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCAGTC GAAAACCTTT TTAACAACCA AACGCAAAAC GCCCGCATCG
1151 AGTTGCGCCA CCAACCCATA GGTGCTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTTACAAC AAAAATCCAG TGCTTTATCT GCCATATCCG AAGCGGTAA
1251 ACAACCGATG CTGCTTGACA ACAAGTGCA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGCG AACTGGGAC AACTTCACGC TTGAAGGAGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT TCAGTACGAC AAAGCATTGA TTGATCGGGA
1401 AAATACTACT AACCAACCCC TGCCCGACCT CGCGCGCAC CGCCAAACCG
1451 CCCGCTCATT CGCACTTTCG GGCAACTGGT ATTTACGCCC ACAACACAAA
1501 CTCAGCCTGA CCGCCTCCCA TCAGGAACGC CTGCGCTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAAACACG TCGCCACCAA CACCTTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGCGGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 TAACTACATT TACGCCCAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GTTACAACCA ATCCGGCGCC
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTCCGGCG ACTATGTACG AGGCCGCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGAGAA GATGCCTACG GCAACGTCC TTTTATCGCA
1951 CAGGACGACC AAAATGCCCC CCGTGTTCGG GCTGCGCGCC TCGGCTTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGTATCGA TGCCAATTG GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAAACTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAAT TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTTCTC TCTGATACGC CGCAATGGG CCGCAGCTTT
2251 ACCGCGGCGG TGAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 604; ORF 149-1>:

m149-1.pep

```

1 MAQTLKPIV LSILLINTPL LAQAHETEQS VDLETVSUVG KSRPRATSG
51 LHTSTASDKI ISGDTLROKA VNLGDALDGV PGIHASQYGG GASAPVIRGO
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDT ALSQQVEILR GPVTLLYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSSELGLRL SSGNLEKLT SGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIG
251 VAYSRRRDQY GLPAHSHEYD DCHADIIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPNGLSCG FHDDDNAHAH THSGRPWIDL RNKRYELRAE WKQFPFGFEA
351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVQ
401 YLQKSSALS AISEAVQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIQYD KALIDRENY NHPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY

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551 EGDWQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
 601 DFYGAEGEII FKPTPRYRIG VSGDYVRGRL KNLPSLPGRE DAYGNRPFFIA
 651 QDDQNAAPRV AARLGFHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
 701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSE
 751 TGGVNVKF*

m149-1/g149-1 96.2% identity in 758 aa overlap

	10	20	30	40	50	60
m149-1.pep	MAQTTLKPIVLSILLINTPLLAQAHETEQSVDLETVSUVGKSRPRATSGLLHTSTASDKI					
g149-1	MAQITLKPIVLSILLINTPLLAQAHETEQSVGLETVSUVGKSRPRATSGLLHTSTASDKI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
g149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m149-1.pep	SPDHAIMVDTALSQQVEILRGVPTLLYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL					
g149-1	SPDHAIMVDTALSQQVEILRGVPTLLYSSGNVAGLVDVADGKIPEKMPENGVSSEAGLRL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m149-1.pep	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTSGISGL					
g149-1	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTSGISGL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m149-1.pep	SWVGEKGFIVGAYSDDRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI					
g149-1	SWVGEKGFIVGAYSDDRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m149-1.pep	DYDNFGLSCGFHDDNAHAHTHSGRPWIDLNRKRYELRAEWKQFPFGFEALRVHLNRNDY					
g149-1	DYDNFGLSCGFHDDNAHAHTHSGRPWIDLNRKRYELRAEWKQFPFGFEALRVHLNRNDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m149-1.pep	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGQVQLQKSSALSASEAVKQPM					
g149-1	HHDEKAGDAVENFFNNKTHNARIELRHQPIGRLKGSWGQVQLQKSSALSAPETVQQPM					
	370	380	390	400	410	420
	430	440	450	460	470	480
m149-1.pep	LLDNKVQHYSHFFGVEQANWDNFTLEGGVRVEKQKASIYDKALIDRENYNHPPLDLGAH					
g149-1	LIDNNVRHYSHFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNQPLDLGAH					
	430	440	450	460	470	480
	490	500	510	520	530	540
m149-1.pep	RQTARSAFALSGNWFYTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKR					
g149-1	RQTARSAFALSGNWFYTPHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKR					
	490	500	510	520	530	540
	550	560	570	580	590	600
m149-1.pep	SNNIELALGYEGDRWQYNLAAYRNRFGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSGA					
g149-1	SNNIELALGYEGDRWQYNLAAYRNRFGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSGA					
	550	560	570	580	590	600
	610	620	630	640	650	660
m149-1.pep	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFFIAQDDQNAAPRV					
g149-1	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDPYGKRPFIAQADQNAAPRI					
	610	620	630	640	650	660

a149-1.seq

This corresponds to the amino acid sequence <SEO ID 606: ORF 149-1.a>:

a149-1.pap

1	MAQTTLKPIV	LSILLINTPL	LSQAHGTEQS	VGLETVSUVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRQKA	VNLGDALDGV	PGIHASQYGG	GASAPVIRRG
101	TGRRIRKIVL	HGETGDMADF	SPDHAMVDS	ALSQSQVEILR	GPVTLIYSSG
151	NVAGLVDVAD	GKIKEKMPEN	GVSHELGLRL	SSGNLEKITS	GGINIGLGNK
201	FVLHTEGQYR	KSGDYAVPRY	RNLKRLPDSH	ADSGTGSILQ	SWVGEGKFGI
251	AAYSDDRRDQ	GLPAHSHEYD	DCHADLIWQK	SILINKRYLQL	YPHLLTEEDI
301	DYDNPGLSCG	FHDDDDAHAA	AHNGKPIWDL	RNRKRYELRAE	WKOPFPFGFEA


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351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVO
401 YLGQKSSALS ATSEAVKQPM LLDNKVQHYS FFGVEQANWD NFFLEGGVRV
451 EKQKASIRYD KALIDRENY NHPPLDLGAH RQTARSAFALS GNWYFTPOHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKR SNNIELALGY
551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSLPGRE DAYGNRPLIA
651 QADQNAAPRV AARLGVHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

a149-1/ml49-1 98.0% identity in 758 aa overlap

a149-1.pep	10	20	30	40	50	60
	MAQTTLKPIVLSILLINTPLLQAAGTEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI					
ml49-1	MAQTTLKPIVLSILLINTPLLQAAGTEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI					
	10	20	30	40	50	60
a149-1.pep	70	80	90	100	110	120
	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
ml49-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
	70	80	90	100	110	120
a149-1.pep	130	140	150	160	170	180
	SPDHAIMVDSALSQQVEILRGVPTLLYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL					
ml49-1	SPDHAIMVDTALSQQVEILRGVPTLLYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL					
	130	140	150	160	170	180
a149-1.pep	190	200	210	220	230	240
	SSGNLEKLTSGGINIGLGNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTSGISGL					
ml49-1	SSGNLEKLTSGGINIGLGNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTSGISGL					
	190	200	210	220	230	240
a149-1.pep	250	260	270	280	290	300
	SWVGEKGFIGAAYSDDRDQYGLPAHSHEYDDCHADI IWQKSLINKRYLQLYPHLLTEEDI					
ml49-1	SWVGEKGFIVAYSDDRDQYGLPAHSHEYDDCHADI IWQKSLINKRYLQLYPHLLTEEDI					
	250	260	270	280	290	300
a149-1.pep	310	320	330	340	350	360
	DYDNFGLSCGFHDDDAHAHAHNGKPWDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY					
ml49-1	DYDNFGLSCGFHDDDAHAHAHNGKPWDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY					
	310	320	330	340	350	360
a149-1.pep	370	380	390	400	410	420
	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGVOYLGQKSSALSATSEAVKQPM					
ml49-1	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGVOYLGQKSSALSATSEAVKQPM					
	370	380	390	400	410	420
a149-1.pep	430	440	450	460	470	480
	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPPLDLGAH					
ml49-1	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPPLDLGAH					
	430	440	450	460	470	480
a149-1.pep	490	500	510	520	530	540
	RQTARSAFALSGNWYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKR					
ml49-1	RQTARSAFALSGNWYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKR					
	490	500	510	520	530	540
a149-1.pep	550	560	570	580	590	600
	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSGA					
ml49-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSGA					
	550	560	570	580	590	600
	610	620	630	640	650	660

426

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a149-1.pep  DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPLIAQADQNAPRVP
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m149-1       DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFIAQDDQNAPRVP
              610      620      630      640      650      660

              670      680      690      700      710      720
a149-1.pep  AARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||
m149-1       AARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
              670      680      690      700      710      720

              730      740      750      759
a149-1.pep  WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
              ||||||||||||||||||||||||||||||||||||||||||||||||
m149-1       WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
              730      740      750

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 607>:

```

g150.seq (partial)
1  ..TACTGCAAGG CAGACCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT
51  CACCGCCCGC CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGGA
101 GCGGTTTCGA TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGTTT
151 GACAACGATC CGGCACTGGT CGGGGAAATC CTAGACCTGC TCGGCATCAA
201 TCCGGCAACG GAAATACAGG CGGGCGGAAA AACCTGCGG GTTGCCCTCCG
251 CACTGTTATC CCATTTGAA CTACGCGAAA ACACCCCGC CTTTGTCAAA
301 GGCTATGCCA CGTTCGCCGA TAATGACGAA CTCGACCGTA TTGCTGCCGA
351 CAACGCCGTT TTGCAAGGCT TTGTGCAAAG CACGCCGATT GCCGGTGTGC
401 TGCACCGCTT CCCGGCAAAA CTGACGGCGG AACAAATCGC CGGCCTGCTG
451 CGCCCGCTTG CGCCGCGCCT GTATTCGATT TCCTCGTCGC AGGCGGAAGC
501 GGGGGACGAA GTGCACCTGA CCGTCGGCGC AGTGCCTTTC GAACACGAAG
551 GGCGCGCCAG GCGGGCGGCG GCATCGGGTT TCTTGCCTGA CCGGCTGGAA
601 GAGGACGGCA CGGTGCGCGT GTTTGCGGAA CGCAACGACG GCTTCAGGCT
651 CCCCGAAGAC AGCCGCAAGC CGATTGTGAT GATCGGCTCC GGTACCGGCG
701 TCGCACCGTT CCGCGCCTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA
751 GGCAGAAACT GGCTGATTTT CGGCAATCCG CATTTTGCCG CCGACTTCCT
801 CTATCAGACC GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGAT
851 ATGACTTCGC CTGGTCGCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC
901 AAAATCCGCG AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC
951 GCATATCTAT GTGTGCGGCG ATGCGGCAAA AATGGCAAAA GAAGTGAAG
1001 CCGCCTTGCT GGATGTGATT ATCGGGGCGG GGCATTGCGA CGAAGACGGC
1051 CCAGAAGGAT ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA
1101 TGTATTATGA

```

This corresponds to the amino acid sequence <SEQ ID 608; ORF 150.ng>:

```

g150.pep (partial)
1  ..YCKADFPFAA LLANQKITAR QSDKDVRHIE IDLSGSDLHY LPGDALGVWF
51  DNDPALVGEI LDLLGINPAT EIQAAGKTLF VASALLSHFE LTQNTPAFVK
101 GYATFADNDE LDRIAADNAV LQGFVQSTPI AGVLHRFPK LTAEQFAGLL
151 RPLAPRLYSI SSSQAEAGDE VHLTVGAVRF EHEGRARAGG ASGFFADRLE
201 EDGTVRVFAE RNDGFRLEPED SRKPIVMIGS GTGVAPFRAF VQORAAENAE
251 GRNWLIFGNP HFAADFLYQT EWQQFAKDG F LHRDYFAWSR DQEEKIYVQD
301 KIREQAEGLW OWLQEGAHY VCGDAAKMAK EVEAALLDVI IGAGHSDDED
351 AEGYLDMLRE EKRYQRDVY*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 609>:

```

m150.seq
1  ATGCAGAACA CAAATCCGCC ATTACCGCCT CTGCCGCCCG AAATCAAGCA
51  GTCCTGTGCG GGGCTGGACG CGGCACAATG GCGGTGGCTG TCCGGCTACG
101 CTTGGGCAAA AGCAGGAAAC GGGGCATCTG CAGGACTGCC CGCGCTTCAG
151 ACGGCATTGC CGGCGGCGA ACCTTTTTC GTAACCGTCC TTTCGCCTC
201 GCAAACCGGC AATGCGAAAT CCGTTGCCGA CAAAGCGGCG GACAGCCTGG
251 AAGCCGCCGG CATCCAAGTC AGTCGCGCCG AACTGAAAGA CTATAAGGCG
301 AAAAACATCG CCGCGGAACG CCGCCTGCTG CTGGTTACCT CCACCCAAGG
351 CGAAGGCGAA CCGCGGAAAG AAGCCGTCGT GCTGCACAAA CTGCTGAACG
401 GCAAAAAAGC CCGGAAATTG GACAACTCC AATTGCGCGT ACTGGGTTTG

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451 GCGGACAGTT CCTATCCGAA TTTCTGTCAG GCAGGTAAAG ATTTGACCG
501 GCGTTTTTGAA GAATTGGGCG CAAAACGCT GCTCGAACGC GTTGATGCGG
551 ATTTGGACTT TACCGCCTCC GCAAACGCTT GGACAGATAA TATCGCCGCA
601 CTCTTAAAAG AAGAAGCCGC AAAAAACCGG GCAACGCCCG CGCCGCAGAC
651 AACGCCCCCC GCGGCCTTC AGACGGCACC GGATGGCAGG TACTGCAAGG
701 CAGCCCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT CACCGCCCGC
751 CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGA GCGGTTGCGA
801 TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGGTTT GACAACGATC
851 CGGCACTGGT CAGGGAAATC CTAGACCTGC TCGGCATCGA TCCGGCAACG
901 GAAATACAGG CGGGCGGAAA GATGATGCCG GTTGCAGCGG CACTTTCATC
951 TCATTTGAA CTCACGCAA AACTCCGGC TTTGTCAAA GGCTATGCCG
1001 CGTTCGCCCA TTATGAAGAA CTCGATAAAA TCATTGCCGA TAACGCCGTT
1051 TTGCAGGATT TCGTGCAAAA CACGCCTATT GTCGATGTGC TGCACCGCTT
1101 CCCGGCAAGC CTGACGGCAG AACAATTCAT CCGTTTACTG CGTCCGCTTG
1151 CACCCCGTTT GTATTGATT TCTTCAGCAC AGGCGGAAGT GGGCGATGAA
1201 GTGCATTAA CTGTCGGCGT GGTTCGTTT GAACACGAAG GCCCGCCAG
1251 AACGGGCGGC GCATCGGGT TCCTTGCCGA CCGGCTGGAA GAGGACGGCA
1301 CGGTGCGCGT GTTGTGGAA CGCAACGACG GCTTCAGGCT GCCCGAAGAC
1351 AGCCGCAAGC CGATTGTGAT GATCGGCTCG GGCACCGCG TCGCACCGTT
1401 CCGCGCTTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA GGCAAAACT
1451 GGCTGATTTT CGCAATCCG CATTGTGCC GTGATTTCT CTATCAAACC
1501 GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGGT ACGATTTCG
1551 CTGGTCCCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC AAAATCCGCG
1601 AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC GCATATCTAT
1651 GTGTGCGGCG ATGCGGCAAA AATGGCAAAA GACGTGGAAG CCGCCTTGCT
1701 GGATGTGATT ATCGGGGCG GACATTGGA CGAAGAGGGC GCAGAAGAAT
1751 ATTTGGATAT GCTGCGCGAA GAAAACGCT ATCAGCGTGA TGTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 610; ORF 150>:

m150.pep

```

1  MQNTNPPLPP LPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
51  TALPAAEPFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA
101 KNIAGERRLL LVTSTQGEGE PPKEAVVLHK LLNGKKAPKL DKLQFAVLGL
151 GDSSYPNFCQ AGKDFDRRFE ELGAKRLLER VDADLDFTAS ANAWTDNIAA
201 LLKEEAANKR ATPAPQTPP AGLQTAPDGR YCKAAPFPAA LLANQKITAR
251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDPAT
301 EIQAGGKMMP VARALSSHFE LTQNTPAFVK GYAFAHYEE LDKIIADNAV
351 LQDFVQNTPI VDLVHRFPAS LTAEQFIRLL RPLAPRLYSI SSAQAEVGDE
401 VHLTVGVVRF EHEGRARTGG ASGFLADRLE EDGTVRVFVE RNDGFRLPED
451 SRKPIVMIGS GTGVAPFRAF VQRAAENAE GKNWLI FGNP HFARDFLYQT
501 EWQQFAKDFG LHRYDPAWSR DQEEKIYVQD KIREQAEGLW QWLQEGAHYI
551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 150 shows 91.3% identity over a 369 aa overlap with a predicted ORF (ORF 150.ng) from *N. gonorrhoeae*:

m150/g150

```

                210      220      230      240      250      260
m150.pep      LLKEEAANKRATPAQTTPAGLQTAPDGRYCKAAPFPAALLANQKITARQSDKDVRHIE
g150              YCKADPFPAALLANQKITARQSDKDVRHIE
                10      20      30

                270      280      290      300      310      320
m150.pep      IDLSGSDLHYLPGDALGVWFDNDPALVREILDLLGIDPATEIQAGGKMMPVARALSSHFE
g150              IDLSGSDLHYLPGDALGVWFDNDPALVGEILDLLGINPATEIQAGGKTLFVASALLSHE
                40      50      60      70      80      90

                330      340      350      360      370      380
m150.pep      LTQNTPAFVKGYAFAHYEELDKIIADNAVLDQDFVQNTPIVDVLRFPASLTAEQFIRLL

```


1701 GGATGTGATT ATCGGGGCAG GACATTGGA CGAAGAGGC GCAGAAGAAT
 1751 ATTTGGATAT GCTGCGCGAA GAAAACGCT ATCAGCGTGA TGTTTATTGA

This corresponds to the amino acid sequence <SEQ ID 612; ORF 150.a>:

a150.pep
 1 MQNTNPPLPP MPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
 51 TALPTAEFFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA
 101 KNIAGERRL LVTSTQGEGE PPEEAVVLHK LLNGKKAPKL DKLQFAVLGL
 151 GDSSYPNFCR AGKDFDKRFE ELGAKRLLER VDADLDFAAA ADGWTDNIAA
 201 LLKEEAAKNR ATPAPQTTP AGLQTAPDGR YCKADPFPA LLANQKITAR
 251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI DLLLGIDQAT
 301 EIQAGGKTL P VASALLSHFE LTQNTPAFVK GYAPFADDE LDRIAADNAV
 351 LQGFVQSTPI ADVLHRFPK LTAEQFAGLL RPLAPRLYSI SSSQAEVGDE
 401 VHLT VGAVRF EHEGRARAGG ASGFLADRLE EDGTVRVFVE RNDGFRLEPED
 451 SRKPIVMIGS GTGVAPFRAF VQORAAENAE GKNWLFNGNP HFARDFLYQT
 501 EWQQFAKDG L HRYDFAWSR DQEEKIYVQD KIREQAEGLW QWLQEGAHY
 551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY*

m150/a150 94.8% identity in 599 aa overlap

	10	20	30	40	50	60
m150.pep	MQNTNPPLPPLPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQTALPAAEPFS					
a150	MQNTNPPLPMPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQTALPAAEPFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m150.pep	VTVLSASQTGNAKSVADKAADSLEAAGIQVSRaelKDYKAKNIAGERRL LVTSTQGEGE					
a150	VTVLSASQTGNAKSVADKAADSLEAAGIQVSRaelKDYKAKNIAGERRL LVTSTQGEGE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m150.pep	PPKEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCQAGKDFDRRFEELGAKRLLER					
a150	PPEEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCRAGKDFDKRFEELGAKRLLER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m150.pep	VDADLDFTASANAWTDNIAALLKEEAAKNRATPAPQTTPAGLQTAPDGRYCKAAPPFAA					
a150	VDADLDFAAAADGWTDNIAALLKEEAAKNRATPAPQTTPAGLQTAPDGRYCKADFPFAA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m150.pep	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFNDPALVREILDLLGIDPAT					
a150	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFNDPALVREILDLLGIDQAT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m150.pep	EIQAGGKMPVARALSSHFE LTQNTPAFVKGYAAFAHYEELDKIADNAV LQDFVQNTPI					
a150	EIQAGGKTL P VASALLSHFE LTQNTPAFVKGYAPFADDELDRIAADNAV LQGFVQSTPI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m150.pep	VDVLHRFPASLTAEQFIRLLRPLAPRLYSISSAQAEVGDEVHLT VGVRFEHEGRARTGG					
a150	ADVLHRFPKLTAEQFAGLLRPLAPRLYSISSAQAEVGDEVHLT VGAVRFEHEGRARAGG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m150.pep	ASGFLADRLEEDGTVRVFVERNDGFRLEPDSRKPIVMIGSGTGVPFRAFVQORAAENAE					
a150	ASGFLADRLEEDGTVRVFVERNDGFRLEPDSRKPIVMIGSGTGVPFRAFVQORAAENAE					
	430	440	450	460	470	480
	490	500	510	520	530	540
m150.pep	GKNWLFNGNP HFARDFLYQT EWQQFAKDGFL HRYDFAWSR DQEEKIYVQDKIREQAEGLW					

430

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a150      GKNWLF FGNPHFARDFLYQTEWQQFAKDGFLHRYDFAWSRDQEEKIYVQDKIREQAEGLW
           490      500      510      520      530      540

           550      560      570      580      590      600
m150 . pep  QWLQEGAHYVCGDAAKMAKDVEAALLDVIIIGAGHLDEEGAEYLDMLREEKRYQRDVYX
           |||||
a150      QWLQEGAHYVCGDAAKMAKDVEAALLDVIIIGAGHLDEEGAEYLDMLREEKRYQRDVYX
           550      560      570      580      590      600

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 613>:

g151.seq

```

1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCACACGTCG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTG
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GCGCGCGAAG
251 TGGAGCGCGT TTTGGGGATG GTGGATTGCG TCGTCTTGT TGGTGACGCA
301 CAGGAAGGTC CGATGCCGCA AACCCGTTTC GTGACCAAAA AAGCCTTGGC
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAACCGTCCG
401 CCCGTCGAG CTGGGTTATC GACCAGACTT TCGAGTTGTT CGACAACTTG
451 GGTGCGACCG ACGAGCAGTT GGATTTCCTG ATGTTTACG CTTAGGTTT
501 GAGCGGCTTT GCCAAGCTGG AAGAAaccga CGAGAGCAGC GATATGCGCC
551 CGctgttcga CACCATCCTA AAATACacgc ctgCACCGAG CCGCAGCGCG
601 GACGAGCCGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
651 CGGCCGCTC GTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
701 AAACCGTTGC CGTGATGAAC CACGAGCAGC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGCTTGGA CGCGTGCCGC TTGAAGAAGC
801 CGAAGCCGGC GACATTGTGA TTATTCCGG TATCGAAGAC ATCGGCATCG
851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCCTGCC GATGTTGAGC
901 GTGACGGAAC CGACGCTGAC GATGGACTTT ATGGTAAACA CCAGCCCGCT
951 CGCAGGTACA GAAGGCAAAT TCGTGACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTTGCC TCGCGTGGA AGACACCGCC
1051 GatgCCGACG TGTTCCGCGT ATCcgGGCGC GCGGAACTGC ACCTGACGAT
1101 TTTGCTGGAA AATATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAGC
1151 CGCGCGTCGT GTACCGAGAC ATCGACGGTC AAAAAATGCGA ACCTTATGAA
1201 AACCTGACTG TGGACGTACc cgacgacAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCGC CGCGTGCGG AACTGACCAA TATGGAAGC GACGCAACG
1301 GacgCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
1351 CAAGGCGAAT TCATGACCCT GACGCGCGGC GTCGGGCTGA TGAgccacGT
1401 GTTcgacgac tacgcgcccg tcaAACCCGA TATGCCCCGC CGCCACAACG
1451 GCGTactggt GtcccaAGAG CAGGGCGAGG CGTTTGCTTA CGCCTTGTTG
1501 AATCTTGAAG ACCGCGGCCG TATGTTGCTA TCGCCCAACG ACAAATCTA
1551 CGAAGGTATG ATTATCGGCA TCCACAGCCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTCACCAATA TCCGTGCCAG CGGTACCGAC
1651 GAAGCGGTGC GCCTGACCAC GCCGATCAAA CTGacgcTGG AAGGCGCGGT
1701 CGAGTTTATC GACGATGACG AGCTGGTGGG AATCAGCCG CAatccatcc
1751 gcctgcgcat gcgttacctG AGCGaattgg aacgccgccc tcaTTTTAAA
1801 AagctgGATT AA

```

This corresponds to the amino acid sequence <SEQ ID 614; ORF 151.ng>:

g151.pep

```

1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGCHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESS DMRPLFDITL KYTPAPSGSA
201 DEPLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQTVAVMN HEQQIAQGRI
251 NQLLGFKGLE RVPLEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDPDDN QGAVMEELGR RRGELTNMES DGNGRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHFDD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW

```

501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRMYL SELERRRHF
 601 KLD*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 615>:

m151.seq

```

1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCAGTTCG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GCGCGCGAAG
251 TAGAGCGCGT TTTGGGGATG GTGGACTGCG TCGTCTTGT GGTGGACGCG
301 CAGGAAGGCC CGATGCCGCA AACCCTTTTC GTGACCAAAA AAGCCTTGCG
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAGCCGTCCG
401 CTCGTCCGAG CTGGGTTATC GACCAAATT TCGAGCTGTT CGACAACTTG
451 GCGCGGACCG ACGAGCAGTT GGATTTCCCG ATTGTTTACG CTCAGGGTT
501 GAGCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
551 CGCTGTTCTA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
601 GACGAAACGC TGCAACTGCA AATTTCCTAA CTCGACTACG ACAACTACAC
651 CGGCGCGCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
701 AAACCGTTGC CGTCATGAAC CACGATCAGC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGTTTGAA CGCGTGCCGC TTGAAGAAGC
801 CGAAGCGGC GACATCGTGA TTATTTCCGG TATCGAAGAC ATCGGTATCG
851 GCGTAACCAT CACCGACAAA GACAATCCCA AAGGCCTACC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGCT
951 GCGGGGTACG GAAGGCAAT TCGTAACCA CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGTGGGA AGATACCGCC
1051 GATGCCGACG TGTTCCGCGT ATCCGGGCGC GCGGAGCTGC ACCTGACCAT
1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATCGCA ACCGTATGAA
1201 AACCTGACCG TGGATGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAGC GACGGCAACG
1301 GACGCACCCG CTTGCAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
1351 CAAGGCGAAT TTATGACCCT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCCGGC CGCCACAACG
1451 GCGTGCTGGT GTCCCAAGAG CAGGCGGAGG CAGTCGCTTA CGCCTTGTTG
1501 AATCTGGAAG ACCGCGGCCG TATGTTCTGA TCGCCCAACG ACAAATCTA
1551 CGAAGGCATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
1651 GAAGCCGTTT GCTGACCAC GCCAATCAAG CTGACGCTGG AAGGTGCGGT
1701 TGAGTTTATC GACGATGACG AACTCGTTGA AATCACGCCG CAATCCATCC
1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCACTTTAAA
1801 AAGCTGATT GA

```

This corresponds to the amino acid sequence <SEQ ID 616; ORF 151>:

m151.pep

```

1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDITL KYTPAPSGSA
201 DETLQLQISQ LDYDNYTGRL GIGRIILNGRI KPGQTVAVMN HDQQIAQGRI
251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IIGVTTITDK DNPKGLPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLOKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDVPDDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARLIGF
451 QGEFMTLTRG VGLMSHVFD YAPVKPDMFG RHNGVLVSQE QGEAVAYALW
501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHF
601 KLD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 151 shows 99.2% identity over a 603 aa overlap with a predicted ORF (ORF 151.ng) from *N. gonorrhoeae*:

m151/g151

	10	20	30	40	50	60
m151.pep	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT					
g151	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m151.pep	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
g151	AIDYEGCHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m151.pep	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN					
g151	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m151.pep	DMRPLFDITILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
g151	DMRPLFDITILKYTPAPSGSADEPLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m151.pep	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
g151	HEQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m151.pep	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
g151	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
	310	320	330	340	350	360
	370	380	390	400	410	420
m151.pep	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDV PDDNQGAVMEELGR					
g151	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDV PDDNQGAVMEELGR					
	370	380	390	400	410	420
	430	440	450	460	470	480
m151.pep	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMFG					
g151	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMFG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m151.pep	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
g151	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
	490	500	510	520	530	540
	550	560	570	580	590	600
m151.pep	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK					
g151	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRMYLSELERRRHFK					
	550	560	570	580	590	600

m151.pep KLDX
 ||||
 g151 KLDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 617>:

```
a151.seq
1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCCACGTCG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GCGGGCGAAG
251 TAGAGCGAGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG
301 CAGGAAGGCC CGATGCCGCA AACCCGTTTC GTGACCAAAA AAGCCTTGCC
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA TAAATCGAC AAACCGTCCG
401 CCCGTCCGAG CTGGGTCAAT GACCAAACCT TCGAGCTGTT CGACAACTTG
451 GCGCGCACCG ACGAGCAGTT GGATTTCCCG ATTGTTTATG CTTCCGGTCT
501 GTCCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATCGGTC
551 CGCTGTTCTG TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
601 GACGAAACGC TGCAACTGCA AATTTCCTCA CTCGACTACG ACAACTACAC
651 CCGCCGCCTC GGTATCGGTC GTATCTTGAA CGGACGTATC AAGCCCGGTC
701 AAGTTGTTGC CGTCATGAAC CACGATCAAC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGTTTAGAA CGCGTGCCGC TTGAAGAAGC
801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATTGAAGAC ATCGGCATCG
851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCCTGCC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGTT
951 GGCAGGTACG GAAGGCAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGTGGA AGATACGCC
1051 GATGCCGACG TGTTCCGCGT ATCCGGGCGC GCGGAGCTGC ACCTGACCAT
1101 TTTGCTGGA AATCATGCCG GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAAATGCGA ACCGTATGAA
1201 AACCTGACCG TGGACGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCCG CGCGTGGCG AACTGACTAA TATGGAAGC GACGGCAACG
1301 GACGCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGCTTC
1351 CAAGGCGAAT TTATGACCCT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCTGGC CGCCACAACG
1451 GCGTGCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTTG
1501 AATCTGGAAG ACCGCGGCCG TATGTTCTGA TCGCCCAACG ACAAATCTA
1551 CGAAGGTATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGTTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
1651 GAAGCCGTTT GCCTGACCAC GCCGATTAAG CTGACGCTGG AAGGTGCGGT
1701 CGAGTTTATC GACGATGATG AGCTGGTAGA AATCACGCCG CAATCCATCC
1751 GTCTGCGCAA CGCTTACTTG AGCGAATTGG AACGCCGCCG CCATTTCAAA
1801 AAGCTAGATT GA
```

This corresponds to the amino acid sequence <SEQ ID 618; ORF 151.a>:

```
a151.pep
1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVVLVDA
101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDITL KYTPAPSGSA
201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQVVAVMN HDQQTAAQGR
251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPGLPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLOKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDVPDDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHVDD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
501 NLEDGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGGK LTNIRASGTD
551 EAVRLTTFIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHFK
601 KLD*
```

m151/a151 99.8% identity in 603 aa overlap

10 20 30 40 50 60

m151.pep	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
a151	
	10 20 30 40 50 60
m151.pep	70 80 90 100 110 120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL
a151	
	70 80 90 100 110 120
m151.pep	130 140 150 160 170 180
	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFFIVYASGLSGFAKLEETDES
a151	
	130 140 150 160 170 180
m151.pep	190 200 210 220 230 240
	DMRPLFDITLKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRIKPKGQTVAVMN
a151	
	190 200 210 220 230 240
m151.pep	250 260 270 280 290 300
	HDQQIAQGRINQLLGFKGLERVPLEEAAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
a151	
	250 260 270 280 290 300
m151.pep	310 320 330 340 350 360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDLQKELLTNVALRVEDTADADVFRVSGR
a151	
	310 320 330 340 350 360
m151.pep	370 380 390 400 410 420
	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQAVMEELGR
a151	
	370 380 390 400 410 420
m151.pep	430 440 450 460 470 480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG
a151	
	430 440 450 460 470 480
m151.pep	490 500 510 520 530 540
	RHNGVLVSQEQGEAVAYALWNLEDRGMFVSPNDKIYEGMIIGHSRDNDLVVNPLKGKK
a151	
	490 500 510 520 530 540
m151.pep	550 560 570 580 590 600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELEERRHFK
a151	
	550 560 570 580 590 600
m151.pep	KLDX
a151	KLDX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq

```

1  ATGAAAAaca aaACCaaagt ctgGGacttc cCaccgcc ttTCCactG
51  GctgcttgCC gCATCCctgc CCTTTATGTG gtatagCGCA AAAGCCGGCG
101 GcgataTGCT GcaatgGCAC ACGCGCGTCG GGCTGCTCGT CCTTTTCCTG

```

```

151 CTCGTATTCC GCCTCTGCTG GGGCATTGTTGG GGCAGcgATA CCGCCCCGTTT
201 CTCccgTtTC GTCCGAGGTT GGGCAGGTAT ACGCGGCTAT CTGAAAAAcg
251 gCATTCCCGA ACAtatcCAG CCGGACACA ACCCCTTGGG CGCACTgatg
301 gtcGTTGCGC TTTTGgccgc cgtcTCATTT CAagtcggcA CGGGGCTTTT
351 Tgcccgaat gaaaacacct tcagcaCCaA cggctacctc aaccatttgg
401 tttccgaaca tacgGGCAGC CTTATACGGA AAATCCACCT CAACTTTTTC
451 AAGCTGCTCG CCGTTTTTTC CGCAGTCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCATATTC AAAAAGAAAA ACCTCGTCCG CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CCGGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 620; ORF 152.ng>:

g152.pep

```

1 MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KAGGDMLOWH TRVGLLVLEFL
51 LVFRLCWGIW GSDTARFSRF VRGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAN ENTFTNGYL NHLVSEHTGS LIRKIHLNFF
151 KLLAVFSAVH IAAVAAYRIF KKNLVRPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLLS*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 621>:

m152.seq

```

1 ATGAAAAACA AAACCAAAGT CTGGGACCTC CCCACCCGCC TTTTCCACTG
51 GCTGCTTGCC GCGTCCCTGC CCTTTATGTG GTATAGCGCG AAAGCCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTCGT CCTTTTCCTG
151 CTCGTATTTC GCCTCTGCTG GGGCATTGTTGG GGCAGCGATA CCGCCCCGTTT
201 TTCCCCTTTC GTCCAAGGCT GGGCAGGCAT ACGCGGCTAT CTGAAAAACG
251 GTATTCCCGA ACACATCCAG CCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGCCGCG CGTGTCCTTC CAAGTCGGCA CCGGGCTTTT
351 TGCCGCCGAT GAAAACACCT TCAGCACCAA CGGCTACCTC AACCATTGCG
401 TTCCGAACA TACGGGCGAG CTTATGCGGA AAATCCACCT CAACTTTTTC
451 AAGCTGCTCG CCGTTTTTTC TGCAATCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCGTATTC AAAAAGAAAA ACCTCATCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCAGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CTCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 622; ORF 152>:

m152.pep

```

1 MKNKTKVWDL PTRLFHWLLA ASLPFMWYSA KAGGDMLOWH TRVGLFVLEFL
51 LVFRLCWGIW GSDTARFSRF VQGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAD ENTFTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFSAIH IAAVAAYRVF KKNLILPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVASLA AAAILLLS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 152 shows 95.4% identity over a 218 aa overlap with a predicted ORF (ORF 152.ng) from *N. gonorrhoeae*:

m152/g152

```

          10      20      30      40      50      60
m152.pep  MKNKTKVWDLPTRLFWLLAASLPFMWYSAKAGGDMLOWHTRVGLFVLFLLVFRLCWGIW
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g152       MKNKTKVWDFPTRLFWLLAASLPFMWYSAKAGGDMLOWHTRVGLLVLELLVFRLCWGIW
          10      20      30      40      50      60

          70      80      90     100     110     120
m152.pep  GSDTARFSRFVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g152       GSDTARFSRFVRGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAN
          70      80      90     100     110     120

```

436

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAHIAAAYAAYRVFKKKNLILPMI					
	: : : : :					
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFSAVHIAAAYAAYRIFKKKNLVRPMI					
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	: : : :					
g152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

```
a152.seq
1  ATGAAAAACA AAACCAAAGT CTGGGACTTC CCCACCCGCC TTTTCCACTG
51  GCTGCTTGCC GCATCCCTAC CCTTTATGTG GTATAGCGCG AAAACCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTTAT CCTTTTCCTG
151 CTCGTATTCC GCCTCTGCTG GGGCATTGGG GGCAGCGATA CCGCCCGTTT
201 CTCCCGTTTC GTCCGCGGAT GGTCCGGTAT CAGAGAGTAT ATGAAAAACG
251 GTATTCCCGA ACACGTCCAA CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTGTGCC TTTTGGCCGC CGTGTCTGTC CAAGTCGGCA CAGGGCTTTT
351 TGCCGCCGAT GTAAACACCT TCAGCACCAA CGGCTACCTC AACCATTGGG
401 TTTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCATCT CAACTTTTTC
451 AAAGTCTCG CCGTTTTC CCGAGTCCAC ATCGCCGNCG TCGCCGCATA
501 CCGCGTGTTC AAAAAGAAAA ACCTCGTCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

```
a152.pep
1  MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KTGDMLOWH TRVGLFILFL
51  LVFRLCWGIW GSDTARFSRF VRGWSGIREY MKNGIPEHVQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAD VNTFSTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFSAVH IAXVAAYRVF KKKNLVLPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAIILLS*
```

m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTTRLFHWLLAASLPFMWYSAKAGDMLOWHTRVGLFVLLVFRLCWGIW					
	: : : : :					
a152	MKNKTKVWDFPTTRLFHWLLAASLPFMWYSAKTGGDMLOWHTRVGLFILFLVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNIGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	: : : : :					
a152	GSDTARFSRFVRGWSGIREYMKNGIPEHVQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAHIAAAYAAYRVFKKKNLILPMI					
	: : : : :					
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAVHIAAXVAAYRVFKKKNLILPMI					
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	: : : :					
a152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

```

g153.seq
1  atgggggtttg cttacAgtat gacgtatatc gaggtCGGga taccggaggc
51  ggcataccgtc ctttCgctGC CCGAGATgat ggcctgatG GTGTTtCagg
101 attATGGTTT TttggcCGAA GTGATGTTTG TgctgaCTTT cGGCGcgcCG
151 GTTCTGTTtC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GGCAGGCGAT GATGGTGGAT GTGTTTTTTG TTCCACTCT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AAAGGTTGCG TTCGGGCCGG CGTTTTATCT
351 GATGTTTCGG CTGTGCGTTA TGCTGATTG GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTCCAA ATCGGGCGGC TGACGGGGAA TAATGCGGTT
451 CAGACGGCAT CGGAAGGCAA AACCTGTTGC AGCCGCTGCC TGTATTTccg
501 cgacAGTgcc gaatccCCCT GCGGGGTGTg cgCGcgga CTgtacggcg
551 gacggccgaa aagtCTGAGt atttCgtCGG CGTTTCtgac ggcggcggtT
601 GTTTTGtATT TCCctgCcaa TATCctgceg attatGattt cgtccaATCc
651 tgccgccacg GAGGcCAACA CCATCTTTAG CCGCATCGCT TATATGTGGG
701 ACgagggcgA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGCTGC TGAAGATTGC GGCAATGTCG GTTTTGATTG CCGCGGCACG
801 GTTCGCTTTG CCGGCGGGCG CAAAGAAATT GTCGCACCTC tacCGCATCA
851 CCGAAGCGGT CCGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT
901 TTGATGTGTT CGTTCcaca TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACACC GCGCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAACGAAA CGGAAAAATA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

```

g153.pep
1  MGFAYSMTYI EVGIPEAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRVV VRLRQAMMVD VFFVSTLVAY
101 IKLSSVAKVR FGPAPYLMFA LSVMLIRTSV SVPQHWWVFQ IGRLTGNNAV
151 QTASEGKTC SRCLYFRDSA ESPCGVCGAE LYGGRPKSLs ISSAFLTAHV
201 VLVFPANILP IMISSNPAAT EANTIFSGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIAAARFAL PAGAKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFHTYAA RVIPGSAAVY FCLVVILTML SAYYFDPRLl WDKRASDGIA
351 FNETEKYD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

```

m153.seq
1  ATGGCGTTTG CTTACGGTAT GACGTATATC GAGGTGCGGA TACCGGGTGC
51  GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG
101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACTTT CCGCGCGCCG
151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GACAGGCGAT GATGGTGGAT GTGTTTTTTG TTCCACTTT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AGAGGTTTCG TTCGGGCCGG CGTTTTATCT
351 GATGTTTCGG CTGTGAGTTA TGCTGATTG GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGGA TAATGCGGTT
451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTTCCG
501 CGACAGTGCC GAATCCCCCT GCGGCGTGTG CGGTGCGGAA CTGTACCGCC
551 GACGGCCGAA AAGTCTGAGT ATTTGCTCGG CGTTTCTGAC GCGGCGGTT
601 ATTTTGtATT TCCCTGCCAA TATCCTGCCG ATTATGATT CGTCCAATCC
651 TGCCGCCACG GAGGTCAATA CCATCCTTAA CCGCATCGCT TATATGTGGG
701 ACGAGGCGA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGCTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCCCG
801 CTTGCGTTTG CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA
851 CCGAAGCGGT CCGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT
901 TTGATGTGTT CGTTCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACACC GCGCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

```

m153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRVV VRLRQAMMVD VFFVSTLVAY

```

[illegible]

a153.seq							
1	ATGGCGTTTG	CTTACGGTAT	GACGTATATC	GAGGTCGGGA	TACCGGGTGC		
51	GGCATCCGTC	TTTTCGCTGC	CCGAGATGAT	GCGCCTGATG	GTGTTTCAGG		
101	ATTATGGTTT	CTTTGCCGAA	GTGATGTTTG	TGCTGACCTT	CGCGCGCCCG		
151	GTTCTGTTTC	TGCTGCTGTG	CCTGTATGTC	TATGCCGCGC	TGATACGGAA		
201	ACAGGCGTAT	CCTGCGCTGC	GTTTGGCAAC	GCGTGTGATG	GTGCGCTTGA		
251	GACAGGCGAT	GATGCTGGAT	GTGTTTTTTG	TTTCCACTTT	GGTGGCGTAT		
301	ATCAAGCTCT	CGTCTGTGGC	AGAGGTTCCG	TTCGGATCGG	CGTTTTATCT		
351	GATGTTTCGG	CTGTGCGTTA	TGCTGATTCC	GACTTCGGTA	TCGGTTCCCC		
401	AGCATTGGGT	GTATTTTCAA	ATCGGGCGGC	TGACGGGGGA	TAATGCGGTT		
451	CAGACGGCAT	CGGAAGGTAA	AACCTGTTGC	AGCCGCTGCC	TGTATTTCCG		
501	CGACAGTGCC	GAATCCCCCT	GCGGCGTGTG	CGGTGCGGAA	CTGTACCGCC		
551	GACGGCGGAA	AAGTCTGAGT	ATTTCTGCGG	CGTTTCTGAC	GCGCGCGGTT		
601	ATTTTGTATT	TCCCTGCCAA	TATCCTGCCG	ATTATGATTT	CGTCCAATCC		
651	TGCCGCCACG	GAGGTCAATA	CCATCCTTAA	CGGCATCGCT	TATATGTGGG		
701	ACGAGGCGCA	CAGGCTGATT	GCGGCGGTTA	TTTTCAGCGC	GAGTATTTTG		
751	GTGCCGGTAC	TGAAGATTGC	GGCAATGTCG	GTTTTGATTG	CGTCCGCCCG		
801	CTTCGCTTTG	CCAACGGGTG	CAAGAATAAT	GTGCGACCTC	TACCGCATCA		

```

851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTTCCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCCC GCGCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLCLYV YAALIRKQAY PALRLATRV VRLRQAMVD VFFVSTLVAY
101 IKLSSVAEVR FGSAYFLMFA LSVMLIRTSV SVPQHWVYFQ IGRITGDNV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL ISSAFLTA
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDR LI AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFH TYAA RVIPGSAAVY FCLVVILT ML SAYYFDPRL WDKRASDGI
351 FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV
a153	MAFAYGMTYIEVGIPGAASVLSLPEMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV
m153.pep	YAALIRKQAYPALRLATRVVRLRQAMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA
a153	YAALIRKQAYPALRLATRVVRLRQAMVDVFFVSTLVAYIKLSSVAEVRFGSAFYLMFA
m153.pep	LSVMLIRTSVSPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE
a153	LSVMLIRTSVSPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE
m153.pep	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDR LI
a153	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDR LI
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII
m153.pep	LMCSFH TYAARVIPGSAAVYFCLVVILT ML SAYYFDPRL WDKRASDGI AFNETEKHDX
a153	LMCSFH TYAARVIPGSAAVYFCLVVILT ML SAYYFDPRL WDKRASDGI AFNETEKHDX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CAGCCTCAAG CACGCGTCCG
51  CAAAACAAC accttctct CCGCGTCTG GCTGGTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTAAAG AAATCCGCA CAGGGGCGCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATCGAAG TCAACAATAC
201 GGTCAATTAAG GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTTA CTGCCCACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGcgtaa CCGGTTTGGG TACGCTGCTT TCGGGTTCGT

```

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401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAgcy GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG AccgCATCCT CAACGTcaac AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAAATCG AAAGCGCGCA TTTCGACccg
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAAT COGCCCTCT GCCTGCCCTG
751 CTGTCAGGCG CGATTTTATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCTT GtgaATACA AAGGGCtga
951 TGTcggCTAG GTTTCAGATG TCCCTTATT TGACCGCAAT gacagCCTGC
1001 ACCTgtTTGA aaacggctgg aTtcccGtac gCATCCGCAT cgagccTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAGCAAAGC AAAGAGCATT GGAACAACA
1101 ATTCCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGCGCGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TCGGACCGCA TACCGTTTAT GCAGGCGATA CCGTCATCGC
1251 CACACGGGGC GCGGTTTGG ATGACTTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACaaatT CAACAATCTG CCATTggata aaACCGTTGC CGAATTGAAC
1351 GGCTCGCTCG CGAACTCAA GTCCGCACTC AAATCCGCCA ATGCCGCCCT
1401 AAGCTCCATT GacaAACTGG TCGgcaatCC GCAGACGCAA AACATCCCGA
1451 ACGAACTGAA CCAAACTCTG AAAGAGTTGC GCATAACCCT GCAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGAgacgta caAAATacgc tgCaaAGTTT
1551 GGACAAAACC TTAAAagacy TtcaACCCGT CATTAACACT TTGAaAGAAa
1601 aacCCaaCgc actGATTTtc aacaACAGCA GCAAAGAccc tATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

```

g154.pep
1 MTDNSPPPNNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51 VVTLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGLTLL SGSYIAFTPG KSGEAKDVFO
151 VGDIPPVTAI GQSGRLRLNLI GKNDRIILNVN SPVLYENFMV GIESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLSNAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVRIEIPS
351 RLEINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGKK MIELNDQPSA
401 SPKLRPHTVY AGDTVIAIRG GGLDDLQVKL ADLLDKFNNL PLDKTVAEIN
451 GSLAELKSAL KSANAALSSI DKLVGNPQTQ NIPNELNQTQ KELRITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NNSSKDPIPK
551 GSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

```

m154.seq
1 ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51 CAAAAACAAC ACCTTCCTCT CTGCCGCTCG GCTGGTTCGG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCAATCAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TCGCGGACGA CAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCGGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAAGC GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA TTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAAT COGCCCTCT GCCTGCCCTG
751 CTGTCGGGCG CGATTTTATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTCCGCC GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTTCGACG TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAACAACA
1101 ATTTACAGAG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCA

```



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1201 TACACCTAAGC TGCAGCCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTTC
1301 TCGACAAGTT CGACAACTG CTTTAGATA AGACGGTGC CGAATTGAAC
1351 GGTTTCGCTT CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAACCCTG AAAGAGTTGC GCACAACCCT GCAAGGCGTA
1501 TCGCCGCAAT CGCCTATCTA CGGCGACGTA CAAATACGC TGCAAAGTTT
1551 GGACAAAACT TTAAGAGACG TTCAACCCGT GATTAATACT TTGAAAGAAA
1601 AACCCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

```

m154.pep
1  MTDNSPPFNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTL SSGYIAFTPG KSDEAKDVPQ
151 VQDIPPVTAI QSGLRRLNLI GKNDRIILNVN SPVLYENFMV QQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQFQT ALNKGTLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVABL
451 GSLAELKSTL KSANAALSSI DKLVGKPTQ NIPNELNQTL KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154 / g154 97.8% identity in 553 aa overlap

	10	20	30	40	50	60
m154.pep	MTDNSPPFNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
g154	MTDNSPPFNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m154.pep	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
g154	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m154.pep	SGVTGLGTL LSGSYIAFT PGKSDRAKDVP QVDIPPVTA IGQSGLRRLNL IGKNDRIILNVN					
g154	SGVTGLGTL LSGSYIAFT PGKSGRAKDVP QVDIPPVTA IGQSGLRRLNL IGKNDRIILNVN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m154.pep	SPVLYENFMV QQVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
g154	SPVLYENFMV QQVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m154.pep	KLSAPLPALL SGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ					
g154	KLSAPLPALL SGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m154.pep	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
g154	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
	310	320	330	340	350	360
	370	380	390	400	410	420
m154.pep	KEHWKQFQT ALNKGTLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATQG					
g154	KEHWKQFQT ALNKGTLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATRG					

442

	370	380	390	400	410	420
	430	440	450	460	470	480
m154.pep	GGLDDLQVKLADLLDKFDKPLDKTVAEIENGSLAELKSTLKSANAALSSIDKLVGKPQTQ					
	: : : : :					
g154	GGLDDLQVKLADLLDKFNNPLDKTVAEIENGSLAELKSALKSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154.pep	NIPNELNQTLKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	: : : : :					
g154	NIPNELNQTLKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540
	550					
m154.pep	NSSSKDPIPKGSRX					
	:					
g154	NNSSSKDPIPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGCTG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCATCAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TCGCGGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTC AAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCAATTA CACCATCTTC ATCCAAAGCC CCAAGGACAA
651 ACTGATTCAT TCCGCCAGCC GTTCTGGCTT GGAAGCGGCG ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTCGGGCG CGATTTTCATT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGATGACCGT TCGCTGTACT ACACGCGGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT CGGTTGCGCT GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTTCGATG TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATTCCCGTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGGAAT TCAATGCCGA CGAACAAAGC AAAGAACATT GGAAACAACA
1101 ATTTAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCAGCAAA ATGATTGAGT TGAACGATCA GCCTTCGCGC
1201 TCGCCCAAGC TCGGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTGCTTG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAAACCCTG AAAGAGTTGC GCACAACCCT GCAAGGCGTA
1501 TCGCCTCAAT CGCCTATCTA CGGCGACGTA CAAATACGCG TGCAAGTTT
1551 GGACAAAACC TTAAGAGAGC TTCAACCCGT CATTAACTT TTGAAAGAAA
1601 AACCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154.pep
1  MTDNSPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFQ

```

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151 VQDIPPVTAI QOSGLRLNLI GKNDRIILNVN SPVLYENFMV GQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTGSGI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAEKSTL KSANAALSSI DKLVGKPQTQ NIPNELNQTl KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154/a154 100.0% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPNHGAQARVRKNNTFLSAVWLVPILIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
a154	10	20	30	40	50	60
	MTDNSPPPNHGAQARVRKNNTFLSAVWLVPILIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
m154.pep	70	80	90	100	110	120
	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGVEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
a154	70	80	90	100	110	120
	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGVEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
m154.pep	130	140	150	160	170	180
	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVQVQDIPPVTAIGOSGLRLNLIGKNDRIILNVN					
a154	130	140	150	160	170	180
	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVQVQDIPPVTAIGOSGLRLNLIGKNDRIILNVN					
m154.pep	190	200	210	220	230	240
	SPVLYENFMVGQVESAHFDPSPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTGSGI					
a154	190	200	210	220	230	240
	SPVLYENFMVGQVESAHFDPSPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTGSGI					
m154.pep	250	260	270	280	290	300
	KLNSAPLPALLSGAISFDSPKTKNSKNVKSSEDSTLYDSRSEVANLPDDRSLYYTAFFKQ					
a154	250	260	270	280	290	300
	KLNSAPLPALLSGAISFDSPKTKNSKNVKSSEDSTLYDSRSEVANLPDDRSLYYTAFFKQ					
m154.pep	310	320	330	340	350	360
	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
a154	310	320	330	340	350	360
	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
m154.pep	370	380	390	400	410	420
	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASEPKLRPHTVYAGDTVIATQG					
a154	370	380	390	400	410	420
	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASEPKLRPHTVYAGDTVIATQG					
m154.pep	430	440	450	460	470	480
	GGLDDLQVKLADLLDKFDKLPLDKTVAELNGSLAEKSTLKSANAALSSIDKLVGKPQTQ					
a154	430	440	450	460	470	480
	GGLDDLQVKLADLLDKFDKLPLDKTVAELNGSLAEKSTLKSANAALSSIDKLVGKPQTQ					
m154.pep	490	500	510	520	530	540
	NIPNELNQTlKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
a154	490	500	510	520	530	540
	NIPNELNQTlKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					

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```

                    550
m154.pep      NSSSKDPIPKGSRX
              |||||
a154          NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1   atGAAaatcg GtataCCACG CGAGTCatta tcCGGCGAAA cccgcgtagc
51  ctgcAcgccc gCCACCGTTG CCctgctggg caAactAGGC TTTGAAACCG
101 TTGtcgaAAG CGGTGCAggt TTGGCGGCAA GTTTggaCGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGCCTGCC
201 TTTAATTAT AAGGTCAACG CGCCGTCCGA AGGCGAGCTG CCGCTGCTCA
251 AAGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAGG CCTTGC GCGC CAAGAAAGTC AACGCGCTGG CGATGGACAT
351 GGTTCCTCCG ATTTCCCGCG CTCAGGCCTT GGACGCTTTG TCTTCAATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT CACTGCCGCC GGCAAAGTGC CGCCTGCGCA
501 GGTTCCTGTTG ATTGGCGCCG GTGTGGCGGG TTTGGCGGCA ATCGGTACGG
551 CAAATTCGCT CGGCGCAGTG GTGCGCGCGT TCGATACCCG CTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGTAAG TTcctGAAAC TCGACTTCCT
651 GCAAGAATCG GGCGGCAGCG GAGACGgctA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAAATG AAGCTCTTTG CCGAACAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCATTCCG GGCAAACCCG CTCCCAAGCT
801 GATTACAAA GAAATGGTGG AAAGCATGAA ATCCGGATCC GTCATCGTCG
851 ATTTGGCGGC GACGGGCGGC AACTGCGAAC TCACCCGACC GGGCGAATTG
901 TCCGTAACCG GCAACGGCGT GAAATCATC GGCTACACCG ACATGGCAAA
951 CCGCCTTGCC GGACAGTCTT CCCAGCTTTA CGCCACCAAC TTGGTGAACC
1001 TGACCAAGCT GTTAAGCCCG AACAAAGAcg gcaAATCAC GCTGGACTTC
1051 GAAGacgtGA TTATCCGCAA TATGACCGTT ACCCGcgacg gcgaaATCAC
1101 CTTCCCGCCT CCGcgaTTc aggtTTCgc cggcgCAG CAAAcgccgt
1151 ctgaAAAagc cgcGCCTGCC GCCAagcccg AgccGaaacc tgttCCcctg
1201 tggAAAAaac tcgCGCCCGC CGCcatcgCC GCCGTATTGG tgctgtgGgt
1251 cggCgcggtc gcaccgcag CATTCTTGAA CCACTTTATC GTCTTCGTCC
1301 TCGCCTGCGT CATCGGCTAC CATGTCGTTT GgaacgTCAG CCACTCGCTG
1351 CACACACCGC TGatgtcgtt aaccaaCgcc atctccGGCA tcatggtcgt
1401 cggCGCGCTG CTGCAATCG GTCAGGGcaa cggcttcgtT TCgtGCTGT
1451 CGTTTGTTC CATCCTGATT GCCGGCATCA ATATCTTCGG CGGCTTTGCG
1501 GTTACACGGC GTATGCTGAA TATGTTAAG AAAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1   MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWACPLIY KVNAPSEGEL PLLKEGQTIV SFLWPRONEA
101 LVEALRAKKV NALAMDVPR ISRAQALDAL SSMANISGYR AVIEAANAFA
151 RFFTQGITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDLQES GSGDGYAKV MSDEFIAAEM KLF AEQAKEV
251 DIIITTAaip GKPAKLITK EMVESMKSGS VIVDLAATGG NCELTRPGEL
301 SVTGNVVKII GYTDMANRLA GSSQLYATN LVNLTKLLSP NKDGEITLDF
351 EDVIIRNMTV TRDGEITFPF PPIQVSARPO QTPSEKAAPA AKPEPKPVPL
401 WKKLAPAAIA AVLVLWVGAV APAAFLNHFI VFVLACVIGY HVVWNVSHSL
451 HTPLMSVTNA ISGIMVVGAL LQIGQNGFV SLLSFVAILI AGINIFGGFA
501 VTRRMLNMEK KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1   ATGAAAATCG GTATCCACG CGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CGGTGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGTCTGCC
201 TTTGATTAT AAGGTCAACG CGCCGTCCGA ACAGGAAGTG CCGCTTTTGA
251 ACGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT

```

```

301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCCGC ATTTTCGCGCG CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CGGCTACCGC GCCGTAATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT TACCGCCGCC GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGTCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 CGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 ACAAGAATCG GCGGCGCAGCG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCT
801 GATTACAAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGCAGGGC GGCAACTGCG AACTCACCAG CCCGGGCGAA
901 TTGTCCGTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCAGCTT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGTTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCAGCCG CAGCAAACGC
1151 CTTCTGAAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCC
1201 CTGTGGAAAA AACTCGCGCC CGCCGTCATC GCCCGCTCT TGGTACTGTG
1251 GGTGCGCGCG GTCGCACCCG CAGCATTCCT GAACCACTTT ATCGTGTTCG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTAAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAAA TCGGTCAAGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCGGCA TCAACATCTT CGGCGGCTTT
1501 GCGGTAACAC GGCGTATGCT GAATATGTTT AAGAAAGGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51 QTAGATVADK AAVWVCPLIY KVNAPSEQEL PLLNEGQTIY SFLWPRQNEA
101 LVEALRAKKV NALAMDVPR ISRAQALDAL SSMANISGYR AVIEAANAFA
151 RFFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDRLEV
201 AEQIESMGSK FLKLDFFQES GSGDGYAKV MSDEFIAAEM KLFAEQAQEV
251 DIIITTAIIP GKPAKLIK EMVESMKSGS VIVDLAAATG GNCELTRPGE
301 LSVTNGVKI IGYTDMANRL AGQSSQIYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQP QQTPEKAVP AAKPEPKVPV
401 LWKKLAPAVI AAVLVLVWGA VAPAAFLNHF IVEVLACVIG YYVVWNVSHS
451 LHTPLMSVTN AISGIIIVGA LLOIGQNGF VSLLSFVAIL IAGINIFGGF
501 AVTRRMLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
              10      20      30      40      50      60
m155.pep     MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              |||
g155          MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m155.pep     AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDVPR
              |||
g155          AAVWACPLIYKVNAPSEGELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDVPR
              70      80      90      100     110     120

              130     140     150     160     170     180
m155.pep     ISRAQALDALSSMANISGYRAVIEAANAFAFRFFTGQITAAGKVPPAQVLVIGAGVAGLAA
              |||
g155          ISRAQALDALSSMANISGYRAVIEAANAFAFRFFTGQITAAGKVPPAQVLVIGAGVAGLAA

```

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	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
m155.pep	250	260	270	280	290	300
	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
g155	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAA-TGGNCELTRPGE					
	250	260	270	280	290	
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	300	310	320	330	340	350
m155.pep	370	380	390	400	410	420
	VTHDGEITFPPPPPIQVSAQPOQTPSEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLWVGA					
g155	VTRDGEITFPPPPPIQVSARPOQTPSEKAAPAKPEPKPVPLWKKLAPAAIAAVLVLWVGA					
	360	370	380	390	400	410
m155.pep	430	440	450	460	470	480
	VAPAAFLNHFIIVFLACVIGYVWVNVSHSLHTPLMSVTNAISGIIIVGALLQIGQGNGF					
g155	VAPAAFLNHFIIVFLACVIGYHVWVNVSHSLHTPLMSVTNAISGIMVVGALLQIGQGNGF					
	420	430	440	450	460	470
m155.pep	490	500	510			
	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					
g155	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					
	480	490	500	510		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

```

a155.seq
1  ATGAAATCG GTATCCACG TGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTGAAACCG
101 TTGTCGAAAG CGGCGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAGCAGCAG GCGCAACCGT TGCCGACAAA GCAGCGGTTT GGGCATACCC
201 TTTAATTAT AAGGTTAACG CGCCGTCCGA AGACGAGCTG CCGCTGCTCA
251 AAGAAGGACA GACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAAG CCTTGC GCGC CAAGAAAGTG AACGCGCTGG CAATGGACAT
351 GGTGCCCGC ATTTCGCGCG CGCAGGCTTT GGACGNTTGT TCTNGATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTNTTCA CCGGCCAAAT TACTGCCGCA GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGTGT TCGATACCGC CCTG.AAGTG
601 GCGGAACAAT TAGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 GCAAGAATCG GCGGCAGCG GCGACGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAGATG AAGCTTTTGT CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCN
801 NNTNANCAA GAAATGGTCG AAAGCATGAA ACCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGGACGGG GCAACTGCG AACTACCAA ACAGGGCGAA
901 TTGTTCTGTA CCGGCAACGG CGTGAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGACAGT CTTGCGAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGCTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCGCG ACGGCGAAAT
1101 CACCTTCCCG CTTCCGCCGA TTCAAGTTT CCGCCAACCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGCGCCT GCCGCCAAGC CCGAACCGAA ACCCGTTCCC

```

```

1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTCGGCGCG GTCGCACCG CAGCATTCTT GAACCACTTT ATCGTCTTCG
1301 TCCTCGCCTG CGTCATCGGC TACTATGTCG TTTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GGCGGATGCT GAATATGTTT AGGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```

a155.pep
  1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
 51 QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQITV SFLWPRONEA
101 LVEALRAKKV NALAMDMPV ISRAQALDXL SXMANISGYR AVIEAANAFA
151 RXFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDFFQES GSGDGYAKV MSDEFIAAEM KLFAEQAKEV
251 DIIITTAAP GKPAKXXXX EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LEVTGNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QQTPEKAAP AAKPEPKPVP
401 LWKKLAPAXI AAVLVLVWGA VAPAAFLNHF IVFVLACVIG YVYVWNVVSHS
451 LHTPLMSVTN AISGIIIVGA LLQIGQNGF VSLLSFVAIL IASINIFGGF
501 FVTRRLNMF RKG*

```

m155/a155 95.3% identity in 513 aa overlap

m155.pep	10	20	30	40	50	60
	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK					
a155	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK					
	10	20	30	40	50	60
m155.pep	70	80	90	100	110	120
	AAVWVCPLIYKVNAPSEQELPLLNEGQITIVSFLWPRONEALVEALRAKKVNALAMDMPV					
a155	AAVWAYPLIYKVNAPSEDELPLLKEGQITIVSFLWPRONEALVEALRAKKVNALAMDMPV					
	70	80	90	100	110	120
m155.pep	130	140	150	160	170	180
	ISRAQALDALSSMANISGYRAVIEAANAFAFRFTGQITAAGKVPPAQVLVIGAGVAGLAA					
a155	ISRAQALDXLSXMANISGYRAVIEAANAFAFRXFTGQITAAGKVPPAQVLVIGAGVAGLAA					
	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDFFQESGGSGDGYAKVMSDEFIAAEM					
a155	IGTANSLGAVVRVFDTRLXVAEQLESMGGKFLKLDFFQESGGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
m155.pep	250	260	270	280	290	300
	KLFAEQAKEVDIIITTAAPGKPAKPLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
a155	KLFAEQAKEVDIIITTAAPGKPAKXXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE					
	250	260	270	280	290	300
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
a155	LFVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	310	320	330	340	350	360
m155.pep	370	380	390	400	410	420
	VTHDGEITFPPPIQVSAQPQQTPEKAVPAAPKPEPKVPLWKKLAPAVIAAVLVLVWGA					
a155	VTRDGEITFPPPIQVSAQPQQTPEKAAPAAKPEPKVPLWKKLAPAXIAAVLVLVWGA					
	370	380	390	400	410	420

448

	430	440	450	460	470	480
m155.pep	VAPAAFLNHFIVFVLACVIGYYVWVNSHSLHTPLMSVTNAISGIIIVVGALLQIGQGNGF					
a155	VAPAAFLNHFIVFVLACVIGYYVWVNSHSLHTPLMSVTNAISGIIIVVGALLQIGQGNGF					
	430	440	450	460	470	480
	490	500	510			
m155.pep	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					
a155	VSLLSFVAILIASINIFGGFFVTRMLNMFKKGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 643>:

```

g156.seq
1  ATGACTTTCG CCTATTGGTG CATTCTGATT GCCTGCCTAT TGCCGCTTTT
51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCTCG CGGTTTTCTG GCACATACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTGCAACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG ATTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT GCGCTCGCTG ATGTGGGCGG GCGGATTTGC
351 CTGCACCGTC GGACTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 644; ORF 156.ng>:

```

g156.pep
1  MTFAYWCILI ACLKPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQONGFEA FAPFAAVLT AHATGNAGQA TVNTLAGLEI LFRLAFIWCY
101 IADKAALRSL MWAGGFACTV GLFVAAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 645>:

```

m156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTGCCTAT TGCCGCTTTT
51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGGTTTTCTA GCGCACACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTGCAACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC GCGCAATCG ACCATCAACA
251 CGCTTGCCCTG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAT
301 ATCGCCGACA AAGCCGCTAT GCGCTCACTG ATGTGGGCAG GCGGATTTGC
351 CTGCACCGTC GGGCTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 646; ORF 156>:

```

m156.pep
1  MTFAYWCILI ACLKPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQONGFEA FAPFAAVLT AHATGNAQS TINTLACLEI LFRLAFIWCY
101 IADKAAMRSL MWAGGFACTV GLFVAAA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m156 / g156 96.1% identity in 127 aa overlap

	10	20	30	40	50	60
m156.pep	MTFAYWCILIACLKPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA					
g156	MTFAYWCILIACLKPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m156.pep	FAPFAAVLTAHATGNAQSTINTLACLEIFLRLAFIWCYIADKAAMRSLMWAGGFACTV					


```

g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWAGGFACTV
              70          80          90          100          110          120

m156.pep  GLFVAAAX
            |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCAGCCGC
201 CGTTTGTACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG CCTGTTTCATC CTGTCCGCC TCGCCTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTTGT
351 CTGCACCGTC GGGCTGTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAAARA
51  HAAQONGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LRLAFIWCY
101 IADKAALRSL MWVGGFVCTV GLFVVAAX*

```

m156/a156 90.6% identity in 127 aa overlap

```

              10          20          30          40          50          60
m156.pep      MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA
              |||||
a156          MTFAYWCILIAYLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAAARAHAAQONGFEA
              10          20          30          40          50          60

              70          80          90          100          110          120
m156.pep      FAPFAAAVLTAHATGNAAQSTINTLACLFI LRLAFIWCYIADKAAMRSLMWAGGFACTV
              |||||
a156          FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWVGGFVCTV
              70          80          90          100          110          120

m156.pep      GLFVAAAX
              |||||
a156          GLFVVAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
1  atgaggaacg aggAAAAACg cgcctgcgc cgcaattgC gCgGcgggcg
51  ttcgcAAATg GGgagagacg tGCGgCGGC GGCGgCgata Aaaatcaacc
101 gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGTATTgg
151 cCGATGGGCA AGGAATTGcg TTTGGGCGgc tTgtcCGCG CGGCGCAAAA
201 ACGCgCGGCA AAactctatc tgccttATAT CGAACCgCAC ACGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGGAACGGGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCCTG TGTCGGCATA GACCGGAAG
401 GCTACCGTTT GGGGCAGGCA GCGGCTATT ACGATGCGAC GCTTTCGGCG
451 ATGAAATACC GTTGCAGGC GAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551 TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

g157.pep

```

1 MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLLKRYI KRGRKIGVYW
51 PMGKELRLGG FVRAAQKRG A KLYLPYIEPH TRRMWFTYP ERGMERERKR
101 GRAKLHVPOF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGAFACQLVD RLPREAHDL LDGFVSEAGI LCF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

m157.seq

```

1 ATGAGGAACG AGGAAAAACG CGCCTGCGC CGCGAATTGC GCGGGCGGCG
51 TTCGCAATG GGGCGGGACG TCGGGGCGGC GGCAACGGTA AAAATCAACG
101 ACCTGCTCAA ACGTTATATT AAAAAAGGCG GGAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACC GCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GCCGATGGAG TAAACAAGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTT GCAGGTCGGA AAAAGCGTGT
351 GCATGATTG AACCTCCTGC TTGTGCCAGT GGTGCGTATG GACAGGCTGG
401 GCTACCGCTT GGGACAGGCA GCGGCTATT ACGATGCGAC GCTTTCAGCG
451 ATGAAATACC GTTGCAGGC AAAAACCGTG GCGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTGCCG TCGAGGCGCA CGACCGGTCT TTGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

m157.pep

```

1 MRNEEKRALR RELRGRRSQM GRDVRAAATV KINHLLKRYI KKGRKIGVYW
51 PMGKELRLDG FVRAAQKRG A ELYLPYIEPR SRRMWFTYP ADGVKQERKR
101 GRAKLHVPOF AGRKRVHDL NLLVFPVGM DRLGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGAFACQLVD RLPVEAHDRS LDGFVSEAGI LCF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRSQMG RDVRAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG					
g157	MRNEEKRALRRELGRRSQMG RDVRAAAAIKINRLLKRYIKRGRKIGVYWPMGKELRLGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m157.pep	FVRAAQKRGAEYLPYIEPRSRMWFTYPADGVKQERKRGRAKLHVPOFAGRKRVHDL					
g157	FVRAAQKRGAKLYLPYIEPHTRRMWFTYPYPERGMERERKRGRAKLHVPOFAGRKIRVHGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m157.pep	NLLVFPVGM DRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
	::					
g157	SVLLVPLVGI DREGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPREAHDLP					
	130	140	150	160	170	180
	190					
m157.pep	LDGFVSEAGILCFX					
g157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

a157.seq

```

1 ATGAGGAACG AGGAAAAACA CGCCTTGGCG CGAGAGTTGC GCCGCGCCCCG
51 CGCGCAGATG GGGCATCAAG GCGGGTTGGC GCGGGGGCAA ACGATTAACC

```

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACCTTATC TGCCTTATAT CGAACCGCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAACGGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCCGCATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GCGGCTATT ACGATGCGAC GCTTGCGGCG
451 ATGAAATACC GTTTCAGGC AAAAACCCTG GCGGTGGGCT TTGCCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACCGCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

```

a157.pep
  1 MRNEEKHALR RELRRARAQM GHQRLAAGQ TINRLLKRYI KRGRKIGVYW
 51 PMGKELRLDG FVRAAQKRGK KLYLPYIEPR SRRMWFTYPY ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGFAQCFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

```

              10      20      30      40      50      60
m157.pep    MRNEEKRALRRELGRRSQMGRDVRAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG
              |||||:||||| :|||: | | ||:|||||:|||||:|||||
a157        MRNEEKHALRRELRRARAQMGHQRLAAGQTINRLLKRYIKRGRKIGVYWPMGKELRLDG
              10      20      30      40      50      60

              70      80      90      100     110     120
m157.pep    FVRAAQKRGAEYLYPYIEPRSRMWFTYPADGVKQERKGRAKLHVPOFAGRKKRVHDL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a157        FVRAAQKRGAKLYLPYIEPRSRMWFTYPESGMERERIRGRAKLNVPQFAGRKIRVHGL
              70      80      90      100     110     120

              130     140     150     160     170     180
m157.pep    NLLVVPVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS
              ::|||:|||:| |||||:|||||:|||||:|||||:|||||:|||||
a157        SVLLVPLVGIDREGYRLGQAGGYDATLAAMKYRLQAKTVGVGFACQFVDRLPREPHDLL
              130     140     150     160     170     180

              190
m157.pep    LDGFVSEAGILCFX
              |||||:|||||
a157        LDGFVSEAGILCFX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

```

g158.seq
  1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAG
 51 CGGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAacCTGctc
151 aACCGCACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGCGG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTCGCGT GGATTCCGCG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCGG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCcgac TTTCGCTCGT TTCTTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCCT TACGGGCCGG AGAATTGGAC
451 GATTCCGGGC TCGTGCACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCTCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGAtgC GCAGGGAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAAACA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```

801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG
 851 TATTTTGGGA TTTTITAGTG AAGGAACTGG GAAAAAATAT GAATAGAACG
 901 AATACCAAAT AA

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

g158.pep
 1 MKTNSEELTV FVQVVESGSF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLNLT EEGAQYFRR AQRILQEMAAA ETEMLAVHEV PQGVLRVDSA
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSS EYINLIERKV DIALRAGELD
 151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE
 251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNL RLRVFLDFLV KELGKNMNR
 301 NTK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

m158.seq
 1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTCAAG TGGTGGAAG
 51 CGGCAGCTTC AGCCGTGCGG CCGAGCAGTT GCGATGGCA AATTCTGCCG
 101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC
 151 AACCGCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATT
 201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGCG GAAACCGAAA
 251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG TGTGAGCGT GGATCCGCG
 301 ATGCCGATGG TGCTGCATCT GCTGCGCGCG CTGGCAGCAA AATTCAACGA
 351 ACGCTATCCG CATATCCGAC TTTCGCTCGT TTCTTCCGAA GGCTATATCA
 401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCGCG AGAATTGGAC
 451 GATTCCGGGC TCGGTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT
 501 CGCCAGTCCT GAATACCTGG CAAAACACGG CACGCCGCAA TCTACAGAAG
 551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT
 601 ACATGGGCGG TTTTAGATGC GCAGGAAAT CCCTATAAGA TTTCACCGCA
 651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGT
 701 GCGGTATTGT TTGCTTATCA GATTTTTTGG TTGACAACGA CATCGCTGAA
 751 GGAAAGTTAA TTCCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC
 801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG
 851 TATTTTGGGA TTTTITAGTG GAGGAACTGG GAAACAATCT CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

m158.pep
 1 MKTNSEELTV FVQVVESGSF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLSLT EEGAQYFRR AQRILQEMAAA ETEMLAVHEI PQGVLSVDSA
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSS EYINLIERKV DIALRAGELD
 151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHQC LGFTEPGSLN
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE
 251 GKLIPLLAEQ TSKTHPFNA VYYSKAVNL RLRVFLDFLV EELGNNLCG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVESGSFSRAAEQLAMANSAVSRIVKRLEEKLGVNLLNRTTRQLSLT					
g158	MKTNSEELTVFVQVVESGSFSRAAEQLAMANSAVSRIVKRLEEKLGVNLLNRTTRQLNLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRR AQRILQEMAAA ETEMLAVHEI PQGVLSVDSAMPMVLHLLAPLAAKFNERYP					
g158	EEGAQYFRR AQRILQEMAAA ETEMLAVHEV PQGVLRVDSAMPMVLHLLAPLAAKFNERYP					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m158 . pep	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
g158	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSHFRVVASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158 . pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSSCGIVCLS					
g158	SAEDLANHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSSCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158 . pep	DFLVDNDIAEGKLIPLLAETSDKTHPFNAVYYSKAVNLRRLRVFLDFLVEELGNNLCGX					
g158	DFLVDNDITEGKLIPLFAEQTSNKTHPFNAVYYSKAVNLRRLRVFLDFLVKELGKNMNRT					
	250	260	270	280	290	300
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158 . seq

1	ATGAAAACCA	ATTCAGAAGA	ACTGACCGTA	TTGTGTCAG	TGGTGGAAAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCGTCCG
101	TAAGCCGCAT	CGTCAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGAAGGCG	TGTTGCGCGT	GGATTCCGCG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCGG	CTGGCAGCAA	AATTCACGCA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCCGG	AGAATTGGAC
451	GATTCCGGGC	TGCGTGACG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCGG	CCACCAATGT	TAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTTAGATGC	GCAGGGAAT	CCCTATAAGA	TTTCACCGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTACAGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTTTGG	TTGACAACGA	CATCGCTGAA
751	GGAAAGTTAA	TTCCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGCACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTTTGA	TTTTTTAGTG	GAGGAAC TGG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158 . pep

1	MKTNSEELTV	FVQVVESGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRRR	QRILQEMAAA	ETEMLAHVEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFENERYP	HIRLSLVSSE	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQC	LGFTTEPGSLN
201	TWAVLDAQGN	PYKISPHFTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTHPFNA	VYYSKAVNLR	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

	10	20	30	40	50	60
m158 . pep	MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
a158	MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158 . pep	EEGAQYFRRRQRILQEMAAEETEMLAHVEIPQGVLSVDSAMPVVLHLLAPLAAKFENERYP					
a158	EEGAQYFRRRQRILQEMAAEETEMLAHVEIPQGVLRVDSAMPVVLHLLAPLAAKFENERYP					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m158.pep	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYSDKAVNLRRLRVFLDFLVEELGNLNCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYSDKAVNLRRLRVFLDFLVEELGNLNCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

g160.seq
1  ATGGAcattc  tgGACAAact  ggtcgatCTC  GCccaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATG  gcATGaaacc  TTGCAACGCG
101 AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  GCGGTTATCT  CTGCATCGAC
151 GCGGAAACTT  CCCCgcGTCC  GGTcGGCAGC  GGCgATATTG  TATTTTCCCC
201 GCGCGGCTTG  GGTcATGTGT  TGAGCCACGA  CGGAAAATAC  GGAGAAAGTT
251 TACAACCGGA  CATACGACAA  AACGGCACAT  TTATGGTCAA  ACAGTGCGGC
301 AACGGGCTGG  ATATGAGCCT  GTTTTGCGCC  CGTTCCGCT  ACGACACCCA
351 CGCCGATTG  ATGAACGGGC  TGCCGGAAC  CGTTTTCTG  AACATTGCC
401 ATCCAAGTTT  GCAGTATGTG  GTTCAATGC  TGCAACTGGA  AAGCGAAAAA
451 CCTTTGACGG  GGACGGTTTC  CGTGGTCAAC  GCATTACCGT  CCGTCCTGCT
501 GGTGCTTATC  CTGCGCGCCT  ATCTCGAACA  GGATAAGGAT  GTCGAATCT
551 CGGGCGTATT  GAAAGGTTGG  CAGGACAAAC  GTTTGGGACA  TTTGATCCAA
601 AAGGTGATAG  ACAAACCGGA  AGACGAATGG  AATATTGACA  AAATGTTGC
651 CGCCGCCAAT  ATGTcGCGCG  CGCAACTGAT  GCGCGCTTC  AAAAGCCAAG
701 TCGGACTCAG  CCCGcACGCC  TTTGTGAACC  ATATCCGCCT  GCAAAAAGGC
751 GCATTGCTGC  TGAAGAAAAAC  CCGGATTTCG  GTTTGGAGG  TCGCGCTGTC
801 GGTGGGCTTT  CAGTCGGAAA  CGCATTTTCG  CAAGGCGTTC  AAACGGCAAT
851 ATCACGTTTC  GCCGGGCAA  TACCGGAAAG  AAGGCGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng>:

```

g160.pep
1  MDILDKLVDL  AQLTGSADVQ  CLLGGQWHEH  LQREGLVHIV  TAGSGYLCID
51  GETSPRPVGT  GDIVFFPRGL  GHVLSHDGKY  GESLQPDIRQ  NGTFMVKQCG
101 NGLDMSLFCA  RFRYDTHADL  MNGLPETVFL  NIAHPSLQYV  VSMLQLESEK
151 PLTGTVSVVN  ALPSVLLVLI  LRAYLEQDKD  VELSGVLKGW  QDKRLGHLIQ
201 KVIDKPEDEW  NIDKMVAAN  MSRAQLMRRF  KSQVGLSPHA  FVNHIRLQKG
251 ALLLKKTPDS  VLEALSVGF  QSETHFGKAF  KRQYHVSPGQ  YRKEGGQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```

m160.seq
1  ATGGACATTC  TGGACAAACT  GGTcGATTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101 TGCAACGCGA  AGGATTGGTA  CACATTGTTA  CATCGGGCAG  CGGCTATCTC
151 TGCATCGACG  GCGAAACTTC  CCCGCGTCCG  GTCAGTACAG  GGGATATTGT
201 ATTTTCCCG  CGCGGCTTGG  GTCATGTGTT  GAGCCACGAC  GGAAATGCG
251 GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACGGTCAAG
301 CAGTGCGGCA  ACGGACAGGA  TATGAGCCTG  TTTTGCGCCC  GTTTCGGCTA
351 CGACACCCAC  GCCGATTGTA  TGAACGGGCT  GCCTGAAACC  GTTTTCTGA
401 ACATTGCCCA  TCCGAGTTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451 AGCAAAAAAC  CTTTGACGGG  GACGGTTTCC  ATGGTCAACG  CATTGTCGTC

```

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501 CGTCCTGCTG GTGCTTATCC TGC GCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAAC CCGGATTGCG TTTGTGCGGT
801 CGCACTGTCT GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AggCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 KQGALLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      MDILDKLVDL AQLTGSADVQ CLLGGQW--- HETLQREGLV HIVTAGSGYL CIDGETSPRP
          10      20      30      40      50

          70      80      90      100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      VGTGDIVFFP RGLGHVLSHD GKYGESLQPD IRQNGTFMVK QCGNGLDMSL FCARFRYDTH
          60      70      80      90      100     110

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGT VSMVNALSSVLL VLILRAYLEQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SEKPLTGT VSVVNALPSVLL VLILRAYLEQ
          120     130     140     150     160     170

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKM VAAANMSRAQLM RRFKSRVGLS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKM VAAANMSRAQLM RRFKSQVGLS
          180     190     200     210     220     230

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLKKNPDSVLSVALS VGFQSETHFG KAFKRQYHVSPGQYRKEGGQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      PHAFVNHIRL QKGALLKKT PDSVLEVALS VGFQSETHFG KAFKRQYHVSPGQYRKEGGQ
          240     250     260     270     280     290

m160.pep KX
          ||
g160      KX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
1 ATGGACATTC TGGACAAACT GGTCGATTTC GCCCAATTGA CGGGCAGTGT
51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```

456

```

101 TGCAACGCGA AGGATTGGTA CACATTGTGA CATCGGCAG CGGCTATCTC
151 TGCATCGACG GCGAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTCCCG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAAATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGCGGCA ACGGACAGGA TATGAGCCTG TTTTGCGCC GTTCCCGTA
351 CGACACCCAC GCCGATTGA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCGTC
501 CGTCCTGCTG GTGCTTATCC TGCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTGTGCGGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGTCAAT ACCGGAAGA AGGCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```

a160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
 51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKFE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

m160/a160 100.0% identity in 301 aa overlap

```

              10      20      30      40      50      60
m160.pep      MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
              |||
a160           MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
              10      20      30      40      50      60

              70      80      90      100     110     120
m160.pep      VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
              |||
a160           VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
              70      80      90      100     110     120

              130     140     150     160     170     180
m160.pep      ADLMNGLPET VFLNIAHPSL QYVVSMLQLES KKPLTGTV SMVNALSSVLL VLILRAYLEQ
              |||
a160           ADLMNGLPET VFLNIAHPSL QYVVSMLQLES KKPLTGTV SMVNALSSVLL VLILRAYLEQ
              130     140     150     160     170     180

              190     200     210     220     230     240
m160.pep      DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
              |||
a160           DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
              190     200     210     220     230     240

              250     260     270     280     290     300
m160.pep      PHAFVNHIRL QKGALLLKKNPDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
              |||
a160           PHAFVNHIRL QKGALLLKKNPDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
              250     260     270     280     290     300

m160.pep      KX
              ||
a160           KX

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGGCGCGACA CCTCCGCAC
201 GCCCCATTGG AAAAACCCTT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTttg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCTG TTTACACGCA GGCGGTGCTG CTCCTTGATT
401 TTGCCGCGCT GGTATTGCTG CTTAATCCCT CGTCCGCGAG CGGTGAGGAA
451 CCGGCGGCAC TCGCCGGGCT GGCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGCAACC GGCGTGGCGA TGTCGTCggt ttgggagacg
601 Ctgaccggct ggCACAcccT GTCCTTTcca tcggcagttt ATCtgtCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAAct GtcgatgAcg cGCGcctaca
701 aaGTCGCGCA CAAATTCACG GTTGCCCTCGC tttcctaTat gaccgtcGTC
751 TTTTCCGCCC TGTCTGCCGC ATTTTCTCTg ggcgaagagc ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCCAT TGCCTTCAAA CAGCGGCTGC AAGCCCTCTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1  MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRLMFS
51  TVTLGAAAVL RRDTFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSSIFL AVFSFLILKE RISVYTOAVL LLGFAGVLL LNPFSRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTTACCATTG TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCCTT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACTGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCTG TTTACACGCA GGCGGTGCTG CTCCTTGATT
401 TTGCCGCGCT GGTATTGCTG CTTAATCCCT CGTCCGCGAG CGGTGAGGAA
451 ACGGCGGCAC TCGCCGGGCT GGCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCGTCGGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCGTG
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCTACA
701 AAGTCGCGCA CAAATTCACG GTTGCCCTCGC TTTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTCTCTG GCGGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1  MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRLMFS
51  TVALGAAAVL RRDxFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTOAVL LLGFAGVLL LNPFSRSGQE

```

151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
 201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
 251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
 301 *

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m161 / g161 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	: : : : :					
g161	MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRMFLSTVTLGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLILKE					
	: : : : :					
g161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLTTGVTLSYTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFAVLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	: : : : :					
g161	RISVYTQAVLLLGFAVLLNPSFRSGQEPALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
	: : : : :					
g161	WRVVFYLSATGVAMSSVWATLTGWHTLSFSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	: : : : :					
g161	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR					
	250	260	270	280	290	300
m161.pep	X					
g161	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 671>:

a161.seq

1	ATGGATACCG	CAAAAAAGA	CATTTTAGGA	TCGGGCTGGA	TGCTGGTGGC
51	GGCGGCTGC	TTTACCATTA	TGAACGTATT	GATTAAAGAG	GCATCGGCAG
101	AATTTGCCCT	CGGCAGCGGC	GAATTGGTCT	TTTGGCGCAT	GCTGTTTTC
151	ACCGTTGCGC	TCGGGGCTGC	CGCCGTATTG	CGTCGGGACA	CCTTCCGCAC
201	GCCCCATTGG	AAAAACCACT	TAAACCGCAG	TATGGTCGGG	ACGGGGGCGA
251	TGCTGCTGCT	GTTTACGCG	GTAACGCATC	TGCCTTTGGC	CACCGGCGTT
301	ACCCTGAGTT	ACACCTCGTC	GATTTTTTTG	GCGGTATTTT	CCTTCCTGAT
351	TTTGAAAGAA	CGGATTTCGG	TTTACACGCA	GGCGGTGCTG	CTCCTTGGTT
401	TTGCCGGCGT	GGTATTGCTG	CTTAATCCCT	CGTCCGCAG	CGGTCAGGAA
451	ACGGCGGCAC	TCGCCGGGCT	GGCGGGCGGC	GCGATGTCGG	GCTGGGCGTA
501	TTTGAAAGTG	CGCGAACTGT	CTTTGGCGGG	CGAACCCGGC	TGGCGCGTCG
551	TGTTTTACCT	TTCCGTGACA	GGTGTGCGCA	TGTCATCGGT	TTGGGCGACG
601	CTGACCGGCT	GGCACACCCT	GTCCTTTCCA	TCGGCAGTTT	ATCTGTCGTG
651	CATCGGCGTG	TCCGCGCTGA	TTGCCCAACT	GTCGATGACG	CGGCGCTACA
701	AAGTCGGCGA	CAAATTCACG	GTTGCCTCGC	TTTCCTATAT	GACCGTCGTT
751	TTTCCGCTC	TGTCTGCCGC	ATTTTTTCTG	GCCGAAGAGC	TTTTCTGGCA
801	GGAAATACTC	GGTATGTGCA	TCATCATCCT	CAGCGGTATT	TTGAGCAGCA

851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLES
51 TVALGAAAVL RRDTRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLIKE RISVYTOAVL LLGFAGVLL LNPSFRSGQE
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL AEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLESSTVALGAAAVL					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLESSTVALGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLIKE					
a161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLIKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTOAVLLLGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTOAVLLLGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTTRAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVFSALSAAFFLAELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq
1 ATGTTATT TTGACGACTTT GTTTTTTGTG TGTGTTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAAGAAG
101 TCATTTTTTAC CGAGTTCAGC TGGTTTTATG TTTAACGTT TTCCATTTTt
151 ctgGGTTTTc tgctGATACT CTCGGTCAGC GGTTTGGGAA ACATcagGCT
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTCCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCCTGGGCC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCAATTATT TTCGGACATT ACGGTCGGCG CGCCGGAACG
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTACG
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC

```

451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG ACCCCTGTGT
801 TTACCTGTGT TCGGCATTTC GCGACAACAT AGGGAACATC CTCGGAATC
851 TGGTGCGCCT CAGTTTGAAG ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTCCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATT CCCTGTTTTT TGTAACCTCT GCCGACTCCG GGATTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGCGGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAATGCGGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAGTGTA
1501 TTTTGACCGG GCGGCAAGTG GAAAGAACGG CTGGTGCGGA TAATGAGCCA
1551 GACGAGGAG CAGGATATTT TAAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

g163.pep

```

1 MVILTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFESIF
51 LGFLILSVS GLGNIRLGRD EDVPEFGFLS WLAMLFAAGM GVGLMFFGVA
101 EPLMHYFSDI TVGAPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFGVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAADPTVYLL SAFGDNIGNY LGNLVRLSLK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISK RTIREFVFGV LLIPGLFGLV
351 WFTVFGNTAI WLDNGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVRIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDEMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

m163.seq

```

1 ATGGTTATTT TGACGACTTT GTTTTTTGTTG TGTGTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAAAGAG
101 TCATTTTAC CGAGTTCAGC TGGTTTTATG TTTAACGTT TTCCATTTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTCTG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTGTA TGCAATATT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCCTTCACG
401 CTTGGTTCGG GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCCGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

```

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651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGTGCT GTTTTTTGT TTGGCGGCGG GACCCACTGT
801 TTACCTGTTG TCGGCATTCT GCGACAACAT AGGGAACATC CTCGGAAATC
851 TGGTGCGCCT CAGTTTTTAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGCGGGTT TGCTCATCC CCGGCCTGTT CGGCGTTTGT
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAAACG CTGCTTTTTA
1151 AATCTTTTAA TTACCTCCCC CTGCCCAGAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTTGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTGGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CTTGCACTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTGAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACAGACT GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AAATGTTTCA TCGGGACGAG CCCGCAATCG AGTTCGTATC
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

m163.pep

```

1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPALRS CFYPLKEKI SGRFGDAID MALLATFFGI ITTLGFASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSLNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISK RTIREFVFGV LLIPGLFGLV
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKEFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLIM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKQT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163 98.6% identity in 660 aa overlap

```

              10      20      30      40      50      60
m163.pep  MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS
          |||
g163      MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS
              10      20      30      40      50      60

              70      80      90      100     110     120
m163.pep  SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
          :|
g163      GLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITVGAPEHRQQ
              70      80      90      100     110     120

              130     140     150     160     170     180

```

462

m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	190 200 210 220 230 240
	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	250 260 270 280 290 300
	GVKVLSEINLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
g163	GVKVLSEINLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRLSLKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	310 320 330 340 350 360
	WFESWTVLYWAWWCWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
m163.pep	370 380 390 400 410 420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	430 440 450 460 470 480
	ITSRDKGLSAPRWQAVMWGVLSAVAVLLMRSGGLGNLQSM TLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGVLSAVAVLLMRSGGLGNLQSM TLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	490 500 510 520 530 540
	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQE QDILKFLKQTASPAMHELQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVRIMSQTQE QDILKFLKHTASPAMHELQR
	490 500 510 520 530 540
m163.pep	550 560 570 580 590 600
	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVS DQLINDGKLPHIR
g163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVS DQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	610 620 630 640 650 660
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

```

a163.seq
1  ATGGTTATTT TGACGACTTT GTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGTTTATG TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT

```

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201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCCTTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGTCTTGCCT TTTTGTGCT GTTTTTTGT TTGGCGGCGG GTCCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACAC CTCGGAATC
851 TGGTGCGCCT CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTCGGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTAA
1151 AATTTCTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCGG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGCTCG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTGAGCCTG TGGAAAGGAT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTGCGGC
1751 AGGATGTATC CGACCACTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

```

a163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFFVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAAGM GVGLMFFGVA
101 EPIMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSLNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYERHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLEFVL
351 WETVFGNTAI WLNDGVAGGV LEKMTSSPET LLEKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

          10      20      30      40      50      60
m163.pep  MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFFVLTFSIFLGFLILSVS
          |||||
a163      MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFFVLTFSIFLGFLILSVS
          10      20      30      40      50      60

          70      80      90     100     110     120
m163.pep  SLGNIRLGRDEDEVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ

```

	70	80	90	100	110	120
a163	SLGNIRLGRDEVDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTAFEHRQQ					
	130	140	150	160	170	180
m163.pep	QALLHTVEHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI					
a163	QALLHTVEHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI					
	190	200	210	220	230	240
m163.pep	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLLIIAAVMSLAVVSAISGVGK					
a163	MALLATFFGIITTLGFGASQLGAGLQEIIGWIAENSFSVQVLLIIAAVMSLAVVSAISGVGK					
	250	260	270	280	290	300
m163.pep	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP					
a163	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP					
	310	320	330	340	350	360
m163.pep	WFESWTVLYAWWCWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI					
a163	WFESWTVLYAWWCWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI					
	370	380	390	400	410	420
m163.pep	WLNDGVAGGMLEKMTSSPETILLEKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN					
a163	WLNDGVAGGVLEKMTSSPETILLEKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN					
	430	440	450	460	470	480
m163.pep	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL					
a163	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL					
	490	500	510	520	530	540
m163.pep	WKGLSADKKYFETRNVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKQTASPAMHELQR					
a163	WKGLSADKKYFETRNVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKHTASPAMHELQR					
	550	560	570	580	590	600
m163.pep	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR					
a163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR					
	610	620	630	640	650	660
m163.pep	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE					
a163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE					
	610	620	630	640	650	660
m163.pep	X					
a163	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

g164.seq (partial)

```

1 ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51 CAAGGCGCGC TTCCTGTTCG CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAAACGCCC GTCGAAAAAA TCATTGGGAC GGACAAAAGC
151 CGGCCGGCCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201 CCGCTTCCCC GAAAAACCCG ACTTGGGCGC CCAACCCCGG ATAAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTCTg ccgatgTTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAAtc cgttttCCcC ttttccaacG TTTTGAAAAA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTTAGATG GTTCAACCGC
601 ATCCGCCTGT TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651 CGATTTTAAA GCCAAGTTCC CCGCGGCCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCCGTC GTCGCCGTC AATACGCCGA ACGGCAAAAA
751 GCGCGCAGCG TCGGCATCCC CCTGCCCGGT TTGGAAGCCA AAGCCGTCGA
801 TGAAGAATTG GTCGAAGTGC CGCGCGCGCA AGTGGGCGAA CTGATCGTCA
851 GGGGCGGTTT GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901 GAAACCATCG TCAACGGCTG GTTGAAACG GCGGATTTG TTACCATAGA
951 CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAGAT TTGATTATTT
1001 CCAAAGGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTATC GCGGTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTGG
1151 GCGAGGACGA aatccgcgc caccTGCGTA CCGTGTGGC AAATTTCAAA
1201 ATCCCAAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

g164.pep (partial)

```

1 ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51 RPAGETAEGD AFFENVRRFP EKPDLGROPR INDLAHIIYT SGTTHGHPKGA
101 LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151 SILLVKSVP FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWYFRWFNR
201 IRLFISGGAP LAEQITLDFK AKFPRAKLE GYGLSEASPV VAVNTPERQK
251 ARSVGIPLP LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKDD LIISKQONVY PREIEEIHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRVTLANFK
401 IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

m164.seq

```

1 ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51 CAAAAACGGA AACGGCACGG CAGTGTTCTG CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCCGGCA CACGGTCGCG CTGGCGGTTT CCAATTCAC
201 AGAATTTATT ACCGCCTATT TCGCCATCTC CGCCATCGGC GCGGTCGCCG
251 TACCGATGAA CACATTTTGG AAAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGCGCTGT CAAAAGAATT
351 GCGGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAATCATT TGGACGGACA
401 AAAGCCGTCC GACCGCGGAA ACGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGATAAAA
501 TGATTTGGCA CACATCATCT ACACCTCCG CACGACGGGG CATCCCAAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTCT CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTT CAACGTTTTG
751 AAACAGACAC TGCTCAAACG CGGACCGTG TTTTGGGCG TACCCGCGAT
801 TTACACCGCG ATGAGCAAGG CGAAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATTCT CCTGTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAGGCTA

```

```

951 CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGA AGCCAAAGCC
1051 GTCGATGAAG AATTGGTGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301 ACAAACCTGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEEI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201 RIFKISKDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNV L
251 KQTLKRA TVFLGVP AIYTA MSKAKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFP RAKLLEGY GLS EASPVVAVNT PERQKAR SVGIPLPGLEAKA
351 VDEELVEVP RGEVGE LIVRG GSVMRGY LNM PAATDETI VN GWLKTGD FVT
401 IDEDFIFIV DRKKDLI ISK QONVYP REIE EEIYKL DAVE AA AVIGVKDR
451 YADEEIVAFV QLKEGMD LGE NEIRRH LRTV LANFKIP QI HFKDGLPRNA
501 TGKVLKRV LK EQFDGN K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

```

          60      70      80      90      100      110
m164.pep  GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK
g164      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          10      20      30
          120     130     140     150     160     170
m164.pep  ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT
g164      ELAGLKAQTPVEKIIWTDKSRPAGETAEGDAFFENVRRFPEKPD LGRQPRINDLAHIIYT
          40      50      60      70      80      90
          180     190     200     210     220     230
m164.pep  SGTTHGHPKGALISYANLFANLNGIERIFKISKRD RFIVFLPMFHSFTLTAMVLLPIYMAC
g164      SGTTHGHPKGALISYANLFANLNGIERIFKISKRD RFIVFLPMFHSFTLTAMVLLPIYMAC
          100     110     120     130     140     150
          240     250     260     270     280     290
m164.pep  SIILVKSVPFSNV LKQTLKRA TVFLGVP AIYTA MSKAKIPWYFRWFNRIRLFISGGAP
g164      SIILVKSVPFSNV LKQALLKRA TVFLGVP AIYTA MSKAKIPWYFRWFNRIRLFISGGAP
          160     170     180     190     200     210
          300     310     320     330     340     350
m164.pep  LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKAR SVGIPLPGLEAKAVDEEL
g164      LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKAR SVGIPLPGLEAKAVDEEL
          220     230     240     250     260     270
          360     370     380     390     400     410

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m164.pep  VEVPRGEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
|||||
g164      VEVPRGEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          280      290      300      310      320      330

          420      430      440      450      460      470
m164.pep  LIISKQNVYPREIEEEIYKLDVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
|||||
g164      LIISKQNVYPREIEEEIHKLDVEAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
          340      350      360      370      380      390

          480      490      500      510
m164.pep  HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
|||||
g164      HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
          400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAAACGGC AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGGGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCCTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTGT AAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCTT GTTCGCCTCG GCCGGCTGT CAAAAGAATT
351 GCGGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTGAAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCAAC CCGGATAAA
501 TGATTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTGCGCTAAT CAGCTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTTGGTC AAATCCGTTT TCCCTTTTC CAACGTTTGT
751 AAACAGGCAC TGCTCAAACG CGGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA CGAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATCCG CCTGTTTATC AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAGGCTA
951 CGGACTGAGC GAAGCCTCGC CCGTCGTCGC CGTCAATACG CCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGA AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCTGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1  MNRTYANFYE MLTAACRKNQ NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPGKALISYA NLFANLNGIE
201 RIFKISKDRD FIVFLPMFHS FTLTAMVLLP IYMACSIIIV KSVFPFSNVL
251 KQALLKRATV FLGVPAIYTA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEVGELIVRG GSVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDGFIFIV DRKKDLISK QONVYPREIE EEIYKLDVE AAIVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRLRTV LANFKIPKQI HFKDGLPRNA

```

501 TGKVLKRVLK EQFDGNK*

m164/a164 98.3% identity in 517 aa overlap

m164.pep	10	20	30	40	50	60
	MNRTYANFYEMLAACRKNGNGTAVFDGKEKTAYRALKQEAEEAAYLQNIQVKGFGDTVA					
a164	MNRTYANFYEMLTAAACRKNGNGTAVFDGKEKTAYRALKQEAEEAAYLQNIQVKGFGDTVA					
	10	20	30	40	50	60
m164.pep	70	80	90	100	110	120
	LAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
a164	LAVSNSTEFITAYFAVSAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
	70	80	90	100	110	120
m164.pep	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDLAGRQPRINDLAHIIYTSGETTG					
a164	KAQTPVEKIIWTDKSRPDGMAEGDAFFEDVRRFPEKPDLAGRQPRINDLAHIIYTSGETTG					
	130	140	150	160	170	180
m164.pep	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKRDGFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
a164	HPKGALISYANLFANLNGIERIFKISKRDGFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
	190	200	210	220	230	240
m164.pep	250	260	270	280	290	300
	KSVFPFSNVLKQTLKTRATVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
a164	KSVFPFSNVLKQALLKTRATVFLGVPAIYTAMSKTKIPWYFRWFNRIRLFISGGAPLAEQT					
	250	260	270	280	290	300
m164.pep	310	320	330	340	350	360
	ILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEELVEVPR					
a164	ILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEVAVDEELVEVPR					
	310	320	330	340	350	360
m164.pep	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLISK					
a164	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLISK					
	370	380	390	400	410	420
m164.pep	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
a164	GQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
	430	440	450	460	470	480
m164.pep	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLEQFDGNKX					
a164	LANFKIPKQIHFKDGLPRNATGKVLKRVLEQFDGNKX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq

1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC

```

51  GACTTTGGGC GTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cCGGTGGAAC
151 AACGcCGGca CGGGGCATTc CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCGc GGAAGGCAAG
301 TTGGAagaCA ATTCCTTCAT CAATGCcgtg ccgcatatGT Ctttggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtccgCTGAT TATGCGCGGC CGGgacgaa ACCAACCCGT
501 CGCCGCCAAC TATTCGCCG Aaggcacgga tgtcgATTc GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAA AACCAGATTc
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTcG GTCCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGTGGGGCG
1051 AATATGCCGC TGACCAAATA CcTGCTGGgC gAaTTGCgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

```

g165.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFRTQKLFEN MEFSTDNRKI
151 SDWAPLIMRG RDENQPVAA YSAEGTDVDF GRITROMVKY LQKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLQK
251 SGIPEGKGYG GLPVSGLFFR NSNPETAQEH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

```

m165.seq (partial)
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGAAC
151 AACGCCGCA CGGGGCATTc CGcGCTGTGc GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGc GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTCGATTc GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAA AACCAGATTc
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCGG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTcG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGTGGGGCG
1051 AATATGCCGC TGACCAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

```

m165.pep (partial)
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFRTQKLFEN MEFSTDNRKI
151 SDWAPLMMRG RDENQPVAA YSAEGTDVDF GRITROMVKY LQKGVKTEF

```

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m165.pep	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
g165	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQRFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165	ELNYAPLGADGVINPARALNIAEQFHVSQRFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m165.pep	HCSYLQKRYDAFKTQKLFENMEFSTDNRKISDWAPLMRGRDENQPVAANYSAEGTDVDF					
g165	HCRYLQKRYDVFKTQKLFENMEFSTDNRKISDWAPLMRGRDENQPVAANYSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m165.pep	GRLTRQMVKYLOGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA					
g165	GRLTRQMVKYLOGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDWQLTLRTRFLFLGA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m165.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYGOASVGAPPMSVPHL					
g165	GGGALTLLQKSGIPEGKGYGGLPVSGLFFRNSNPETAEQHNAKVYGOASVGAPPMSVPHL					
	250	260	270	280	290	300
	310	320	330	340	350	
m165.pep	DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK					
g165	DTRNVDGKRHLMFGPYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
	310	320	330	340	350	360
g165	ELRX					

```

a165.seq
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGCGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTCTGG GAAATCACC
101 TGATTGAACG CTTGGAAGAT TGGCGCTTGG AATCGTCAA CGCGTGAAC
151 AACGCCGGCA CGGGGCATT CCGCTGTGCG GAATTGAAC ATGCCCGTT
201 GGGTGCAAT GGGATTATCG ATCCGGCGCG CGCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGCGCA CGTTGGTCCG GGAAGGCAAG
301 TTGGAAGACA ATTCCCTCAT CAATCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAACCT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCTCGTAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCGG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGCGTAAA AACCGAGTTC

```

```
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCGCA ACCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAATTCC TCAAGCAAGG CTCATTATG GATTGTCGCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGGCA AACCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTAA
```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

a165.pep

```
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALE ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVNED HCSYLOKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAA N YSAEGTDVDF GRLTRQMVKY LQKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALLLQK
251 SGIEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQSLM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASILEYYPEA NPDDWELITA QORVQIIKID
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLEL VPGYGIKLE NPERADEIIA YTAKVLDI*
```

m165/a165 99.7% identity in 356 aa overlap

```
10 20 30 40 50 60
m165.pep MAEATDVVLVGGGIMSATLGVLLELEPSWEITLIERLEDVALESSNAWNAGTGHSALE
a165 MAEATDVVLVGGGIMSATLGVLLELEPSWEITLIERLEDVALESSNAWNAGTGHSALE
10 20 30 40 50 60
70 80 90 100 110 120
m165.pep ELNYAPLGANGIIDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVNED
a165 ELNYAPLGANGIIDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVNED
70 80 90 100 110 120
130 140 150 160 170 180
m165.pep HCSYLOKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGDRDENQPVAA N YSAEGTDVDF
a165 HCSYLOKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGDRDENQPVAA N YSAEGTDVDF
130 140 150 160 170 180
190 200 210 220 230 240
m165.pep GRLTRQMVKYLQKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQTLRTRFLFLGA
a165 GRLTRQMVKYLQKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQTLRTRFLFLGA
190 200 210 220 230 240
250 260 270 280 290 300
m165.pep GGGALLLQKSGIEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASV GAPPMSVPHL
a165 GGGALLLQKSGIEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASV GAPPMSVPHL
250 260 270 280 290 300
```

g165-1.seq

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

g165-1.pap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

n165-1.seq

1	ATGGCTGAAG	CGACAGACGT	TGCTCTGGTG	GGCGCGGCA	TTATGAGCGC
51	GACTTTGGGC	GTTTTCGCTA	AAGAATCTGA	ACCGTCTTGG	GAATCAGCCC
101	TAGCTGAAGC	CTTGGGAAGT	GTGGCGTTGG	AATCGTCAAA	CGCGTGGAAC
151	AACGCCGACG	CGGGGCATTC	CGCGCTGTGC	GAATTGAATC	ATTGCCGGTT
201	GGGTGCAAA	GGGATTATG	ATCCGGCCGG	CGCCCTCAAT	ATTGCCGAAC
251	ATGTTTCATG	CAGCCGCCAG	TTTGGGGCGA	CGCTCGTTCG	GGAAAGCGCA
301	TGGGAAGACA	ATTCTTCAT	CGATGCCGTG	CCGCATATGT	CTTTGGTGAT
351	GAATGAAGAC	CATTGTTCTT	ATCTTCAAAA	ACGTTATGAC	CGGTTTAAAA
401	CCCAAAAAT	TTTTGAAAT	ATGGAATTTT	CCACGATCG	GACAAAATTT
451	TCCGATTGGG	CTCCGCTGAT	GATGCGCGG	CGGGACGAAA	ACCAACCGGT
501	CGCCGCCAAC	TACTCCGCCG	AAGGTACGGA	TGTCGATTTC	GGACGGCTGA
551	CGCGCCAAAT	GGTGAATAT	TTGCAGGGCA	AGGCGGTAAA	AACCGAGTTC
601	AACCGCCACG	TGGAAGACAT	CAACGCGGAA	TCCGACGTGG	CGTGGGTGCT
651	CAAAACCGCC	GATACCCGCA	ACCCGACGG	GCAGCTCACC	CTCCGTATCC
701	GC TTCCTCTT	CCTCGGCGCG	GGCGGCGGCG	CGCTGACCC	GCTGCAAAAA
751	TCCGGCATCC	CCGAAGGCCA	AGGCTACGGC	GGCTTCCCCG	TGTCGGCCAGT
801	GTTCCTTCGC	AACAGCAACC	CGGAAACCGC	CGCAACACAC	AACGCCAACT


```

851 TGTACGGGCA GGCTTCCGTC GCGCGCGCCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTTCGCCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGTGGGCG GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACT CCGGAGGCA AACCCGACG
1151 ACTGGGAATC CATCACCGCA GGGCAACGCG TCCAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCACGC
1251 CGACGGCTCA CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACGCTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GCGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTATTGGA TATTAA

```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

```

m165-1.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALE ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDNRKI
151 SDWAPLMRGR RDENQPVAA N YSAEGTDVDF GRLTRQMVKY LQGGKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAQH NAKVYQASV GAPPMSVPHL
301 DTRNVGKRHL MFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLEYYPEA NPDDWELITA GQRVQIIKID
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165-1/g165-1 89.7% identity in 428 aa overlap

m165-1.pep	10	20	30	40	50	60
	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALE					
g165-1	10	20	30	40	50	60
	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALE					
m165-1.pep	70	80	90	100	110	120
	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165-1	70	80	90	100	110	120
	ELNYAPLGADGVINPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
m165-1.pep	130	140	150	160	170	180
	HCSYLQKRYDAFKTQKLFENMEFSTDNRKISDWAPLMRGRDENQPVAAANYSAEGTDVDF					
g165-1	130	140	150	160	170	180
	HCRYLQKRYDVFKTQKLFENMEFSTDNRKISDWAPLMRGRDENQPVAAANYSAEGTDVDF					
m165-1.pep	190	200	210	220	230	240
	GRLTRQMVKYLQGGKGVKTEFNRHVEDIKRESGAWVLKTADTRNPDGQLTLRTFLFLGA					
g165-1	190	200	210	220	230	240
	GRLTRQMVKYLQGGKGVKTEFNRHVEDIKRESGAWVLKTADTRNPDGQLTLRTFLFLGA					
m165-1.pep	250	260	270	280	290	300
	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAAPPMSVPHL					
g165-1	250	260	270	280	290	300
	GGGALTLLQKSGIPEGKGYGGLPVSGLFFRNSNPETAQHNAKVYQASVGAAPPMSVPHL					
m165-1.pep	310	320	330	340	350	360
	DTRNVGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG					
g165-1	310	320	330	340	350	360
	DTRNVGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
m165-1.pep	370	380	390	400	410	420
	ELRKTKEERFASLLEYYPEANPDWELITAGQRVQIIKIDSEKGGVLQFGTEIVAHADGS					
g165-1	370	380	390	400	410	420
	ELRKTKEERFASLLEYPR-QTRRLVLITQXTR-HIIXYDS-KLRVLQLYEIVPRDARSR					
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
:
g165-1 ILERRGASRXALISADDTAPSAPVLESVX
420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq
1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51 GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTG CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTTCATG CAGCCGCCAG TTTTGGGCGA CGTTGGTTCG GGAAGGCAAG
301 TTGGAAGACA ATTCCCTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATGTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTAAAAA
401 CCCAAAAAT TTTTGAAAT ATGGAATTTT CCACCGATCG GAACAAAAAT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCTG
501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCTCTCT CCTCGGCGCG GCGGCGGCGG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGGTTTCCCG TGTCGGGCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAG
851 TGTACGGGCA GGCTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAATTCC TCAAGCAAGG CTCACTTATG GATTGGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCCG TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAATACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAACAT CATCACCGCA GGGCAACCGG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTAA

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSAIC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAA NYSAGTDVDF GRLTRQMVKY LQKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GORVQIIKID
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

a165-1/m165-1 99.4% identity in 488 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNAGTGHSAIC					
m165-1	MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNAGTGHSAIC					
	10	20	30	40	50	60
	70	80	90	100	110	120
a165-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED					
m165-1	ELNYAPLGANGIIDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
a165-1.pep	HCSYLQKRYDAFKTKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAA NYSAGTDVDF					
m165-1	HCSYLQKRYDAFKTKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAA NYSAGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240

```

a165-1.pep  GRLTRQMVKYLGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
m165-1      GRLTRQMVKYLGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190      200      210      220      230      240

              250      260      270      280      290      300
a165-1.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYGOASVGAPPMSVPHL
m165-1      GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYGOASVGAPPMSVPHL
              250      260      270      280      290      300

              310      320      330      340      350      360
a165-1.pep  DTRNVGDKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
m165-1      DTRNVGDKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG
              310      320      330      340      350      360

              370      380      390      400      410      420
a165-1.pep  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
m165-1      ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
              370      380      390      400      410      420

              430      440      450      460      470      480
a165-1.pep  LAALLGASPGASTAVPLMIRLMHQCFFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
m165-1      LAALLGASPGASTAVPLMIRLMHQCFFPERTPSWEDRLKELVPGYGIKLNENPERADEIIA
              430      440      450      460      470      480

              489
a165-1.pep  YTAKVLDIX
m165-1      YTAKVLDIX

```

a165-1/p33940

sp|P33940|YOJH_ECOLI_HYPOTHETICAL_60.2_KD_PROTEIN_IN_ECO-ALKB_INTERGENIC_REGION
>gi|1736851|gnl|PID|d1016718 (D90850) ORF ID: o372#5; similar to [SwissProt Accession Number
P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical
to 490 residues of YOJH_ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct
identical to GB: ECOHU49_33
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548
Score = 458 bits (1167), Expect = e-128
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

```

Query: 3  EATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALCEL 62
+ TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL
Sbjct: 30  QETDVLLIGGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSALMEL 89

Query: 63  NYAPL GANGI IDPARALNIAEQFHSRQFWATLVAEGKLED-NSFINAVPHMSLVMNEDH 121
NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
Sbjct: 90  NYTPQNADGSISIEKAVAINAEAFQISRQFWAHQVERGLRTPRSFINTVPHMSFVWGEDN 149

Query: 122  CSYLQKRYDAFKTQKLFENMEFSTDNRNKISDWAPLMMGRDENQPVAANYSAEGTDVDFG 181
++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
Sbjct: 150  VNFLRARYAALQQSSLFRGMRYSIEDHAQIKEWAPLVMEGRDPQKVAATRTEIGTDVNYG 209

Query: 182  RLTRQMVKYLGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
+TRQ++ LQ K ++ V +KR D W + AD +N Q
Sbjct: 210  EITRQLIASLQKSNFSLQLSSEVRALKRNDNTWTVTVDLKNGTAG-NIRAKFVFIGA 268

Query: 241  XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYGOASVGAPPMSVPHL 300
Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
Sbjct: 269  GGAALKLLQESGIPEAKDYAGFPVGGQFLVSENPDVNNHHLAKVYGKASVGAPPMSVPHI 328

Query: 301  DTRNVGDKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
Sbjct: 329  DTRVLDGKRVVLFPGPFATFSTKFLKNGSLWDLMSSTTSNVMPMMHVGLDNFDLVKYLVS 388

Query: 361  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVXXXXXX 420
++ ++E+RF +L EYYP+A +DW L AGORVQIIK+D+EKGGVL+ GTE+V
Sbjct: 389  QVMLSEEDRFEALKEEYPOAKKEDWRLWQAGORVQIIKRDAEKGGLRLGTEVVSDDQQT 448

Query: 421  XXXXXXXXXXXXXVPLMIRLMHQCFFERT--TPSWEGRLKELVPGYGIKLNENPERADEI 478

```

P+M+ L+ + F +R +P W+ LK +VP YG KLN + +
 Sbjct: 449 IAALLGASPGASTAAPIMLNLEKRVFGDRVSSPOWQATLKAIVPSYGRKLNQDVAATERE 508
 Query: 479 IAYTAKVLDI 488
 + YT++VL +
 Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq
 1 atggcgccgg cggaaataaa acgccccctc gctgtcgatt tccagcacat
 51 agcgtccgtt ctgcacggcg gcatagccgc ttttgccctgc ctgatagggg
 101 tgcagggcgg aatgcgaaat caggtaatca gtcagtttgc cgccgtcttc
 151 ggcgatattg cccaccagtt tggcaaaciaa ggtatggcac acgcccgttt
 201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg
 251 acgacggcct ccaagtcggt gggatgcttt ccggtcagcc ggacggcgtt
 301 ttgttccggc aagcctttaa tcggataact gatttgtttt ttgccgtcgt
 351 tggttttgcc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta
 401 ttgtcgatgt atttgacttt gaaaaccggg ttcggcgcgcc tttgtccgac
 451 attttgccgc tgttccgccc tattttcggg tttgccgcag gcggcaagca
 501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc
 551 tgatgggttc aaaatgccgt ctgaaatgcc gtctgaaacg tggcaggcgg
 601 aggttcggac ggcattgggt ttatttcaac gggcggatgc cgaccgcac
 651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgct tttgcgcgc
 701 ctgcctgcaa aatctcttcg atttgcggaag gattagaggt caatgcggtg
 751 tag

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep
 1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF
 51 GDIAHQFGKQ GMAHAVFREPA RRRVLSVGFH TFADDGFOVV GMLSGQPDGV
 101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDF ENRFRALCR
 151 ILRLFRIRIF FAAGGKQQA AOHGKRYFOH SALLMVSKCR LKCRLLKGRRR
 201 RFGRHWVYFN GRMPTASRTL SNNSRASLRA FCAPACKISS ICEGLEVNAL
 251 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq
 1 ATGGCGGCGG CGGAAATAAA ACGCCCCTTC GCTGTGCGATT TCCAGCACAT
 51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCCTGC CTGATAGGGT
 101 TGCAGGGCGG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC
 151 GGCATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT
 201 CTGCCCAACC TGCCGACTG TCCTTATCAT CCGTTTCCAT ACATTGCGC
 251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT
 301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTGTGTTT TTGCCGTCGT
 351 TGGTTTTGCC TTCGCTGCTT TGTCCCAAAT CCAAACCGGC AATCGCCGTA
 401 TTGTGCATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC
 451 GTTTTGCGGC TGTACCGCG TATTTwCGGA TTTGCCGCaC GGCaaRGcAG
 501 CAGGCAGCCG CCCAATACGG CAAAaAwGT wTTCAGCATT CCACaYTCCT
 551 GATGGTTTCA AAATGCGGTC TGAAACGCGG CAGGCGGAGG TTCGGACGGC
 601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATCgGT ACTTTGTCCA
 651 ATAATTGCGG TGCTTCTTTA CGCGCTTTCG CCGCGCCTGC CTGCAAAATC
 701 TCTTCGATT GCGAAGGGTC GCGGTCAGC TCGTTGTAG

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep
 1 MAAAEIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN *VIRQFAAVF
 51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI
 101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRALYR
 151 VLRLYRRIXG FAATAQQQA AQYKXXXQH STXLMVSKCR LKGRRRRFRG
 201 HRVHFNGRMP TASGTLSNNS RASLRAFAAP ACKISSICEG SAVSSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 204 shows 82.0% identity over a 250 aa overlap with a predicted ORF (ORF 204.ng) from *N. gonorrhoeae*:

m204/g204

	10	20	30	40	50	60
m204 . pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIGLQGGMRNXVIRQFAAVFGDIAHQFGKQ					
g204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIGLQGGMRNQVISQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204 . pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
g204	GMAHAVFRPARRRVL SVGFHTFADDDGFQVVGMLSGQPDGVLFRQAFNRITDLFFAVVGFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m204 . pep	FAALSQIQTNRRIVDIYDFENRFRRLALYRVLRLYRRIXGFAATAXQQAAYGKXXQH					
g204	FATLSQSQTGNRRIVDFDFENRFRRLALYRVLRLYRRIXGFAATAXQQAAYGKXXQH					
	130	140	150	160	170	180
	190	200	210	220	230	
m204 . pep	STXLMVSKCRLK----RGRRRRFGHRVHFNGRMPTASGTLNNNSRASLRAFAAPACKISS					
g204	SALLMVSKCRLKCRLLKGRRRRFGHRVHFNGRMPTASRTLSNNNSRASLRAFCAPACKISS					
	190	200	210	220	230	240
	240					
m204 . pep	ICEGSAVSSLX					
g204	ICEGLEVNAL					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

a204 . seq

```

1  ATGGCGGCGG CGGAAATAAA ACGCCCCCTC GCTGTCGATT TCCAGCACAT
51  AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCTGC CTGATAGGGT
101 TGCAGGCGCG AATGCGAAAT CAGGTAATCC GTCAGTTTGC CGCCGTCTTC
151 GGCGATATTG CCCACAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTG
201 CCGCCAGCC CGAAGGCGCG CCCTTCCGT CGGTTTCCAT ACATTGCGG
251 ACGACGGCTT CCAAGTCGTT GGGATGCTTG CCGGTCAGCC GGACGACGTT
301 TTGTTCCGGC AAGCCTTT .....

```

This corresponds to the amino acid sequence <SEQ ID 702; ORF 204.a>:

a204 . pep

```

1  MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVIRQFAAVE
51  GDIAHQFGKQ GMAHAVCRPA RRRALSVGFH TFADDGFQVV GMLAGQPDV
101 LFRQAF....
151 .....KRFR
201 HWVYFNGRIP TASRTLNNNS RASLRAFCAP ACKISSICEG SAVSSL*
```

478

m204/a204 54.5% identity in 246 aa overlap

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIQLGGMRNXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIQLGGMRNOVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTLIIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
a204	GMAHAVCRPARRRALSFGFHTFADDGFQVVGMLAGQPDVLFQAF-----					
	70	80	90	100		
	130	140	150	160	170	180
m204.pep	FAALSQIQTGNRRIVDIYDFENRFRRLYRVLRLYRRIXGFAATAXQAAAQYKXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKCRLKRGRRRFGRHVRHFNGRMPTASGTLNNSRASLRAFAAPACKISSICEG					
a204	-----KRFGRHWVVFNGRIPTASRTLNNNSRASLRAFCAPACKISSICEG					
	110	120	130	140	150	
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

g205.seq

```

1  atgctgaaaa taccttttgc cgtggtgggc ggctgcctgc tgcttgccgc
51  ctgcggaaca tccgaaaata cggcggaaca gccgcaaat gcggcacaaa
101 gcgcgccgaa accggttttc aaagtcaaat acatcgacaa tacggcgatt
151 gccggtttgg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaaca aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgtcgt cgcaaatgt
301 atggaaaccg acggaagga cgcgccttcg ggctgggagg aaaacggcgt
351 gtgccatacc ttgttgcca aactggtggg caatatcgcc gaagacggcg
401 gcaaactgac tgattacctg atttcgcatt ccgccctgca accctatcag
451 gcaggcaaaa gcggctatgc cgccgtgcag aacggacgct atgtgctgga
501 aatcgacagc gagggggcgt tttatttccg ccgccccat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

g205.pep

```

1  MLKIPFAVLG GCLLLAACGK SENTAEQPON AAQSAPKPVF KVKYIDNTAI
51  AGLALGQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNTA EDGKLTGYL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

m205.seq

```

1  ATGCTGAAWA CwTyTTTTGC CGTATTGGGC GGCTGCCTGC TGCyTtGCCG
51  tCGGGCAAAT CCGwAAATAC GGCGGTACAG CCGCAAAACG CGGTACAAAG
101 CGCGCCGAAA CCGGTTTTCA AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTGGA TTTGGGACAA AGCAGCGAAG GCAAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGGA AGCCGTCAGC GGCAAATGTA
301 TGAAACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTTGCCAA ACTGGTGGGC AATATCGCCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TTTCGCATGC CGCCCTGCAA CCCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCCGC CGCCGCCATT ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

m205 . pep
 1 MLXTXFAVLG GCLLXCRCGK SXNTAVQPON AVQSAPKPVF KVIYIDNTAI
 51 AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
 101 METDDKDDPA GWAENGVCHT LFAKLVGNIA EDGGKLT DYLVSHAALQPYQ
 151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

m205/g205

	10	20	30	40	50	60
m205 . pep	MLXTXFAVLGGCLLXCRCGKSXNTAVQPONAVQSAPKPVFKVIYIDNTAIAGLDLGQSSE					
g205	MLKIPFAVLGGCLLLAACGKSENTAEQPNAAQSAPKPVFKVIYIDNTAIAGLALGQSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m205 . pep	GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDDSPAGWAENGVCHT					
g205	GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m205 . pep	LFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFFYFRRRH					
g205	LFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFFYFRRRH					
	130	140	150	160	170	180
m205 . pep	YX					
g205	Y					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

a205 . seq (partial)
 1 TCCGAACCTC TTAAAGGCTT GCCGGAACAA AACGTCGTCC GGCTGACCGG
 51 CAAGCATCCC AACGACTTGG AAGCCGTCGT CGGCAAATGT ATGGAAACCG
 101 ACGGAAAGGG CGCGCCTTCG GGCTGGGCGG CAAACGGCGT GTGCCATACC
 151 TTGTTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG GCAAACCTGAC
 201 GGATTACCTG ATTTGCGATT CCGCCCTGCA ACCCTATCAG GCAGGCAAAA
 251 GCGGCTATGC CGCCGTGCAG AACGACGCT ATGTGCTGGA AATCGACAGC
 301 GAGGGGGCGT TTTATTTCCT CCGCCGCCAT TATTGA

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

a205 . pep (partial)
 1 SEPLKGLPEQ NVVRLTGKHP NDLEAVVGKC METDGKGAPS GWAANGVCHT
 51 LFAKLVGNIA EDGGKLT DYLVSHAALQPYQ AGKSGYAAVQ NGRYVLEIDS
 101 EGAFYFRRRH Y*

m205/a205 88.3% identity in 111 aa overlap

	50	60	70	80	90	100
m205 . pep	KVIYIDNTAIAGLDLGQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC					
a205	SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC					
	10	20	30			
	110	120	130	140	150	160
m205 . pep	METDDKDDSPAGWAENGVCHTLFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQ					

g205-1.seq (partial)

```
1 ATGCTGAAAA TAcCTTTTGC CGTGTGTGGGC GGCTGCCTGC TGCTTGCCGC
51 CTGCGGCGAAA TCCGAAAATA CGGCGGAACA GCCGCAAAAT GCGGCACAAA
101 GCGCGCGGAAA ACCGGTTTTC AAAGTCAAAT ACATCGACAA TACGCGGATT
151 GC CGGTTTGG CTTTGGGACA AAGTAGCGAA GCGAAACCA ACACGCGCAA
201 AAAACAAATC AGTTATCGGA TTAAGGCTT GCCGGAACAA AACGCCGTCC
251 GGCTGACCGG AAAAGATCCC AACGACTTGG AAGCCGTCGT CGGCAAAATGT
301 ATGGAACCGG ACGGAATCGA CGCGCTTGG CGATGGGCGG AAAACGGCGT
351 GTGCCATACC TTGTTTGCCA AACTGGTGGG GAATATCGCC GAAGACGCGT
401 GCAAACTGAC TGATTACCTG ATTTGCAATT CCGCCCTGCA ACCCTATCAG
451 CAGAGCAAAA CGCGGTATGC CGCCGTGAC AACGGACGCT ATGTGCTGGA
501 AATCGACAGC GAGGGGGCGT TTTA
```

g205-1.pep (partial).

```
1  MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51 AGIALGGSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVKTI LFAKLGVGNIA EDGGKLT DYL ISHSALQPYQ
151 AKSGSYAAVO NGRVYLEIDS EGAF
```

m205-1.seq..

```
1 ATGCTGAAAA CATCTTTTGC CGTATTGGGC GGCTGCCTGC TGCTTGCCGC
51 CTGCGGCGAA TCCGAAAATA CGGCGGACCA CGCGCAAAAC GCGGTACAAA
101 CCGCGCCGAA ACCGGTTTTC AAAGTCAAA ATATCGACAA TACGGCGATT
151 GCCGGTTTGG ATTTGGGACA AAGCAGCGAA GGCAAAACCA ACGACGGCAT
201 AAAACAAATC AGTTATCCGA TTAAGAGCTT GCCGGAACAA AATGTTATCC
251 GACTGATCGG CAAGCATCCC GGCAGCTTGG AAGCCGTCAG CGGCAAAATG
301 ATGGAACACG ATGATAAGGA CAGTCCGGCA GTTTGGGCAG AAAACGGCGT
351 GTGCCATACC TTGTTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG
401 GCAAAGTACG GGATTACCTA GTTTCGCATC CCGCCCTGCA ACCCTATCAG
451 GCAGGCAAAA GCGGCTATGC CGCCGTCAG AACGGACGCT ATGTGTCGGA
501 AATCGACAGC GAAGGGGCGT TTTATTTCG CGCCGCCCAT TATTGA
```

m205-1.pap

1	<u>MLKTSFAVLG</u>	<u>GCLLLAACGK</u>	SENTAEQPQN	AVQSAPKPVF	KVKYIDNTAI
51	AGLDLGQSSE	GKNTDGGKKI	SYPIKGLPEQ	NVIRLIGKHP	GDLEAVSGKC
101	METDDKDSPA	GWAENGVCIT	LFAGLVGNIA	EDGGKLTDL	VSHAALQPYQ
151	KAGQQAAYAO	NGRYVLECHS	EGAFYFRHRH	Y*	

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAACGKSENTAEQPNAAQSAPKPVFKVKYIDNTAIGLALGQSSE					
m205-1	MLKTSFAVLGGCLLLAACGKSENTAEQPNNAVQSAPKPVFKVKYIDNTAIGLDLGQSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT					
m205-1	GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKQDSPAGWAENGVCHT					


```

              70      80      90      100      110      120
            130      140      150      160      170
g205-1.pep  LFAKLVGNI AEDGGKLT DYLI SHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAF
m205-1      LFAKLVGNI AEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
            130      140      150      160      170      180
m205-1      YX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 713>:

```

a205-1.seq (partial)
1  CCTCTTAAAG GCTTGCCGGA AAAAAACGTC GTCCGGCTGA CCGGCAAGCA
51  TCCCAACGAC TTGGAAGCCG TCGTCGGCAA ATGTATGGAA ACCGACGGAA
101 AGGCGCGGCC TTCGGGCTGG GCGGCAACG GCGTGTGCCA TACCTTGTTT
151 GCCAAACTGG TGGGCAATAT CGCCGAAGAC GCGGCAAAAC TGACGGATTA
201 CCTGATTTTC CATTCGCCCC TGCAACCTTA TCAGGCAGGC AAAAGCGGCT
251 ATGCCGCCGT GCAGAACGGA CGCTATGTGC TGGAAATCGA CAGCGAGGGG
301 GCGTTTTATT TCCGCCGCCG CCATTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 714; ORF 205-1.a>:

```

a205-1.pep (partial)
1  PLKGLPEQNV VRLTGKHPND LEAVVGKCM ETDGKGAPSGW AANGVCHTLF
51  AKLVGNI AEDGGKLT DYLI SHSALQPYQAG KSGYAAVQNG RYVLEIDSEG
101 AFYFRRRHY*

```

m205-1/a205-1 89.0% identity in 109 aa overlap

```

              50      60      70      80      90      100
m205-1.pep  KYIDNTA IAGLDLGSSEK TNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCM E
a205-1      PLKGLPEQNVVRLTGKHPNDLEAVVGKCM E
              10      20      30

            110      120      130      140      150      160
m205-1.pep  TDDKDSPAGWAENG VCHTLFAKLVGNI AEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNG
a205-1      TDGKGAPSGWAENG VCHTLFAKLVGNI AEDGGKLT DYLI SHSALQPYQAGKSGYAAVQNG
              40      50      60      70      80      90

            170      180
m205-1.pep  RYVLEIDSEGAFYFRRRHYX
a205-1      RYVLEIDSEGAFYFRRRHYX
              100      110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 715>:

```

g206.seq
1  atgttttccc cgcacaaaac ctttttcctc tgtctcggcg cactgctcct
51  cgcctcatgc ggcacgacct ccggcaaaaca ccgccaaccg aaaccctaaac
101 agacagtccg gcaaatccaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctcggactca tcggcacgcc
201 ctacaaatgg ggcgcagca gcaccgcaac cggcttcgac tgcagcggca
251 tgattcaatt ggtttacaaa aacgcctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atccccgaca gccgcctcaa
351 ggccggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgaat tcattccatgc ccccggcagc
451 ggcaaaacca tcaaaaccga aaaactctcc acaccgtttt acgcaaaaaa
501 ctaccttgga gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 716; ORF 206.ng>:

```

g206.pep
1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT

```

51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPR
 101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS
 151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 717>:

m206.seq
 1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
 151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
 201 CTACAAATGG GCGGCGAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
 251 TGATTCAATT CGTTTACAAr AACGCCCTCA ACGTCAAGCT GCCGCGCACC
 301 GCCCGCGACA TGGCGGCGGC AAGCCGsAAA ATCCCGGACA GCCGCTCAA
 351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
 401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
 451 GGCAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTT ACGCCAAAAA
 501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

m206.pep..
 1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
 51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
 101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
 151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
g206	MFSPDKTLFLCLGALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS					
	10	20	30	40	50	60
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRXKAGD					
g206	LGLIGTPYKWGGSSTATGFD CSGMIQLVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRXKAGD					
g206	LGLIGTPYKWGGSSTATGFD CSGMIQLVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	LVFFNTGGAHRYSHVGLYIG NGEFIHAPSSGKTIKTEKLS TPFYAKNYLGAHTFFTEX					
g206	IVFFNTGGAHRYSHVGLYIG NGEFIHAPSGKTIKTEKLS TPFYAKNYLGAHTFFTE					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 719>:

a206.seq
 1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
 151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
 201 CTACAAATGG GCGGCGAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
 251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
 301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCGGACA GCCGCCTTAA
 351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
 401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
 451 GGCAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTT ACGCCAAAAA
 501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
  1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
 51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP
101 ARDMAAASRK IPDSRLKAGD LVFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TFFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYKNALNVKLPRPTARDMAAASRKIPDSRXKAGD					
a206	LGLIGTPYKWGGSSTATGFD CSGMIQFVYKNALNVKLPRPTARDMAAASRKIPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
  1 atgctgcggc atttaggaaa cgacttcgcc ttgggcgcgt tgtttttcga
 51 tgctgcgggt gatgtgccac tgctgggcga tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcgggttcag ataggtttgg gcgaacatcg ttgccgccat aatgatgggc
251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgccccag tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt cttcgaaaag ctgcatcatc gcttgcgtgt gcgccatacg
451 gtcgtgcgcg tatttttctt tgatggtctg cagttcgggt gcggcggcac
501 gcattttcgc catcgaaagg taggaggcgt tggtaaatgg atacagtacg
551 gctttgacga tgatggtcaa aacgacgatt gccagcccc agttgccgat
601 aatgttgtgc agttggttca ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggtgtcggc gatgtttgcy
701 ataacggatg tggtttgagg accggcatac aggttgaccg ccattttcgg
751 ttttggcccc cgggttgga tagcgggtaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
  1 MLRHLGNDEA LGALFFDAV DVPLLGDGQE VVDHPVENQT GREEEHDGE
 51 NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AEVGNPAQP
101 RCLAQFYGGE QCPVQADEDG DLQQHRTAA QRVDPLVFKE LHRLLLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQEP EERRCEPVYFT VVFCQLQVVG DVCNCGCLR TGIQVDRHFR
251 FWPPGWDG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
  1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGGTT GTTTTTCGAT
 51 GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAAGAGG TTGTTGACTA
101 CCGAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTTCGCC TGCATCGGGT CGGTCGGCGG
201 CGGGTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
```

```

301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAGC TGCATCATCG CCTGTTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGGCGGCACG
501 CATTTTCGCC ATAGAGCGGT AAGAGGCGTT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTTGTGCA GTTGGTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTGCGCG ATGTTTGC GA
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTGATGGA GGCTTCGgTT
751 TCGCGCCGTT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTGCT TCGGCGCTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT TGCCTTTTAG GTTGAGAAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT GCCGAGCCAG CCGGTCGGGG TTTTGCGGAT GTATTTCGGCC
951 TCGGATTTGC CGGATTTGGC ATCGTCGTCC AAGTCGGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
1 MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDGE
51 NQRHDFHHFR LHRVGRRRVQ ISLGEHRCRH NDQDQVVG VGAAEVGNPTQP
101 RCLAQFYGGE QCPIQSDG DLQHRQAAA QRVDFLVCVK LHHRLLLRHT
151 VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW IQYGFDDDG* NDNRPAFVAD
201 DVVQLVQEP EERGEPVYFA VVFGQLQVVG DVCDDGCGLR AGVEVDGGFG
251 FAPFWMAAKG TLTVLVLSL LRLMSMLHS PAAQTLCLPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng)

from *N. gonorrhoeae*:

```

m209/g209
10      20      30      40      50      60
m209.pep MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDG ENQRHDFHHFR
|||||
g209      MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDHPVENQT GREEEEHDG ENQRHDFHHFR
10      20      30      40      50      60

70      80      90      100     110     120
m209.pep LHRVGRRRVQ ISLGEHRCRH NDQDQVVG VGAAEVGNPTQPRCLAQFYGGEQCPIQSDG
|||||
g209      LHRVGRRRVQ IGLGEHRCRH NDQDQVVG VGAAEVGNPAQPRCLAQFYGGEQCPIQADEG
70      80      90      100     110     120

130     140     150     160     170     180
m209.pep DLQHRQAAA QRVDFLVCVK LHHRLLLRHT VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW
|||||
g209      DLQHRQTA AQRVDFL VFEKLHRL LLLRHTV VAVFFDGL QFGCGGTHFR HRTVGGVGQW
130     140     150     160     170     180

190     200     210     220     230     240
m209.pep IQYGFDDDGXNDNRPAFVADDVVQLVQEP EERGEPVYFA VVFGQLQVVG DVCDDGCGLR
|||||
g209      IQYGFDDDGQNDDCPAPVADNVVQLVQEP EERRCEPVYFTVVFQQLQVVG DVCDDGCGLR
190     200     210     220     230     240

250     260     270     280     290     299
m209.pep AGVEVDGGFGF-APFWMAAKG TLTVLVLSL LRLMSMLHS PAAQTLCLPL GWRIQVDMK
:||||
g209      TGIQVDRHFRFWPPGWD SG
250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
1 ATGCTGCGGC ATTAGGAAA CGACTTCGCC TTGGGCGCGT TGTTTTTCGA

```

```
51 TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGATC
101 ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151 AACCAAAGGC ATGATTTTCA TCATTTTCGC CTGCATCGGG TCGGTCGGCG
201 GCGGGTTCAG ATAGGTTTGG GCGAACATCG TTGCCGCCAT AATGATGGGC
251 AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AACCAGCCA
301 AGGTGCCTGG CGCAATTCTA CGGAGGCGAA CAATGCCCAA TACAATCCGA
351 TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401 ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGTCT GCGCCATACG
451 GTCGTCGCCG TATTTCTCTT TGATGGCTTG CAGTTTGGGC GCGCGGGCAC
501 GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551 GCTTTGACGA TGATGGTTAA AACGATAATC GCCCAGCCCC AGTTGCCGAT
601 GATGTTGTGC AGTTGGTTCA AAAGCCAATA GAGGGGGGAG GCGAACCAGT
651 GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTGTCTCGC GATGTTTGCG
701 ATAACGATG TGGTCTGTGG GCCGCGTAG AGGTTGATGG AGGCTTCGGT
751 TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGCTGACGC TGGTGCTGTA
801 CAGCTTGTCG TTGCGGCGTT TGATGTCGAT ACGGCAGTCG CCAGCGGCGC
851 AAACGCTTTG TCCGCCTTTG GGTGAGGA TCCAGGTGGA CATGAAGTGG
901 TGTTCATCA TGCCGAGCCA GCCGTCGGG GTTTTGCCTG TGTATTGCGC
951 CTCGGATTG CCGGATTGG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```
a209.pep
1 MLRHLGNDFAL LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEEHDGE
51 NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDQDVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSEDEG DLQQRQAAA QRVDFLVCVK LHHGLLLRHT
151 VVAVFLFDGL QFGRGGTHFR HRTVRGVGQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQKPK EGGGEPVYFA VVFGQLQVVG DVCNCGGLW AGVEVDGGFG
251 FAPFWIAAKG TLTVLVLSLS LRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*
```

m209/a209 95.6% identity in 341 aa overlap

```
10 20 30 40 50 60
m209.pep MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEEHDGENQRHDFHHFR
|||||
a209 MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEEHDGENQRHDFHHFR
10 20 30 40 50 60

70 80 90 100 110 120
m209.pep LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSEDEG
|||||
a209 LHRVGRRRVQIGLGEHRCRHNDGQDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSEDEG
70 80 90 100 110 120

130 140 150 160 170 180
m209.pep DLQQRQAAAQRVDFLVCVKLHHRLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
|||||
a209 DLQQRQAAAQRVDFLVCVKLHHGLLLRHTVVAVFLFDGLQFGCGGTHFRHRTVRGVGQW
130 140 150 160 170 180

190 200 210 220 230 240
m209.pep IQYGFDDDGXNDNRPAFVADDVVQLVQEPPEERGGEPPVYFAVVGQLQVVGDVCDGCGLR
|||||
a209 IQYGFDDDGXNDNRPAFVADDVVQLVQKPEGGGEPVYFAVVGQLQVVGDVCDNCGGLW
190 200 210 220 230 240

250 260 270 280 290 300
m209.pep AGVEVDGGFGFAPFWMAAKGTLTLVLVLSLSLRLMSMLHSPAAQTLCLPLGWRIQVDMKW
|||||
a209 AGVEVDGGFGFAPFWIAAKGTLTLVLVLSLSLRLMSIRQSPAAQTLCPPLGWRIQVDMKW
250 260 270 280 290 300

310 320 330 340
m209.pep CSIMPSQPVGVLRMYSASDLPDLASSSKSEKLTFWKLPSGVX
```

```

a209      |||||
          CSIMPSQPVGLRMYASDLPDLASSKSEKLTFWKLPSGVX
          310      320      330      340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

```

g211.seq
1  atgttgcgga ttgctgctgc caatcagttg ggcggtcgaa atggtgcggc
51  ggtgggaaac ggggtcgata agtttggcg tggtgctgat aatcaggttg
101 agtttttga aggaacctg attgtagtcg gcgctccgg gcgtgccgt
151 gtaacggtag ccgtggcgca attcgagcgt gcgtttgttg tccttcagcg
201 agaagttacc ttctttggcg aagatgatgt tgcgcgccg gttttgtcc
251 tgttcgcgca ggaacaggtt ttcatgatg ccgattcgg tgcgaaagg
301 ttcgacgaaa taaaccctgc cgttgcgctt gcccaagtta ttgaactcgc
351 cggcttcac caagacaat tcctgcttct gttcaaaat ttcggcatat
401 tcgcggtcgc gcagctctgc ccacggatc acccaaagct gcagacggc
451 aatcaggatg gcaaacggca cggcaactg catgacggg cgtatccact
501 gtttcaacgc caatccgcag gatag

```

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

```

g211.pep
1  MLRIAAANQL GGRNGAAVGN GVDKFRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVLQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFVKVG
101 FDEINPAVAL AQVIELAGFH QRQFLLLQD FGIFAAALC PRYHPKLHDG
151 NQDKRHKGL HDGAYPLFQ QSAG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

```

m211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTCGATG AGTTTGGCG TGGTCTGAT AATCAGGTTG
101 AGTTTGTGA AGGAACCTG ATTGTAGTCG GCGGTCGCG GCGTGCCGT
151 GTAACGGTAG CCGTGGCGCA ATTCGAGCGT GCGTTGTGT TCGTTCAGCG
201 AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTGCGGCC GTTTTGTCC
251 TGTTGCGCA GGAACAGGTT TTTCATGATG CCGGATTCG TATCGAAGGT
301 TTCGACAAA TAAACCCTGC CGTTGCGCTT GCCCAAAGT TGAACTCGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAAACGGCA CGCAAAGT CATCACGGG CGTATCCATT
501 GTTCAATGC CAATCCGAG GATAG

```

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

```

m211.pep
1  MLRVAAANQL GGRNGTAVGN GVDEFGRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVVQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGIEG
101 FDKINPAVAL AQTVELACLH QRQFLLLQD FSVFAAAXLC PRYHPKLHDG
151 NQNGKRHKGL HHRAYPLFQC QSAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

```

m211/g211
          10      20      30      40      50      60
m211.pep  MLRVAAANQLGGRNGTAVGNVGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g211      MLRIAAANQLGGRNGAAVGNVVDKFRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER
          10      20      30      40      50      60
          70      80      90     100     110     120
m211.pep  AFVVVQREVTFFGEDDVVAAVFVLFAQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH

```

```
a211.seq
  1  ATGTTGCGGG  TTGCTGCTGC  CAATCAGTTG  GCGGGTCGGA  ATGGTACGGC
51  GGTGGGAAAC  GGGGTCGATG  AGTTTGGGCG  TGGTGCTGAT  AATCAGGTTG
101 AGTTTTTTGGA AGGAAACCTG  ATTGTAGTCG  GCGCGTCCGG  GCGTGCCGCT
151 GTAACGGTAG  CCGTGGCGCA  ATTCGAGCGT  GCGTTTGTTG  TCGTTCAGCG
201 AGAAGTTACT  TTCTTTGGCG  AAGATGATGT  TGCTGCCGCC  GTTTTTGTCC
251 TGTTGCGGCA  GGAACAGGTT  TTTCATGATG  CCGGATTCGG  TATCGAAGGT
301 TTCGACAAAA  TAAACCCTGC  CGTTGCGCTT  GCCCAAAGCT  TTGAACCCGC
351 CTGCCTCCAC  CAAAGACAAT  TCCTGCTTCT  GCTTCAGGAT  TTCAGCGTAT
401 TCGCGGCTGC  GTAGCTCTGC  CCACGGTATC  ACCCAAAGCT  GCATGACGGC
451 AACCAAACG  GCAAACGGCA  CGGCAAAGCT  CATCACCGGG  CGTATCCATT
501 GTTTCAGTGC  CAATCCGCAG  GATAG
```

a211.pep

1	MLRVAAANQL	GGRNGTAVGN	GVDFEGRGAD	NQVEFLEGNL	<u>IVVGASGRAA</u>
51	VTVAVAQFER	AFVVVQREVT	FFGEDDVVAA	VFVLFAGEQV	FHDAGFGIEG
101	FDKINPAVAL	AQTVEPACLV	<u>QRQFLLLQD</u>	<u>FSVFAAA*LC</u>	PRYHPKLHDG
151	NQNGKRHGKL	HHRAYPLFOC	OSAG*		

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
a211	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVVQREVTFFGEDDVVAAVFVLFAQEQQVFHDAGFGIEGFDKINPAVALAQTVELACLH					
a211	AFVVVVQREVTFFGEDDVVAAVFVLFAQEQQVFHDAGFGIEGFDKINPAVALAQTVEPACLH					
	70	80	90	100	110	120
	130	140	150	160	170	
m211.pep	QRQFLLLLQDFSVFAAAXLCPRYHPKLHDGNQNGKRHGKLLHHRAYPLFQCQSAGX					
a211	QRQFLLLLQDFSVFAAAXLCPRYHPKLHDGNQNGKRHGKLLHHRAYPLFQCQSAGX					
	130	140	150	160	170	

g212.seq (partial)

```
1 atggacaatc tcgtatggga cggcattccc gacatccgca cactcgacca
51 aaccatccgc aaacacgcac acccgctcaa cctgattgtc tgccctccccg
101 ataatcagat tcccgatttt caaacgcac aagatgcttc ggactcggaa
151 tgcggtctga agcaccggtt ggatcaggca acccagtgcc tccagttcga
201 cagcatcaac ctcatcgaac acatcctgcc cgatgtccgc ttctggctgg
251 ttcccccttc acgcaccgc cgcctgcacg aacatttcca ccaattttcc
301 tggcagaccg aagcatcccg gcaaacggaa agcaagtccg acaaaacctg
351 gtttgacatt ccacaaacat ccgaacggaa aaaaccggaa cacgtcctcg
```

```

401 tcatcgggtgc aggcattgcc ggcgcatcga cggccacgc cttagcatca
451 cacggcattt ccgttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaaatctcg ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctcggacaca tcctgcccga ctccgacact tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattgggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgcg aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgtcc
851 gcacctcct cagccatccg ctgatcgaac tatatgaaa cacaacgtta
901 accggcattt cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 ccaatttacc gccacacaca tcatctactg caccggcgcg cacagcccct
1001 gcctgcccga aaccaacctc gccgccctac ccctcaggca aatacgcgga
1051 caaacgggcc tcacaccgtc caccctgtt tccgaacaac tgcgttgcg
1101 cgttttcaggc gaaagctaca tcagcccgtc gtggcacgga ctgactgct
1151 acggcgcgag ttttattccc aacagcagca ataccggtg gaacgaagcc
1201 gaagaagcct caaacgccca agcattggca caccttaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRDLQA TQCLQFDSIN LIEHILPDVR FWLVPPSRT R LHEHFHHIS
101 WQTEAIPQTE SKSDKPWFAL PQTSEKPKPE HVLVIGAGIA GASTAHALAS
151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
251 EKIAGIPLNT PYAELCGLY WQHGVLNPP AFVRTLLSHP LIELVENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSNTGWNEA
401 EEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCCTCAA CCTGATTATC TGCCTCCCCG
101 ATAATCAGAT TCCCGATTTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCGTTT GGATCAGGCA ATGCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCTTC ACGCACCCAC CACCTGCACG AACATTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAAACCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGCATATCC GCGCGGGCAA CCGCCACGC CTTAGCATCA
451 CACGGCATT T CCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCAAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCAGGACA
551 CCGAACAGAC CGAACTTTTG CTGCGCGGCT ACGGCTACAC CAAACGCCGTG
601 CTCGGACACA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACAGC GCGTATGGCT CAATCCACCC GCATTGCTCC
851 GCACCCTCCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCCTTG
901 ACCGACATTT CCCACGACGG GGAAGAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCTT
1001 ACCTACCCGA AACCACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TCGGTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTTCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCA ACCCAAACCC CCAAAACAC CAAGGGCACG
1301 CCGCCATACG CTGCGACAGC CCGGACCACC TTCCCTAGT CGGCGCACTC
1351 GCGGACATTG CCGCATGCG GCAGACCTAC ACCAAACTCG CGCTGGACAA
1401 AAACCTACGC ATCGACACCC CATGCCATA CCTGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CCGCACCCGC GGACTCGCCA CCGCCCCAT CTGCGCCGCC

```


15 01 GmCAwTGCAG CCCAAATCst AGGCyTGCCC CATCCCTTTT yAcAAcGCCT
 15 51 gCGCCACGCC cTAcACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA
 16 01 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep

1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE
 51 CRLKHLRDLQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHFHHIS
 1 01 WQTEAIPQTE SKPDKPWFAL POTSERQKPE HILVIGAGIS GAATAHALAS
 1 51 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
 2 01 LGHILPESET WGGNGIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
 2 51 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL
 3 01 TDISHDGEKW IASTPNGTFT ATHIYCTGA NSPYLPETNL AALPLRQIRG
 3 51 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGFASFP NSSHTGWNEA
 4 01 EEASNRQALA HLNPALESSE FAANPNPQKH QGHAAIRCD S PDHLPVGLAL
 4 51 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA
 5 01 XXAAQIXGLP HPFXQRLRHA LHPNRTIIRA IVRRKDLTP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng)
 from *N. gonorrhoeae*:

m212/g212

	10	20	30	40	50	60
m212.pep	MDNLVWDGIPDIRTLDQAIRKHAPPLNLIIICLPDNQIPDFQTAQDASDAECRLKHLRDLQA					
g212	MDNLVWDGIPDIRTLDQTIKHAHPLNLIVCLPDNQIPDFQTAQDASDSECRLKHLRDLQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESKPKDPWFAL					
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRRLHEHFHHISWQTEAIPQTESKSDKDPWFAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m212.pep	POTSERQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
g212	POTSERKKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIHLNYSRTEQQRNHELGLQKHHNH					
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGIHLNYSRTEQQRNHELGLQKHHNH					
	190	200	210	220	230	240
	250	260	270	280	290	300
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP LIGLHEDTPL					
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m212.pep	TDISHDGEKWIASTPNGTFTATHIYCTGANSPLYLPETNL AALPLRQIRGQTGLTPSTPF					
g212	TGISHDGEKWIASTPNGTFTATHIYCTGAHSPCLPETNL AALPLRQIRGQTGLTPSTPF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m212.pep	SEQLRCAVSGESYISPSWHGLHLCYGFASFPNSSHTGWNEAEASNRQALAHLPALSESSE					

```

a212.seq
1 ATGGACAATC TCGCATGGAA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AACCATCCGC AAACACGCAC ACCCGCTCAA CCTGATTGTC TGCCTCCCCG
101 ATAATCAGAT TCCCAATTTT CAAACCGCAA AAGATGCTTC GGACCGGGAA
151 TGCCGTCGTA AGCACCGTTT GGATCAGGCA ACCCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTGATTGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCGC CGCTGCAACG AACACTTCCA CCACATTTC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGTAAGCCCG ACAAACCTG
351 GTTTGCATCT CCACAACACT CGCAACGGCA AAAACCGGAA CATATCTCG
401 TTATCGGAGC GGGCATATCC GCGCGGCGAA CCGCCACGCG CTTAGCATCA
451 TACGGCATT TCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAAAC CGAAGTCTGT CTTGCCGGCT ACGGGTACAC CAAACGCGCT
601 CTCGGACATA TCTGTCCGGA ATCGGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACGCA GGCAGAAGCC
751 GAAAAAATCG CCGGCATCCC TCTGAACAGC CCCTACGCGG AACCATTTATG
801 CGGACTGTTT TGGCAGTAGC GCGTATGGCT CAATCCTCC ACATTCTGTC
851 GCGCCCTCCT CAGCCATCCG CTCATTGGAC TACACAAGAA CACACCGTTA
901 ACCGACATT CCCACGACGG GGAAAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCTT
1001 ACCTACCCGA AACCAACCCT GCCACCTCG CCCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGCCTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCAGGGA CTGCATCTGT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCGCGCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCGGACCACC TTCCCCTAGT CGGCGCACTC
1351 GCGCAGATTG CGCCTATGCA ACAAACTTAC GCCAAACTCG CGCTGGACAA
1401 AAACATATCG ATCGATGCCC CCTGCCCGTA CCTGCCCAAT GCCTACGCCA
1451 ACACCGCCCA CGGCACACGC GGGCTTGCCA CCGCCCCCAT CTGCGCGGCC
1501 GCGGTTGCAG CCGAAATCTT AGGCTTGCCC CATCCCCTCT CAAAACGCCT
1551 GCCCAGCCG CTACACCCCA ACCGCGCCAT CATCCGCGCC ATCGTCAGAA
1601 GGAAGGATCT AACCCTTTAA

```

a212.pap

1	MDNLAWNGIP	DIRTLDQ TIR	KHAHPLNLIV	CLPDNQIPNF	QTAQDASDAE
51	CRLKHLRDLA	TQCLQFDSIN	LIEHILPDVR	FWLVPPSRTR	RLHEHFHHIS
101	WQTEAIPQTE	SKPKDPWFAL	PQTSEKQKPE	HILVIGAGIS	GAATAHALAS
151	YGISVTVLEA	RKAAQASAGN	RQGLLYAKIS	PHDTEQTELL	LAGYGYTKRL
201	LGHILPESET	WGGNGIHLN	YSRTEQQRNH	ELGLQKHNNH	LYRSITQAEA
251	EKIAGIPLNT	PYAEPLCLGF	WQYGVWLNPP	TFVRALLSHP	LIGLHEDTPL
301	TDISHDGEKW	IASTPNGTFT	ATHIIYCTGA	NSPYLPETNL	ATPLPLRQIRG
351	QTGLTPSTPF	SEQLRCAVSG	ESYISPSWHG	LHCYGASFIP	NSSHTGWNEA
401	EEASNROQAL	HLNPALSES	FAANPNPQKH	QGHAAIRCDS	PDHLPLVGAL
451	GDIAAMQQTQ	AKLALDKNYR	IDAPCPYLPN	IVYANTAHGTR	<u>GLATAPICAA</u>
501	AVAAEILGLP	HPLSKRLRHA	LHPNRATIRA	IYVRKDLTP*	

```

          10      20      30      40      50      60
m212.pep  MDNLVVDGIPDIRTLDQAIRKHAPPLNLIICLPDNGIPDFQTAODASDAECRLKHLRDOA
          |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
a212      MDNLAWNGIPDIRTLDQIRKHAHPLNLIVCLPDNGIPNFQTAODASDAECRLKHLRDOA

```

491

	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
a212	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
a212	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
a212	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
a212	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
a212	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
a212	370	380	390	400	410	420
m212.pep	430	440	450	460	470	480
a212	430	440	450	460	470	480
m212.pep	490	500	510	520	530	540
a212	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

```

g214.seq
1  atgatacaaa agatatgtaa gctatttggt ttaattgtaa tttttgcaac
51  ttctcccgtt tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtagctc aacatttccg cctcgtgtgt
201 caacgtcaca cgcggcaggc aaagcgggcg aatccgtgag ggcggaaggt
251 tcgcccgtcc gcttcagcca aacgttggac gggggcaaaag ggacgggtgcg
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgtcgttc
351 tgaccggcaa tgccaaagtg cagcgcggcg gcgacgttgc cgaaggtgcg
401 gtcattacct acaacaccaa aaccgaagtc tatacatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214.pep

```
m214.seq (partial)
      1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
     51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
    101 AGGCCGACCA AGGTTCTGCTC GATCAAGCCA ACCAAAGCAC CACATTTCAGC
    151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCCCGCT
    201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
    251 CGCCAGTCCG CTTCAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
    301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
    351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
    401 TGATTACATA CAACACCAAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
    451 AAATT...
```

```
m214.pep (partial)
  1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
 51  GNVVIRQGT L NISAARVNVT RGRQRRRIE GGRFASPLQ P DIGRRQRHGA
101 RTGKQRCLFI CRQHRS LNR* CQSTARRRC R RRCGDYIQH Q NRSLYHQRQH
151 KI...
```

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng) from *N. gonorrhoeae*:

```

              10      20      30      40      50      60
m214.pep  MIQKICKLFLVLIAFFSASPAFALQSDSRQPIQIEADQGSLDQANQSTTFSGNVVIRQGT
          |||||:::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
g214      MIQKICKLFLVLIIVIFATSPAFALQSDSRRPQIEADQGSLDQANQRTTFSGNVIIIRQGT
          10      20      30      40      50      60

              70      80      90      100     110     120
m214.pep  NISAARVNVTGRQRRRIREGGRFASPLQPDIGRRQRHGARTGKQRCFLICQHRSLNRX
          |||: |||||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
g214      NISASCVNVTGRQRRRIREGGRFARPLQPNVGRGQRDGA RSGKQRYLFLRRKHCHRSRDRQ
          70      80      90      100     110     120

              130     140     150
m214.pep  CQSTARRRCRRRCGDYIQHQNRSLYHQHQHI
          |||:||| ||| :|||:|||:|||:|||:|||:|||
g214      CQSAARRRCRRRCGHYLQHQNRSLYHQHQHEIGCEIRFQNRQGRRHAPFKHTKNRITPM
          130     140     150     160     170     180

g214      PSETETQFRRHLPTEMPRRDY
          190     200

```

```
a214.seq
1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTTCGCTC GATCAAGCCA ACCAAAGCAC CACCATTCAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGTC . GGC AAAGCGCGCG AATCCGTGAG GCGCGAAGGT
251 TCGCCAGTCC GCTTCAGCCA GACATTGGAC TGCAGGCAAG CCGCGGTGCG
301 CGGACAGGCA AACAATCGTTG CTTATTATC TGCAGGCAGC AGCAGTAGCT
```

```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTCGC CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAAATCCG CTTCCAAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGGACGG CATTGCGCA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNVT RGXQRRRIRE GGRFASPLQ P DIGRRQRHGA
101 RTGKQRCLFI CRQHRSLNR* CQSTARRRCR RRCGDYIQH Q NRSLYHQRH
151 KIRRKIRFQI RQGQRRYPAF EYAKIRIIPM PSET*TWFG R HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

```

              10      20      30      40      50      60
m214.pep    MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L
a214         MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L
              10      20      30      40      50      60

              70      80      90     100     110     120
m214.pep    NISAARVNVT RGRQRRRIRE GGRFASPLQ PDIGRRQRH GARTGKQRCLFICRQHRSLNRX
a214         NISAARVNVT RGRQRRRIRE GGRFASPLQ PDIGRRQRH GARTGKQRCLFICRQHRSLNRX
              70      80      90     100     110     120

              130     140     150
m214.pep    CQSTARRRCRRRCGDYIQH QNRSLYHQRH QKI
a214         CQSTARRRCRRRCGDYIQH QNRSLYHQRH QKIRRKIRFQI RQGQRRYPAF EYAKIRIIPM
              130     140     150     160     170     180

a214         PSETXTWFG RHLPTEILKRY L X
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATTGTAA TTTTTCGAAC
51  TTCTCCCGCT TTGCCCCTTC AAAGCGACAG CAGACGGCCC ATCCAAATCG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGTAC CACATTAGC
151 GGCAATGTCA TCATCAGACA GGTACGCTC AACATTCCG CCTCGCGCT
201 CAACGTCACA CGCGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGTT
251 CGCCCGTCCG CTTACAGCAA ACGTTGGACG GGGGCAAAGG GACGGTGCGC
301 GGTCAGGCAA ACAACGTTAC CTATTCCTCC GCAGGAAGCA CCGTCGTCT
351 GACCGGCAAT GCCAAAGTGC AGCGCGGCGG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAA ACCGAAGTCT ATACCATCAA CGGCAGCAGC
451 AAATCGGGTG CGAAATCCGC TTCCAAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
1  MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISASRVNVT RGGKGGESVR AEGSPVRFSQ TLDGGKGTVR
101 GQANNVTYSS AGSTVLTGN AKVQRGGDVA EGAVITYNTK TEVYTINGST
151 KSGAKSASKT GRVSVVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTGCCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTAGC
151 GGAACGTCG TCATCAGACA GGTACGCTC AATATTCCG CCGCCCGCGT

```

494

```

201 CAAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTCAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 748; ORF 214-1>:

m214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51 GNVVIRQGT L NISAARVNVT RGGKGGESVR AEGSPVRF SQ TLDGGKGTVR
101 GQANNVAYSS AGSTVVL TN AKVQRGGDVA EGAVITYNTK TEVYTISGST
151 KSGAKSASKS GRVSVVIQPS STQKSE*

```

m214-1/g214-1 93.8% identity in 176 aa overlap

	10	20	30	40	50	60
m214-1.pep	MIQKICKLFV	LIAFFSASPA	FALQSDSRQP	IQIEADQGS	L DQANQSTTFS	GNVVIRQGT
g214-1	MIQKICKLFV	LIVIFATSP	AFALQSDSR	RP IQIEADQGS	L DQANQSTTFS	GNVVIIRQGT
	10	20	30	40	50	60
	70	80	90	100	110	120
m214-1.pep	NISAARVNVT	RGGKGGESV	RAEGSPVRF	SQ TLDGGKGT	VRGQANNVAYSS	SAGSTVVL TN
g214-1	NISASRVNVT	RGGKGGESV	RAEGSPVRF	SQ TLDGGKGT	VRGQANNVYSS	SAGSTVVL TN
	70	80	90	100	110	120
	130	140	150	160	170	
m214-1.pep	AKVQRGGDVA	EGAVITYNTK	TEVYTISGST	KSGAKSASKS	GRVSVVIQPS	STQKSEX
g214-1	AKVQRGGDVA	EGAVITYNTK	TEVYTINGST	KSGAKSASKT	GRVSVVIQPS	STQKTEX
	130	140	150	160	170	

g214-1/p38685

sp|P38685|YHBN_ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)
>gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF_o185 [Escherichia coli]
>gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185
Score = 97.1 bits (238), Expect = 6e-20
Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

Query: 19 PAFALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L NISAARVNVT --GGKGG 76
PAFA+ D+ QPI IE+DQ SLD TF+GNV++ QGT+ I+A +V VTR G +G
Sbjct: 24 PAFAVTGD TDQPIHIESDQQSLDMQGNVVTF TGNVIVTQGT IKINADKVVVTRPGGEQK 83

Query: 77 ESVRAEGSPVRF SQ TLDGGKGT VRGQANNVAYSSAGSTVVL TN AKVQRGGDVA EGAVIT 136
E + G P F Q D GK V G A+ + Y A VVLTGNA +Q+ +G IT
Sbjct: 84 EVIDGYGK PATFYQMDNGK -PVEGHASQMHYELAKDFVVL TNAYLQQVDSNIRGDKIT 142

Query: 137 YNTKTE 142
Y K +
Sbjct: 143 YLVKEQ 148

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

a214-1.seq

```

1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTACAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCGCGCT
201 CAATGTTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTCAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

a214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS

```

51 GNVVIRQGT L NISAARVNVT RGGKGGESVR AEGSPVRF SQ TLDGGKGT VR
 101 GQANNVAYSS AGSTVVLTGN AKVQRGGDVA EGAVITYNTK TEVYTISGST
 151 KSGAKSASKS GRVSVVIQPS STQKSE*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQKICKLFVLIAFFSASPAFALQSDSRQPIQIEADQGS LDOANQSTTFSGNVVIRQGT L					
m214-1	MIQKICKLFVLIAFFSASPAFALQSDSRQPIQIEADQGS LDOANQSTTFSGNVVIRQGT L					
	10	20	30	40	50	60
	70	80	90	100	110	120
a214-1.pep	NISAARVNVT RGGKGGESVRAEGSPVRF SQ TLDGGKGT VRGQANNVAYSSAGSTV VLTGN					
m214-1	NISAARVNVT RGGKGGESVRAEGSPVRF SQ TLDGGKGT VRGQANNVAYSSAGSTV VLTGN					
	70	80	90	100	110	120
	130	140	150	160	170	
a214-1.pep	AKVQRGGDVA EGAVITYNTK TEVYTISGST KSGAKSASKS GRVSVVIQPS STQKSE X					
m214-1	AKVQRGGDVA EGAVITYNTK TEVYTISGST KSGAKSASKS GRVSVVIQPS STQKSE X					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq
 1 atgaaagtaa gatggcggtta cgggaattgcg ttccatttga tattggcggg
 51 tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa
 101 tgcaggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc
 151 ttggacggaa ggcgggttga cgaacaggga tacttgaaag aacatttgag
 201 cgcgaaagggt gcgaaacagt ttcccgaaaa cagcgacatc cattttgatt
 251 cgccgcatct cgtgttcttc caagaaggca ggctgttgta cgaagtcggc
 301 agcgatgaag ccgtttacca taccgaaaaa aaacaggttc ttttataaaa
 351 caacgttggtg ctgacaaaaa ccgcccagcg caggcgccag gcgggtaaaag
 401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaacc
 451 gatacgcttg tcagtttcca atatggcgcg tcgcacgggc aggcgggccc
 501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga
 551 aagccgcgat ttatgataca aaagatatgt aa

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep
 1 MKVRWRYGIA FPLILAVALG SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS
 51 LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPLVFF QEGRLLYEVG
 101 SDEAVYHTEN KQVLFKNV V LTKTADGRRQ AGKVETEK LK VDTESQYAQT
 151 DTPVSFOYGA SHGQAGGMTY NHKTGMLNFS SKVKAAYDT KDM*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)
 1 ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT
 51 CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA
 101 GCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTTGAG CGCGAAGGGC
 151 GCGAAACAGT TTCCGAAAG CAGCGACATC CATTTTGATT CGCCGCATCT
 201 CGTGTCTTC CAAGAAGGCA GGTGTTGTA CGAAGTCGGC AGCGACGAAG
 251 CCGTTTACCA TACCGAAAAC AAACAGGTTT TTTTAAAAA CAACGTTGTG
 301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA
 351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC GATACGCCTG
 401 CAGTTTCCA ATATGGTGCA TCGCAGGTC AGGCGGGCGG CATGACTTAC
 451 GACCACaawA CAGGCATGTT GAACCTCTCA TCTAAAGTGA AAGCCACGAT
 501 TTATGATACA AAAGATATGT AA

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)
 1 ..SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG
 51 AKQFPENSDI HFDSPLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNV V
 101 LTKTADGKRQ AGKVEAEKLH VDTESQYAQT DTPVSFOYGA SHGQAGGMTY

496

151 DHXTGMLNFS SKVKATIYDT KDM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
		:			
g215	MKVRWRYGIAFPLILAVALG	SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
	10	20	30	40	50
	50	60	70	80	90
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQEGRLLYE	VGSD	EA
	:				
g215	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQEGRLLYE	VGSD	EA
	70	80	90	100	110
	110	120	130	140	150
m215.pep	LT	KTADGKRQAGKVEAE	KLHVD	TESQYAQ	TDTPV
	:				
g215	LT	KTADGKRQAGKVEAE	KLHVD	TESQYAQ	TDTPV
	130	140	150	160	170
	170				
m215.pep	SKVKATIYDTKDMX				
	:				
g215	SKVKAAYDTKDM				
	190				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq

1	ATGAAAGTAA	GATGGCGGTA	CGGAATTGCG	TTCCCATGTA	TATTGGCGGT
51	TGCCTTGGGC	AGCCTGTCGG	CATGGTTGGG	ACGCATCAGC	GAAGTCGAGA
101	TTGAAGAAGT	CAGGCTCAAT	CCCGACGAAC	CGCAATACAC	AATGGACGGA
151	TTGGATGGCA	GCGCGTTTGA	CGAACAGGGA	TACTTGAAAG	AACATTGAG
201	TTCGAAGGGC	GCGAAACAGT	TTCCCGAAAG	CAGCGACATT	CATTTCGACT
251	CACCGCATCT	CGTGTCTCTC	CAAGAAGGCA	GGTTGTGTGA	CGAAGTCGGC
301	AGCGATGAAG	CCGTTTACCA	TACCGAAAAC	AAACAGGTTC	TTTTTAAAAA
351	CAACGTTGTG	CTGACCAAAA	CCGCCGACGG	CAAACGGCAG	GCGGGTAAAG
401	TTGAAGCCGA	AAAGCTGCAC	GTCGATACCG	AATCTCAATA	TGCCCAAAACC
451	GATACGCCTG	TCAGTTTCCA	ATATGGTGCA	TCGCACGGTC	AGGCGGGCGG
501	CATGACTTAC	GACCACAAAA	CAGGCATGTT	GAACCTCTCA	TCTAAAGTGA
551	AAGCCACGAT	TTATGATACA	AAAGATATGT	AA	

This corresponds to the amino acid sequence <SEQ ID 756; ORF 215.a>:

a215.pep

1	MKVRWRYGIA	FPLILAVALG	SLSAWLGRIS	EVEIEEVRLN	PDEPQYTMDS
51	LDGRRFDEQG	YLKEHLSSKG	AKQFP	ESSDI	HFDS
101	SDEAVYHTEN	KQVLFKNNVV	LT	KTADGKRQ	AGKVEAEKLH
151	DTPVSFQYGA	SHGQAGGMTY	DHKTGMLNFS	SKVKATIYDT	KDM*

m215/a215 98.3% identity in 173 aa overlap

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
		:			
a215	MKVRWRYGIAFPLILAVALG	SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
	10	20	30	40	50
	50	60	70	80	90
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQEGRLLYE	VGSD	EA
	:				


```

a215      |||||:|||||
          YLKEHLSSKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNVNV
          70      80      90      100      110      120

          110      120      130      140      150      160
m215.pep  LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVVSFYQGASHGQAGGMTYDHXTGMLNFS
          |||||
a215      LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVVSFYQGASHGQAGGMTYDHXTGMLNFS
          130      140      150      160      170      180

          170
m215.pep  SKVKATIIDTKDMX
          |||||
a215      SKVKATIIDTKDMX
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

g216.seq (partial)

```

1  ..atgatatcga tttcgagctc ggtacccagc gacgaaatca ccgccatcat
51  ccccgcaactc aaacgcaaag acattaccct cgtctgcac accgcccgc
101 ccgattcaac catggcgcgc catgccgata tccacatcac cgcacggtt
151 tgcgaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggct ttgggcgacg cgttggcggt cgtcctgctg cgcgcccgcg
251 cgttcacgcc cgacgacttc gccttgatcc accctgccgg cagcctcggc
301 aaacgcctgc ttttgccgct tgcgcacatt atgcacaaag gcggcggcct
351 gcccgccgct cgactcggca cgccttgaa aggagccatc gtcagcatga
401 gcgagaaagg tttgggcatg tgggcgggaa cggacgggca aaggctgtct
451 gaaaggcctt tttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

g216.pep (partial)

```

1  ..MISISSVPS DEITAIIPAL KRKDITLVC I TARPDMAR HADIHITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVLL RARAFTPDDF ALIHPAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGA I VSMSEKGLGM WAGTDGQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

```

1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGTT
51  GCACGCCGAA GCGGAAGGCT TGCGCGAAAT TGCAGCGGAA TTGACAAAA
101 ACTTCGTCCT TGCGGCAGAC GCGTTGTTGC ACTGCAAGGG CAGGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGGCACGC CTGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGCGA TTTGGGTATG ATTGTGGACA TCGACGTGGT CGTCGCGATT
301 TCCAATTCGG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCACGCTTG TCTGCATCAC CGCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACCGCCG TCATGGCTTT
501 GGGCGATGCG TTGGCGGTG TCCtGCTGCG CgcACGCGCG TTCACGCCCCG
551 ACGATTTCGC CTTGAGCCAT CCTGCCGGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GCGCGCTGCG CTGCCGTCGG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GGCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCGG CCTGTTTCAA GAATGCGACA ATTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATGTGATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

m216.pep

```

1  MAMAENGKYL DWAREVLHAE AEGLEIAAE LXKNFVLAAD ALLHCKGRVV

```

```

51 ITGMVKS GHI GRKMAATMAS TGTPAFFVHP AEAHGD LGM IVDXDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAP TTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGR LKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHTHPKT ISAERLATEA LKVMQANHVN
301 GLLVTDADGV LIGALNMHDL LAARIV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 216 shows 91.8% identity over a 147 aa overlap with a predicted ORF (ORF 216.ng) from *N. gonorrhoeae*:

m216/g216

	70	80	90	100	110	120
m216.pep	TMASTGTPAFFVHPAEAAHGD LGMIVDXDVVVAISNSGESDEIAAIIPALKRKDITLVCI					
g216	MISISSVSPSDEITAIIPALKRKDITLVCI					
				10	20	30
	130	140	150	160	170	180
m216.pep	TARPDSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPDDF					
g216	TARPDSTMARHADIHITASVSQEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPDDF					
	40	50	60	70	80	90
	190	200	210	220	230	240
m216.pep	ALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVTDGQGR					
g216	ALIHAPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKGAIVSMSEKGLGMWAGTDGQRLS					
	100	110	120	130	140	150

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 761>:

a216.seq

```

1 ATGGCGATGG CAGGAAACGA AAAATATCTT GATTGGGCAC GCGAAGTGTT
51 GCACACCGAA GCGGAAGGCT TGCGCGAAAT TGCGGCGGAT TTGGACGAAA
101 ACTTCGCCCT TGCGGCGGAC GCGTTGTTGC ACTGCAAAGG CAGGGTCGTT
151 ATCACGGGCA TGGGCAAGTC GGGACATATC GGGCGCAAAA TGCGGCGAAC
201 CATGGCCTCG ACCGGCACGC CCGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGGCGA TTTGGGCATG ATTGTGGACA ACGACGTGGT CGTCGCGATT
301 TCCAATTCGG GTGAAAGCGA CGAAATCGCC GCCATCATCC CCGCGCTCAA
351 ACGCAAAGAT ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACCGCCG TTATGGCTTT
501 GGGCGATGCG TTGGCGGTTG TCCTGCTGCG CGCCCGCGCG TTCACGCCCG
551 ACGACTTCGC CTTGAGCCAC CCTGCCGGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCTGCG CTGCCGTCGG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGCGGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTT TTGGCGGCGC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 762; ORF 216.a>:

a216.pep

```

1 MAMAGNEKYL DWAREVLHTE AEGLREIAAD LDENFALAAD ALLHCKGRVV
51 ITGMVKS GHI GRKMAATMAS TGTPAFFVHP AEAHGD LGM IVDNDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAP TTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGR LKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHTHPKT ISAERLATEA LKVMQANHVN

```

3 O1 GLLVTDADGV LIGALNMHDL LAARIV*

m216/a216 97.2% identity in 326 aa overlap

	10	20	30	40	50	60
m216.pep	MAMAENGKYLWAREVLHAEAEGLREIAAEELXKNFVLAADALLHCKGRVVITGMVKS GHI					
a216	MAMAGNEKYLWAREVLHTEAEGLREIAADLDENFALAADALLHCKGRVVITGMGKS GHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m216.pep	GRKMAATMASTGTPAFFVHPAEAAHGDLGMIVDXDVVVAISNSGESDEIAAIIPALKRKD					
a216	GRKMAATMASTGTPAFFVHPAEAAHGDLGMIVDNDVVVAISNSGESDEIAAIIPALKRKD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m216.pep	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARA					
a216	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m216.pep	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT					
a216	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m216.pep	DGQGRLLKGVFTDGLRRLFQECDNFTGLSIDEVMHHPKTI SAERLATEALKVMOANHVN					
a216	DGQGRLLKGVFTDGLRRLFQECDNFTGLSIDEVMHHPKTI SAERLATEALKVMOANHVN					
	250	260	270	280	290	300
	310	320				
m216.pep	GLLVTDADGVLIGALNMHDL LAARIVX					
a216	GLLVTDADGVLIGALNMHDL LAARIVX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcggatg acggtttgtt gcggaactg tccgaaaaac ccagccaaag
51  tgctctcttc ctgccatttg acccattcgt ttctcaggtt ttggactgcc
101 ttttggatcat cgggcccggc ttgaacaat gtttcaagca aatcccggca
151 acgcgccacc cattcgccga ccgtcgcagg ttgccgcat atccgggcaa
201 tatccgacag ggtttcgagg aaggcggcaa aacgtccgaa catggcgggt
251 tgattcacgt cggcatacca cgcgctgaca tcctgccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgcccgcga tttctccgtc caatcccca
401 tggacgttca aatcggcaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcgc aaacggcgca acacggcggc ggtttccaaa agcgcgagca
501 ctttgcggac ttcaaaacgg ctttccagca agtcggacac gcactccaac
551 gcataaaaaa acggttgccg gcggctgatt ttcacgtccg aaacggaata
601 cggcaatgcc tgcgcgccgg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgataa ggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence <SEQ ID 764; ORF 217.ng>:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPPYPGNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHQAQYH TVCRLLPGKQ LIRAAHFSV QSPMDVQIGN HIVQKRQIVP
151 GQSETAQHGR GFQKREHFAD FKTAQQVGH ALQRIKKRLP AADFHVNRGI

```

m217.seq

1	ATGGCGGATG	ACGGTGTGCG	GCGGCAACTG	TCCGGAAAT	TGCGCCAATT
51	CGGTTTCCCG	CTCCATTG	ACCCATTCTG	TTTCAAGGTT	TTGGACTGAC
101	TTTTGTGCAT	CGGCTTCAGC	TTGGAACAAT	GTTTCAAGCA	AATCCCGGC
151	ACGCGCCACC	CATTTCGCCA	CGTTGCGGG	CTGCCGCCAT	ATCCGTACAA
201	TATCCGTCAG	GGTTTCGAGG	AAGGCGGCAA	AACGTCCGAA	CATGGCGGTT
251	TGATTACAGT	CGGCATACCA	CGCGTGACA	TCCTGCCACA	TCGGATTGCC
301	GCCTTTGGGC	AGCATCCAGC	CCAAATATCAT	CGGTTCTACC	GCCTGCTTCC
351	AGGTGAACAG	CTGATCCGTG	CCGCCGCGCA	TTTCTCCGTC	CAAACCCAG
401	TGGACGTTCA	AATCGGCAAC	CATGTCGTGC	AAAAGCGGTA	AATCGTCTC
451	AGTCAGTCCG	AAACGGCGCA	ACACGGGCGC	GGTTTCTAAA	AGCACAGCA
501	CTTTATCGAC	TTCAAATCGG	CTTTCCAACA	AGTCGAACAG	GCATGACAAA
551	GCATGAAACA	GCGGTTGGCG	GCGGCTGATT	TTCACGTCTG	ACACGGAATA
601	CGGCAATGCC	TGCGCATCGG	GctGCGCCTG	TCCGAACACG	GCTTCGATAA
651	AAGGCGTATA	GGATTTCGATA	TTCCGGGTTA	A	

m217.pep

```

1  MADDGVRRL SGKLRQGFGR LPFDPFVFKV LDXLLVIGFS LEQCFKQIPA
51 TRHPFADRCG LPPYPYNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRIA
101 AFGQHPAQYH AFYRLLPGEF LIRAAAHFSV QTPVDVQIGN HVVQKRXLVL
151 SQSETAQHGR GFXXHKHFGID FKSAQQOVEQ AXQSMQORLA AADFHVXHGI
201 RQCLRTGLRL SEHKGDKKRI GFDIRG*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m217/g217

	10	20	30	40	50	60
m217.pep	MADDGVRRLQSGKLRQGFRLPFDPFVFKVLDXLLVIGFSLEQCFKQIPATRHPPFADRCG					
	: : : :					
g217	MADDGLLRQLSEKPSQSALFLPFDPFVFEVLDCLLVIGPGLKQCFKQIPATRHPPFADRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m217.pep	LPPYPYNIRQGFEEGGKTSEHGGLIHVGI PRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
	: : :					
g217	LPPYPGNIRQGFEEGGKTSEHGGLIHVGI PRADILPHRVA AFGQHPAQYHTVCRLLPGKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m217.pep	LIRAAAHFSVQTPVDVQIGNHVQKRXIVLSQSETAQHGRGFXKHKHFIDFKSAFQVVEQ					
	: : : : : : :					
g217	LIRAAAHFSVQSPMDVQIGNHIVQKRQIVPGQSETAQHGRGFQKREHFADFKTAFQVQVGH					
	130	140	150	160	170	180
	190	200	210	220		
m217.pep	AXQSMKQRLAAADFHVXHGIRQCLRTGLRLSEHGFDKRRIGFDIRGX					
	: : :					
g217	ALQRIKKRLPAADFHVNRNGIRQCLRAGLRLSEHGFIKKRIGFDIRG					
	190	200	210	220		

a217.seq

1	GTGGCGGATG	ACGGTGTGCA	GCGGCAACTG	TCCGGAATAA	TGCGCCAATT
51	CGGTTTCCGC	CTGCCATTGT	ACCCATTTCG	TTTCGAGGCT	TTGGACTGCC
101	TTTTGGTCAT	CGCCTTCGAC	TTGGAACAAT	GTTTCAAGCA	AATCCCGGCA
151	ACGCGCCACC	CATTTCGTC	CCGTCGCAGG	TTGCCGCCAT	ATCCGTACAA

501

```

201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CAGGCGGGTT
251 TGGTTCACGT CGGCATACCA CGCGCTGACC CCCTGCCACA TCGGATTGCC
301 GCCTTCGGGC AGCATCCAGC CCAATATCAT GCGTCTTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTTCTCCGTC CAAACCCAG
401 CGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGCA AATCGTCCTC
451 AGTCAGTCCG AAATGGCGCA ACACGGGCGC GGTTCCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGTCG GCGGCTGATT TTCACATCCG AAACGGAATA
601 CGGCAATGCC TGC GCGCGCGG GCTGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGGCGTATA GGATTCGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 768; ORF 217.a>:

```

a217.pep
1 VADDGVQRQL SGKLRQFGFR LPFDPFVFEEA LDCLLVIAFD LEQCFKQIPA
51 TRHPFVNRRL LPPYPYNIRQ GFEEGGKTSE QGGLVHVGIIP RADPLPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPADVQIGN HVVQKRQIVL
151 SQSEMAQHGR GF*KKHFID FKSAFQQVEQ A*QSMKQRLS AADFHIRNGI
201 RQCLRAGLRL SEHGFDKRRRI GFDIRG*

```

m217/a217 90.3% identity in 226 aa overlap

m217.pep	10	20	30	40	50	60
	MADDGVRRLSGKLRQFGFRLPFDPFVFKVLDXLLVIGFSLEQCFKQIPATRHHPFADRCG					
a217	VADDGVQRQLSGKLRQFGFRLPFDPFVFEEALDCLLVIAFDLEQCFKQIPATRHHPFVNRRL					
	10	20	30	40	50	60
m217.pep	70	80	90	100	110	120
	LPPYPYNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
a217	LPPYPYNIRQGFEEGGKTSEHGGLVHVGIIPRADPLPHRIA AFGQHPAQYHAFYRLLPGEQ					
	70	80	90	100	110	120
m217.pep	130	140	150	160	170	180
	LIRAAAHFSVQTPVDVQIGNHVVQKRQIVLSQSETAQHGRGFXKKHFIDFKSAFQQVEQ					
a217	LIRAAAHFSVQTPADVQIGNHVVQKRQIVLSQSEMAQHGRGFXKKHFIDFKSAFQQVEQ					
	130	140	150	160	170	180
m217.pep	190	200	210	220		
	AXQSMKQRLAAADFHVXHGIRQCLRTGLRLSEHGFDKRRIGFDIRGX					
a217	AXQSMKQRLSAADFHIRNGIRQCLRAGLRLSEHGFDKRRIGFDIRGX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 769>:

```

g218.seq
1 atggttgccg tggatcctta tacggcaaaa gtggtcaaca ccatgccgcg
51 caatcagggt tggatcaca ctatggatga aatccacggc gatatgatgc
101 tcggtgcggc aggcgattat cttttgaaa cggcagcttc actgaccatt
151 attatggttg tcagcggtt gtacctttgg tgggcgaaac agcgcgcat
201 taaagcgatg ctgctgccgc caaaaagcag ggcgcgttct tggtgccgga
251 atctgcacgg cgcgtttga acttggtgt cggtgatttt actgtgttc
301 tgcctgtcgg gtattgcttg ggcaggtatt tggggcgcca aatcggtga
351 ggcttggaat cagttcccgg ccggcaaatg ggggtgcgaa ccgaaccccg
401 tttcaatcgt gccgaccac ggcgaggtat tgaatgacgg caagggttaag
451 gaagtgccgt ggattttgga gcttatgcct atgcctgtct cagggacgac
501 tgtgggtgaa aacggcatta accccaccga gcccataaac attggaaacc
551 gtcgaccggt tcgcgcggga aatcggttcc aaagggcgtt atcagttgaa
601 tttgcccaaa ggcgaggacg gggatatggac tttgtcgacg gattctatga
651 gttatga

```

This corresponds to the amino acid sequence <SEQ ID 770; ORF 218.ng>:

```

g218.pep
1 MVAVDPYTAK VVNTMPRNQG WYHTMDEIHG DMMLGAAGDY LLETAASLTI

```

51 IMVVSGLYLW WAKQRGIKAM LLPPKSRARS WWRNLHGAFG TWVSLILLLF
 101 CLSGIAWAGI WGGKFVQAWN QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
 151 EVPWILELMP MPVSGTTVGE NGINPTEPNN IGNRRPFRAF NRFRALSVE
 201 FAQRRRGRMD FVAGFYEL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 771>:

m218.seq
 1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCGCGG
 51 CAATCAGGGT TGGTATTACA CGATGGATGA AATCCACAGC GATATGATGC
 101 TCGGTGCGGC AGGCGATTAT CTTTGGGAAA CGGCAGCTTC ACTGACCATT
 151 ATTATGGTTG TCAGCGGCTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT
 201 CAAGGCGATG CTGCTGCCGT CAAAAGGCAr GGCGCGTTCT TGGTGGCGGA
 251 ATCTGCACGG CACGTTTGA ACTTGGGTGT CGTTGATTTT GCTGTGTTC
 301 TGCTGTCCG GTATTGCTTG GCGGGTATT TGGGGCGGCA AGTTCGTACA
 351 GGCTTGGAGT CAGTTCCTG CCGGTAAATG GGGTGTGAA CCGAACCCCG
 401 TTTCAGTCGT GCCGACCCAC GCGAGGTAT TGAATGACGG CAAGGTTAAG
 451 GAAGTGCCGT GGGTTTGA GCTTACGCCT ATGCCTGTTT CAGGGACGac
 501 yGtgGGCAA GACGGCATT ACCCTGACGA GCCGATGACA TTGGAAACCG
 551 TCGACCGCTT TCGCGGnGA AATCGGTTT AAAGGGCGTT ATCAGTTGAA
 601 TTTGCCCAA GCGAGGACG GCGTATGGAC TTTGTGCGAG GATTCTATGA
 651 GTTA

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

m218.pep
 1 MVAVDPYTAK VVSTMPRNQG WYYTMDIHS DMMLGAAGDY LLETAASLTI
 51 IMVVSGLYLW WVKRRGIKAM LLPSKGXARS WWRNLHGTFG TWVSLILLLF
 101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
 151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFRALSVE
 201 FAQRRRRMD FVAGFYEL

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

m218/g218

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQG WYYTMDIHS DMMLGAAGDY LLETAASLTI IMVVSGLYLW					
g218	MVAVDPYTAKVVNTMPRNQG WYHTMDIHS DMMLGAAGDY LLETAASLTI IMVVSGLYLW					
	10	20	30	40	50	60
70	80	90	100	110	120	
m218.pep	WVKRRGIKAMLLPSKGXARS WWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
g218	WAKQRGIKAMLLPPKSRARS WWRNLHGAFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKVWPVLELTPMPVSGTTVGK DGINPDEPMT					
g218	QFPAGKWGVEPNPVSIPTHEVLNDGKVKVWPVLELTPMPVSGTTVGK DGINPTEPNN					
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRFRALSVEFAQRRRGRMD FVAGFYEL					
g218	IGNRRPFRAFNRFRALSVEFAQRRRGRMD FVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

a218.seq

```

1   ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCCGC
51  CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTTCGAC AGGTGATTAT CTTTGGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGC CGCGCAT
201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GCGCGTTCT TGGTGGCGGA
251 ATCTGCACGG CCGGTTTGGG ACTTGGGTGT CGTTGATTTT ACTGTTGTTT
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCCGG CAGGCAAATG GGGTGTGCGA CCGAACCTG
401 TTTCAGTCGT GCCGACCCAC GCGAGGTAT TGAATGACGG CAAGGTTAAG
451 GAAGTGCCGT GGGTTTTGGA GCTTACGCCT ATGCCTGTTT CAGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAAACCG
551 TCGACCGTTT TCGCGG.GA AATCGGTTT AAAGGCGTT ATCAGCTGAA
601 TTTGCCCAAA GCGGAGGACG GCGTATGGAC TTGTGCGCAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

a218.pep

```

1   MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51  IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAEG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRRQALSAE
201 FAQRRGRMD FVAGFYEL

```

m218/a218 95.9% identity in 218 aa overlap

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMD	EHSDMMLGAAGDYLLETAASLTI	IMVVSGLYLW			
a218	MVAVDPYTAKVVSTMPRNQGWYYAMDEI	HSMDMMLGSTGDYLLETAASLTI	IMIISGLYLW			
	10	20	30	40	50	60
m218.pep	WVKRRGIKAMLLPSKXARSWWRNLHGT	FGTWVSLILLFCLSGIAWAGIWGGKFVQAWS				
a218	WVKRRGIKAMLLPPKGRARSWWRNLHGA	FGTWVSLILLFCLSGIAWAGIWGGKFVQAWS				
	70	80	90	100	110	120
m218.pep	QFPAGKWGVEPNPVSVVPTHGEVLNDGK	VEVPWVLELTPMPVSGTTVGK	DGINPDEPMT			
a218	QFPAGKWGVEPNPVSVVPTHGEVLNDGK	VEVPWVLELTPMPVSGTTVGK	DGINPDEPMT			
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSVVPTHGEVLNDGK	VEVPWVLELTPMPVSGTTVGK	DGINPDEPMT			
a218	QFPAGKWGVEPNPVSVVPTHGEVLNDGK	VEVPWVLELTPMPVSGTTVGK	DGINPDEPMT			
	190	200	210			
m218.pep	LETVDRFARXNRRQALSAEFAQRRGRMD	FVAGFYEL				
a218	LETVDRFARXNRRQALSAEFAQRRGRMD	FVAGFYEL				
	190	200	210			

1	atgacgca	ggttaaggaa	gtgccgtgga	ttttggagct	tatgcctatg
51	cctgtctcag	ggacgactgt	gggtgaaaac	ggcattaacc	ccaccgagcc
101	caataacatt	ggaaaccgct	gaccgtttcg	cgcgggaaat	cggtttcaaa
151	gggcgttatc	agttgaattt	gcccaaaggc	gaggacgggg	tatggacttt
201	gtcgcaggat	tctatgagtt	atgacatgat	cagcccggtt	gccgacgcga
251	cggtagcatat	caccagttac	agcggcgaga	tctctgcga	catccgtttt
301	gacgattaca	accggttcgg	caaatctatg	gcggcaagca	ttgcgtctga
351	<u>tatggggact</u>	ttgggctggt	ggagcgtggt	ggcgaacgct	gtgttctgcc
401	ttgccgtgat	ttttatcgcc	atcagcggct	gcgtgatgtg	gtggaaacgc
451	cgtcgcgtcg	gcgtggcggg	cattgttcct	ccggcgcaaa	aaatcaaaact
501	gcccgtctcg	tgggcgatgg	cattgccegt	gctgttgat	gcactgcttt
551	tccgcaccgc	ggtgcttgcc	attgccgtga	tttgctgtgt	ggataccttg
601	ctcgtctcgc	ggattcctgt	gttgaqgaaa	tqgtttaaat	ga

q219.pep

1	MTARLRKCRG	FWSLCLCLSQ	GRLWVKLTALT	PPSPITLETV	DRFAREIGFK
51	GRYQLNLPGK	EDGVWTLSDQ	SMSYDMISPF	ADRTVHIDQY	SGEILADIRF
101	DDYNPFVGKFM	AASIALHMG	LGWWSVLANV	<u>VFCLAVIFIG</u>	<u>ISGCVMWWR</u>
151	RPSGVAGIVP	PAQIKLPVW	<u>WAMALPILLI</u>	<u>ALLEPFTALLA</u>	<u>IAVIWLLDTL</u>
201	LLSRIPVLRK	WFK*			

m219.seq

1	ATGACGGCAA	GGTTAAGGAA	GTGCCGTGGG	TTTTGGAGCT	TACGCCTATG
51	CCTGTTTCAG	GGACGaCyGt	gGGCAAAGAC	GGCATTAACC	CTGACCAGCC
101	GATGACATTG	GA AACCGTCG	ACCGCTTTGC	GCGGnGAAAT	CGGTTTCAA
151	GGCGGTTATC	AGTTGAATTG	GCCCAAAGGC	GAGGACGGCG	TATGGACTTT
201	GTCGCAGGAT	TCTATGAGTT	ACGACATGAT	CAGCCCGTTT	GCCGACCGCA
251	CGGTACATAT	CGACCAGTAC	AGCGGCAAAA	TCCTTGCCGA	CATCCGTTTT
301	GACGATTACT	ACCCGTCGCG	CAAATTTATG	GCGCAAGCA	TTGCGCTGCA
351	TATGGGGATA	CTGGGCTGGT	GGAGCGTGTT	GCGCAACGTC	TTGTTCTGCC
401	TTGCCGTCAT	TTTTATCGGT	ATCAGCGCGT	CGGTGATGTG	GTGGAAACGC
451	CGTCCGACCG	GAGCGGTGGG	CATCGTTCCG	CCGGCGCAGA	AAGTCAAGCT
501	GCCGGATTCG	TGGATGATCG	CATTGCCCGT	ATTGGCAATC	GCACTGCTCT
551	TCCCGATTCG	ACTGCTTGCC	ATTGCCGTGA	TTTGGCTGTT	GCATACGCTG
601	CTGTTTGTGCG	GGATTCTGTG	TTTGAGGAGA	TGGTTTAAAT	GA

m219.pep

1	MTARLRKCRG	FWSRLRLCLFQ	GRXWAKTALT	LTSRXHWKPS	TALRGEIGFK
51	GRYQLNLPGK	EDGVWTLSDQ	SMSYDMISPF	ADRTVHIDQY	SGKILADIRF
101	DDYNPFGKFM	AASIALHMG	LGWWSVLAV	LFCLAVIFIG	ISGCVMWKWR
151	RPTGAPVGIV	PAQVKVLPVW	WMMALPLLAI	ALLFPTSLLA	IAVIWLLDTL
201	LLSRAIVPLRR	WFK*			

Homology with a predicted ORF from *N. gonorrhoeae*

m219/g219

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSRLCLFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
g219	MTARLRKCRGFWSRLCLCLSQGLRWVKALTTPPSPITLETVDRFAREIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m219.pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
g219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFMAASIALHMG					

505

	70	80	90	100	110	120
m219.pep	130	140	150	160	170	180
	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPTGAVGIVPPAQKVLPVWMMALPLLAI					
	: : : : :					
g219	130	140	150	160	170	180
	LGWWSVLANVVFCLAVIFIGISGCVMMWKRRPSGVAGIVPPAQKIKLPVWWAMALEPLLLI					
m219.pep	190	200	210			
	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	: : :					
g219	190	200	210			
	ALLFPTALLAIAVIWLLDTLLLSRIPVLRKWFK					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219.seq
1  ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTTC GCGG.GAAAT CGGTTTCAAA
151 GGGCGTTATC AGCTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CGGTGCATAT CGACCACTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTT GCGGAACGTT TTGTTCTGCC
401 TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAACGC
451 CGTCCGTCCG GCGCGGTGGG CATGGTTCCG CCGGCGCAA AAATCAAGCT
501 GCCCGTCTGG TGGGCAATGG CCGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTAAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219.pep
1  MTARLRKCRG FWSLRCLFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV LFCLAVIFIG ISGCVMMWKR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRW WFK*

```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRCLFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
	: : : : :					
a219	MTARLRKCRGFWSLRCLFQGRWAKTVLTLSRXHWKPSTVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
m219.pep	70	80	90	100	110	120
	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKEMAASIALHMG					
	: : : : :					
a219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKEMAASIALHMG					
	70	80	90	100	110	120
m219.pep	130	140	150	160	170	180
	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPTGAVGIVPPAQKVLPVWMMALPLLAI					
	: : : : :					
a219	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPSGAVGMVPPAQKIKLPVWWAMAVPLLLI					
	130	140	150	160	170	180
m219.pep	190	200	210			
	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	: : :					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 781>:

```
g221.seq
1  atgcacgacc acggcgccat ggatcgccgc ctccccgctt tcggaagtct
51  gatcgggcga gccgtaaaac adatcgacgc tgacggattt gaaccctgcc
101 tcacggggcg catcgatgac ttctttgggt tcttcgtagc tttggatgcg
151 gttgactgcc gcctgcactt tggggtcgaa atcctgaatg ccgacgctca
201 tgcggttgaa gccgagctct cggagcatga ggacggtgtc gcggctgact
251 ttgcgcgggt cgatttcgat ggaatattcg ccggacggta tcagttcgaa
301 atgtttgcgg atcatgcgga agacacgttc gatctgttcg tcgctcaaaa
351 aggtcggcgt gccgccgccg aagtgcagtt gggcaagctg gtgccgtccg
401 ttcagatgtg gagcgagcag ttccatttct ttttcaagat attcgatgta
451 ggtatcggcg cggcctttgt ctttgggtgat gattttgttg cagccgcagt
501 agtagcagat ggtgttgcaa aacggaatgt gaatgtaaag ggaaagcggg
551 ttgtttaa
```

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

```
g221.pep
1  MHDHGAMDRR LPAFGSLMRR AVNXIDADGF EPCLTGGIDD FFGFFVALDA
51  VDCRLHFGVE ILNADAHAVE AESAEHEDGV AADFARVDFD GIFAGRYQFE
101 MFDLHAEDTF DLFVAQKGRR AAAEVQLGKL VPSVQMWSEQ FHFFFKIFDV
151 GIGAAFVFGD DFVAAAVVAD GVAKRNVNVK GKRFV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

```
m221.seq
1  ATGGyGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACCTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCCG TGGGGATTAA CTCGAAATGT TTGCGTATCA TGCGGAAGAC
301 ACGTTCGATC TGTTTCGTCG TCAAAAAGGt GCGTGCCCG CCGAAGTGCA
351 GTTGGGCAAG CTGGTGCCGT CCGTTCAGAT GTGGAGCGAG CAGTTCATT
401 TCTTTTCAA GATATTCGAT GTAGGCATCG GCGCGGCTTT TGTCTTGGT
451 GATGATTTG TTGCAGCCGC AGTAGTAGCA GATGGTGTG CAGAACGGAA
501 TGTGAATGTA AAGGAAAGC GGTGTGTTA A
```

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

```
m221.pep
1  MXVLMXRSLV RQAVNQIDAD GFEPFRFARRI DDFGFFVTL DAVDRRLHFG
51  VEILNADAH VEAESAHEH GVAADFARVD FDGVFAGGDX LEMFAYHAED
101 TFDLFVAQKG ACPAEVQLGK LVPSVQMWSE QFHFFFKIFD VGIGAAFVFG
151 DDFVAAAVVA DGVAERNVNV KGKRFV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng) from *N. gonorrhoeae*:

m221/g221

	10	20	30	40	50
m221.pep	MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFGFFVTLDAVDRRLHFGVE				
	: : :				
g221	MHDHGAMDRRLPAFGSLMRRAVNXIDADGFEPCLTGGIDDFFGFFVALDAVDCRLHFGVE				
	10	20	30	40	50
	60	70	80	90	100
m221.pep	ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDXLEMFAYHAEDTFDLFVAQKGA-				
g221	ILNADAHAVEAESAEHEDGVAADFARVDFDGI FAGRYQFEMFADHAEDTFDLFVAQKGRR				
	70	80	90	100	110
	120	130	140	150	160
	170				

m223.seq

This corresponds to the amino acid sequence <SEQ ID 790; ORF 223>:

m223.pap

1 VEFRRHQVVV GVEPFGHFD ELVFVTARQL EELFQRQVLA VEAAGGNRA
51 GGDQVEDV VVESEIXYGN IGVGSDDLVP VFLAQVFSN QQFLLDFFA
101 PVFFLCEQF AEGADTREA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 223 shows 80.7% identity over a 119 aa overlap with a predicted ORF (ORF 223.ng) from *N. gonorrhoeae*:

m223/g223

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGVEPFGHFDSELVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDVV					
g223	MEFRHQVVVVGVEPFGHFDGELVFVAARQLEELFQRQVLAIEAETGGNRARGYLQVEDVM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYGNEIGVGSDLVFPVFLAQVFSNSQQFLLADEFAPVFFLCEFQFAEGADTREAX					
g223	VESEITYSNVISVRSSLVFPVFLAQVFGNVEQLLFTDLFAPVFFLGEFQFTEGADTREAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 791>:

a223.seq

1	GTGGAATTCA	GGCACCAAGT	AGTGGTAGTT	GGTGTGGAAC	CATTTGGTCA
51	TTTCGATAGC	GAATTGGTCT	TTGTTACCGC	GGCCACGTTG	GAGAAATTGT
101	TCCAAAGATC	GGTTTGGGCT	GTCTGAAGCG	AAGCGGGCGG	GAATCGCGCC
151	GGTGCGGACT	TGCAAGTCGA	GGATGTGGTC	GTAGAAAGTC	AAATCGCCTA
201	CGGCAACGTA	ATCGGCGTTG	GCAGCGGCCT	GGTGTTTCCA	GTTTTTCTCG
251	CGCAAGTCTT	TAGCAACAGC	CAGCAATTCT	TGCTCGCTGA	TTCTTTTGGC
301	CCAGTATTTT	TCTTGTGCGA	ATTTCAATTC	GCGGAAGGCA	CCGACACGCG
351	GGAAAGCTGA				

This corresponds to the amino acid sequence <SEQ ID 792; ORF 223.a>:

a223.pwp

1 VEFRRHQVVVV GVEPFGHFDS ELVFTVARQL EELFQR*VLA VEAAGGNRA
51 GGD LQVEDVV VESEIAYGNV IGVSGSLVFP VFLAQVFSNS QQFLLADEFA
101 PVFFLCEQFQ AEGTDTREA*

m223/a223 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGVPEFGHFDSELVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDVV					
a223	VEFRHQVVVVGVPEFGHFDSELVFVTARQLEELFQRXVLAVEAEAGGNRAGGDLQVEDVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYGNIEIGVSGDLVFPVFLAQVFSNSQQFLLDFFAPVFFLCEFPQFAEGDTRAX					
a223	VESEIAYGNVIGVSGSLVFPVFLAQVFSNSQQFLLDFFAPVFFLCEFPQFAEGDTRAX					

70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 793>:

```
g225.seq
1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgcggtccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101 gcgagcagat tctcagacag tttgccgaag acgaacagcc cgttttacct
151 gtcaaccgag cccccgcccg gcgggcgggc aatgccgacg aactcatcgg
201 cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251 ccgcccggcg gggcggaat gccgacaaac tcatcggcag cgcgatgcgg
301 cttttgggta ttgacctacc ctacggcggc acatcggtgt ctaccggttt
351 tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401 acctgccgcy cagctcgccg gaacaggcgc ggatgggcgc acccgttgcc
451 cgaagcgaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501 cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551 acgcgccgcy cagggggaaa aatatcgaaa tcaccagcct gagccacaaa
601 tattggagcy gcaaatatgc gttcgcccgc cgggtcaaga aaaacgaccc
651 gtcacgcttt ctgaactga
```

This corresponds to the amino acid sequence <SEQ ID 794; ORF 225.ng>:

```
g225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151 RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201 YWSGKYAFAR RVKKNDSRFL LN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 795>:

```
m225.seq (partial)
1  ..TTTCAAACC CGGCAGTTTG GGCGTTTTTG TGGCTGAWGT TTGCCGTCCG
51  CCCCGCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101 TTCTCAGACA GTTTGCCGAA GACGAACAGC CCGTTTTACC CATCAACCGA
151 GCCCCCGCCC GGCGGGCGGG CAATGCCGAC GAACTCATCG GCAGCGCGAT
201 GGGGCTTAAC GAACAGCCCC TTTACCCGT CAACCGAGTC CCCGCCCGGC
251 GGGCGGGCAA TGCCGACGAA CTCATCGGCA ACGCGATGGG GCTTAACGAA
301 CAGCCCGTTT TACCGTCAA CCGAGCCCCC GCCCGCGGG CGGGCAATGC
351 CGACGAACTC ATCGGCAACG CGATGGGACT TTTGGGTATT GCCTACCGCT
401 ACGGCGGCAC ATCGGTTTCT ACCGTTTTTG ACTGCAGCGG CTTTATGCAG
451 CACATCTTCA AACGCGCCAT GGGCATCAAC CTGCCGCGCA CGTCGGCAGA
501 ACAGGCACGG ATGGGTACGC CGGTTGCCCG AAGCGAATTG CAGCCCGGAG
551 ATATGGTGTT TTTCGCGACG CTCGGCGGCA GCCGCATTTC CCATGTCGGA
601 CTTTATATCG GCAACAACCG CTTTATCCAC GCGCCGCGCA CGGGGAAAAA
651 TATCGAAATC ACCAGCCTGA GCCACAAATA TTGAGCGGCG AAATACGCGT
701 TCGCCGCGCG GGTCAAGAAA AACGACCCGT CCCGCTTTCT GAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 796; ORF 225>:

```
m225.pep (partial)
1  ..FSNPAVWAVL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQVLPINR
51  APARRAGNAD ELIGSAMGLN EQPVLVNRV PARRAGNADE LIGNAMGLNE
101 QPVLVNRAP ARRAGNADEL IGNAMGLLGI AYRYGGTSVS TGFDCSGFMQ
151 HIFKRAMGIN LPRTSAEQAR MGTFVARSEL QPGDMVFFRT LGGSRISHVG
201 LYIGNNRFIH APRTGKNIEI TSLSHKYWSG KYAFARRVKK NDPSRFLN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

m225/g225

```

              10      20      30      40      50
m225.pep      FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
              | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g225           MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPVNRAPARRAG
```

510

	10	20	30	40	50	60
m225 . pep	60	70	80	90	100	110
	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA					
g225	NADELIG-----GAMGLNEQPVVRVNRAXARRAGNA					
				70	80	90
m225 . pep	120	130	140	150	160	170
	DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
g225	DKLIGSAMRLGLIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225 . pep	180	190	200	210	220	230
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225 . pep	240	249				
	VKKN D P S R F L N X					
g225	VKKN D P S R F L N					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

```

a225 . seq
1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCCGGCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCGC CCCGGCGGGC
351 GGGCAATGCC GACGAACTCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCCCCCGCCC GCGGGCGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTGACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCTAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTTCG
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

```

a225 . pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVARS ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKN D P S R F L N *

```

m225/a225 87.4% identity in 277 aa overlap

	10	20	30	40	50
m225 . pep	FSNPAVWAVLWLXFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG				
a225	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRXPARRAG				
	10	20	30	40	50
	60	70	79	80	
m225 . pep	NADELIGSAMGLNEQPVLPVNR-----VPARRAGNA				

511

```

a225      |||||
NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
          70          80          90          100          110          120

m225.pep  90          100          110          120          130          140
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAIYRYGGTSVSTGFDCSGF
|||||
a225      DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAIYRYGGTSISTGFDCSGF
          130          140          150          160          170          180

m225.pep  150          160          170          180          190          200
MQHIFKRAMGINLPRTSAEQARMGTFVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
|||||
a225      MQHIFKRAMGINLPRTSAEQARMGTFVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
          190          200          210          220          230          240

m225.pep  210          220          230          240          249
IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSPRFLNX
|||||
a225      IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSPRFLNX
          250          260          270          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 799>:

g225-1.seq

1	atggattctt	ttttcaaacc	ggcagtttgg	gcggttttgt	ggctgatgtt
51	tgcgcgtcgc	cccgcgcctg	ccgacgaagt	gaccaacgct	ctcagcagcc
101	gtcagcagat	ctctcagacg	tttgcggaag	acgaacagcg	cgttttaccg
151	gc caaccgag	cctccgcgccg	gtggggcgggc	aatgcccagc	aactcatcgg
201	cggcgcgatg	gggcttaacg	aacagcccg	tgtacgcgtc	aaccgagccn
251	ccgcgcggcg	ggcgggcaat	ccgcgcaaac	tcatcggcag	cgcatcgctg
301	cttttggggg	tgtcctaccg	ctacgcggcg	acatcggtgt	ctacgggttt
351	tgactgcagc	ggattcatgc	agcacatctt	caaacgcgcg	atgggcatca
401	acCtgccgcg	cacgtcggcg	gaacagcgcg	ggatcggcgc	accggttccg
451	cgaagcgaa	tgcagcccg	ggatatggtg	tttttcgcga	cgctcggcgg
501	cagcgcgcat	tcccatgtcg	gactttatat	cgccaacaac	cgcttcaccc
551	acgcgcgcgcg	cacggggaaa	aatatcgaaa	taccagcct	gagccacaaa
601	tatttggagc	ccaaatatgc	gttcgcccgc	cgggtcaaga	aaaacgacct
651	gtcacgcttt	ctgaactga			

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

g225-1.pap

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51 VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYGG TSVSTGFDSC GFMQHIFKRA MGINLPRTSA EQARGAPVA
151 RSELQPGDMV PFRTLGGSRJ SHVGLYIGNR RFIHAPRTGK NIEITSLSHK
201 YWSGKYAFAR RVKKNDPSRF LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

m225-1.seq

1	ATGGATTCTT	TTTTCAAACC	GGCAGTTTGG	GCGGTTTTGT	GGCTGATGTT
51	TGCGGTCCGC	CCCGCCCTTG	COGACGAGTT	GACCAACyTG	CTCAGCAGCC
101	GCGAGCAGAT	TCTCAGACAG	TTTGCAGAAG	ACGAACACGCC	CGTTTATCCAC
151	ATCAACCGAG	CCCGCGCCCG	CGGGCGGGCG	AATGCCGACG	AACCTACGGG
201	CAGCGCGATG	GGGCTTAAAC	AACAGCCCGT	TTTACCCGTC	AACCGAGTCC
251	CCGCCCCGCG	GGCGGGCAAT	GCGCAAGAAC	TCATCGGCAA	CGCATGGGGG
301	CTTAACGAAC	AGCCGTTTTT	ACCCGTCAAC	CGAGCCCCCG	CCCGCGGGCG
351	GGGCAATGCC	GACGAACTCA	TGCGCAACGC	GATGGGACTT	TGGGTATTG
401	CCTACCGCTA	CGGCGGCACA	TCGGTTTCTA	CCGGTTTTGA	CTGCAGCGGC
451	TTTCATCGAG	ACATCTTCAA	AGCGCGCATG	GGCATCAACC	TGCGCGGCAC
501	GTCCGGCAGAA	CAGGCACGTA	TGGGTACGCC	GGTTCGCCGA	ACGGAATTGC
551	AGCCCCGAGG	TATGTGTGTT	TTCCGCACGC	TGCGGGCGAG	CGCATTTCC
601	CATGTCGGAC	TTTATATCGG	CAACAACCGC	TTCATCCACG	CGCGCGGCAC
651	GGGGAAAAAT	ATCGAAATCA	CCAGCCTGAG	CCACAAATAT	TGGAGCGGCA
701	AATACGCGTT	CGCCCGCCGG	GTCAAGAAAA	ACGACCCGTC	CCGCTTTCGT
751	AATCGA				

This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRAPARRAG NADELIGSAM GLNEQVLPV NRVPARRAGN ADELIGNAMG
101 LNEQVLPVN RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG
151 FMQHIFKRAM GINLPRTSAE QARMGTPVAR SELQPGDMVF FRTLGGSRIS
201 HVGLYIGNNR FIHAPRTGKN IEITSLSHKY WSGKYAFARR VKKNDPSRFL
251 N*

```

m225-1/g225-1 84.9% identity in 251 aa overlap

	10	20	30	40	50	60
m225-1.pep	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG					
g225-1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG					
	10	20	30	40	50	60
m225-1.pep	NADELIGSAMGLNEQVLPVNRVPARRAGNADELIGNAMGLNEQVLPVNRAPARRAGNA					
g225-1	NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA					
	70	80	90	100	110	120
m225-1.pep	DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
g225-1	DKLIGSAMRLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225-1.pep	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR					
g225-1	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225-1.pep	VKKNDPSRFLNX					
g225-1	VKKNDPSRFLNX					
	250					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq

```

1  ATGGATTCTT TTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCGCG CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTGCGGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCC CGCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGCGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTT ACCCGTCAAC CGAGTCCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAACTCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCCCCCGCCC GCGGGCGGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTGACTG CAGCGGCTTC ATGCAGACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGNTTTC CGCACGCTCG GCGGCAGCCG CATTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXFARRAG NADELIGSAM GLNEQVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQVLPVN RVPARRAGNA DELIGNAMGL NEQVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAIYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVARS ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNNDPSRFLN *

```


a225-1/m225-1 88.6% identity in 280 aa overlap

	10	20	30	40	50	60
a225-1.pep	MDSFFKPAVWVWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG					
m225-1	MDSFFKPAVWVWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a225-1.pep	NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA					
m225-1	NADELIGSAMGLNEQ-----VLPVNRVPARRAGNA					
	70	80	90			
	130	140	150	160	170	180
a225-1.pep	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF					
m225-1	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF					
	100	110	120	130	140	150
	190	200	210	220	230	240
a225-1.pep	MQHIFKRAMGINLPRTSABQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF					
m225-1	MQHIFKRAMGINLPRTSABQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF					
	160	170	180	190	200	210
	250	260	270	280		
a225-1.pep	IHAPRTGKNIETSLSHKYWSGKYAFARRVKKNDPSRFLN					
m225-1	IHAPRTGKNIETSLSHKYWSGKYAFARRVKKNDPSRFLN					
	220	230	240	250		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

g226.seq

```

1   ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTGCGGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGccgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggctcgg
351 gccggatacc caattctcct tcccgccctcg tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccgcca
451 tttctgttgc ctccgcctct cctgcgcgcg ctcggcccg ctcattgcg
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551 cagttgtggt cctttctcct Ccgggcctcg cccctccct cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

g226.pep

```

1   MSEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
101 GSVTGIIVTGM YFAAWLGPDT QFSFPRLQY LLFTPSGIPI HTLYARVLP
151 FLLPPPLLR LGPHTLRFT ILPKLRPFK PLLPVVVLSP PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

m226.seq

```

1   ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTGCGGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGCATTGT TACAGGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGTTACAA

```

m226.ppt

1	<u>MNEILRQPSV</u>	<u>LLFLTAVYA</u>	<u>LAIIVRTRTG</u>	<u>NIFCNPLVLS</u>	<u>TIVLIAYLKI</u>
51	<u>LGIDYAVYHN</u>	<u>AAQFIDFWLK</u>	<u>PAVVVLAVPL</u>	<u>YQNRKIFNQ</u>	<u>WLPVIVSOLA</u>
101	<u>GSVTGIVTGM</u>	<u>YFAKWLGAEK</u>	<u>EVVLSLAVGS</u>	<u>VTNPIAIEIT</u>	<u>RSIGGIPAIT</u>
151	<u>AATVIIAGLV</u>	<u>QFIAGYKMLK</u>	<u>NTVVMPPSSK</u>	<u>MSLGTASHAM</u>	<u>GIAASLERSR</u>
201	<u>RMAAYAGLGL</u>	<u>TFNGVLTALI</u>	<u>APLLIPVLGF</u>	*	

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

m226/g226

	10	20	30	40	50	60
m226 . pep	MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	:					
g226	MSEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m226 . pep	AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER					
	:					
g226	AAQFIDFRLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAAWLGPDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m226 . pep	EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG					
	:					
g226	QFSFPPRLQYLLFTPSGIPHTLYARVLPPFLPPPLLPRLGPHTLRRFTILPKKLRFK					
	130	140	150	160	170	180

a226.seq

seq	ATGAACGAAA	TCCTCAGGCA	GCCGAGCATC	CTGCTTTTCC	TCACGCTTGC
51	CGTGTACGCG	CTTGCGATTA	TCTGTGCGAC	GCGCAGGGT	AATATCTTCT
101	GCAACCCCGT	ACTCGTCAGC	ACTATCGTGC	TGATTGCGTA	CCTGAAAAATC
151	CTCGGTATCG	ATTATGCGGT	GTACCAACAAC	GCCGCGCAGT	TTATCGATT
201	CTGGCTCAAG	CCCGCGCTGC	TCGTGCTTGC	CGTGGCGCTC	TACCAAAACC
251	GCCGTAAAAT	CTTCAACCAA	TGGCTGCCCG	TCATCGTTTC	GCAGCTTGGC
301	GGCAGCGTTA	CGGGCATTGT	TACGGGGATG	TATTTTGCCA	AATGGCTGGG
351	CGCGGAACGC	GAGTCGCTC	TCTCGCTGCG	GTCCAAATCT	GTTACCAATC
401	CTATCGCCAT	GGAATCACC	CGCTCATACG	GCGGCATTCC	CGCCATTACC
451	GCCGCCACCG	TCATCATTGC	CGGCCCTGGT	GGACAGATTG	CCGTTTACAA
501	AATGTTGAAA	AACACGGTCG	TTATGCCCTC	ATCTGTCCGA	ATGTCGCTCG
551	GCACGGCTTC	GCACGCGATG	GGCATTTGCC	CCTCGCTCGA	ACGCAGCCGC
601	CGCATGGCGG	CATACGCGGG	GCTGGGGCTG	ACGTTCAACG	GGCTACTGAC
651	CGCGCTGATT	GCGCGCTGTC	TTATCCCGT	TTGGGATT	TGA

a226.pcp

1	<u>MNEILRQPSI</u>	<u>LLFLTAVYA</u>	<u>LAIIVRTRTG</u>	<u>NIFCNPVLV</u>	<u>TIVLIAYLKI</u>
51	<u>LGIDYAVYHN</u>	<u>AAQFIDFWLK</u>	<u>PAVVVLAVPL</u>	<u>YQNRKFTNQ</u>	<u>WLPVIVSQLA</u>
101	<u>GSVTGIVTGM</u>	<u>YFAKWLGAER</u>	<u>EVVLSLAVS</u>	<u>VTNPIAIEIT</u>	<u>RSIGGIPAIT</u>
151	<u>AAATVIIAGLV</u>	<u>QGIAGYKMLR</u>	<u>NTVVMPSXG</u>	<u>MSLGTASHAM</u>	<u>GIAASLERSR</u>
201	<u>RMAAYAGLGL</u>	<u>TFNGVILTALI</u>	<u>APLLIPVLGF</u>	*	

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60

515

```

m226.pep  MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPLVSTIVLIAYLKILGIDYAVYHN
a226      MNEILRQPSILLFLTLAVYALAIIVRTRTGNIFCNPLVSTIVLIAYLKILGIDYAVYHN
           10      20      30      40      50      60

           70      80      90      100     110     120
m226.pep  AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
a226      AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
           70      80      90      100     110     120

           130     140     150     160     170     180
m226.pep  EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG
a226      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG
           130     140     150     160     170     180

           190     200     210     220     230
m226.pep  MSLGTASHANGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
a226      MSLGTASHANGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1   atgaacatca tccgcgcgct cctcatcatc ctcggctgcc tcgccgccgg
51  cgaaaccgcc gttttcctag caggcatcaa actgcccgcc agcatcgctc
101 gcatggcgct gctgtttgcg cttttgcagg cgggttggtc caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaacctga cgctgttcct
201 cgtgccgccc tgcgtggcgg tcatcagcta tttggatttg attgccgacg
251 attggtttc gatactggtt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaaggttca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1   MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLEA LLQAGWLKTS
51  WLQQLTDALM ANLTLFLVFP CVAVISYLDL IADDWFSLV SASASTLCVL
101 LVTGKVRHWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1   ..ACGTCTTtGC TGCAACAGCT TACCGACGCG CTGATGTCGA ACCTGACGCT
51  GTtCCTCGTG CCgCC.TGCG TGGCGGTCAT CAGCTATTG GATTGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCG CCTCCGCCAG cACTTTGTGC
151 GTACTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1   ..TSXLQQLTDA LMSNLTLFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVRH WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

m227/g227

```

m227.pep                                     10      20      30
                                           TSXLQQLTDALMSNLTLFLVPPCVAVISYL
                                           || |||||
g227      TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTLFLVPPCVAVISYL
           20      30      40      50      60      70

           40      50      60

```

516

```

m227.pép    DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
            |||||
g227        DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
            80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51 CGAAACCGCC GTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTCG
101 GCATGGGCGT ACTGTTTGGC CTTTTCAGG CGGTTGGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCCC TGGCTGGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATGGGTTTC GATACTGGTT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301 CTGGTTACAG GCAAGGTTCA CCGCTGGATA CGGAGCATTA TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pép
1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLF LQAGWVKTS
51 WLQQLTDALM ANLTFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pép                                10      20      30
                                TSXLQQLTDALMSNLTFLVPPCVAVISYL
                                || |||||
a227        TAVFLAGIKLPGSIVGMGVLFALLQAGWVKTSWLQQLTDALMANLTFLVPPCVAVISYL
            20      30      40      50      60      70

            40      50      60
m227.pép    DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
            |||||
a227        DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
            80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGTTCAA GCCGTTGAGT
101 CCGATGTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pép
1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGTTCAA GCCGTTGAGT
101 CCGATGTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

a228.pep
 1 MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
 51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
 101 KMKDAAK*

m228/a228 100.0% identity in 107 aa overlap

	10	20	30	40	50	60
m228.pep	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
a228	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
	10	20	30	40	50	60
	70	80	90	100		
m228.pep	AAADAKASAEAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
a228	AAADAKASAEAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

g229.seq
 1 atggctgccc tatcgggcgg cggtgcggtc ttcctgataa tgcttcacaca
 51 tattgcccgc gttcagcgtc agccgccagc gttcgcccaa gcgtcgggag
 101 aaatcgccat tgaagccgcc ggcgaaattg tatcggtgcg cgcccaagag
 151 gttttgcccc acaaacggca cggtgccgaa cgagcgcgtt accgaacggt
 201 tttgatggcc gaacgacagg cgcaggttct gttcgtgaa atctttgtta
 251 tcccaataat gcacgcccgc gctgatgccg ccgtagagga aatgatgccc
 301 gcccgccattg atttcgcgcg acacgcccga gccgtagcgc aaaccgtgtg
 351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgcaaat
 401 tcaatcgttt ttccggacga agcgttggtt atagcggatt aacaaaaatc
 451 aggacaaggc ggcggggcgc aggcagtagc gatggtacgg aaccggttcg
 501 cccggtgctt ggacgcctta gggaaccggt ccctttgagc cggggcgggg
 551 caaccgtac cggtttttgt tcatccgcca tattgtgttg a

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

g229.pep
 1 MAAVSGGGAV FLIMLPHIAR VQRQPPAFAQ ASGEIGIEAA GEIVSAAQAE
 51 VLPDKRHGAE RARYRTVLMA ERQAQVLFAR IFVIPIMHAA ADAAVEEMMP
 101 ALIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFGR SVVYSGLTKI
 151 RTRRRAAGST DGETPVRPVL GRLREPFPLS RGGATRTGFC SSAILC*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

m229.seq (partial)
 1 ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC
 51 GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG
 101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC
 151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCCG CTGATGCCGC
 201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTCGCGCGA CACGCCTAAG
 251 CCCTAGCGCA AACCCTGTGC CTTTTCGCGC AGGCTGTCCG CGGTTTTTCGT
 301 CCAGCTTCTG CCGCAAATT CAATCGTTTT TTCGGACGAA GCGTTGTGTTA
 351 TAGCGGATTA AAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA
 401 AATAGTACGG AACCATTCA CTGGTGCTT CAGCACCTTA GAGAATCGTT
 451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

m229.pep (partial)
 1 ..AQALGEIGIE AADEIVSAAA XEVLLDKRHD AERARYRTVF IAERQAQALF
 51 AEIFVIPIMH AAAADAAYEE MPMARIDFAR HAXALAQTVC LLRQAVGGFR
 101 PASARKFNRF FGRSVVYSGL TKIRTRQRSA DSTNSTEPIH LVLQHLRESR
 151 SLFCSSAILC *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 229 shows 80.5% identity over a 169 aa overlap with a predicted ORF (ORF 229.ng) from *N. gonorrhoeae*:

m229/g209

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g229      MAVVSGGGAVFLIMLPFIARVQRPPAFQAQASGEIGIEAAAGEIVSAAAEVLDPKRHGAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFVIMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||| ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g229      RARYRTVLMARQAQVLFVIMHAAA-DA AVEEMMPARIDFARHAQAVQTVCLL
                70      80      90      100     110

                                100     110     120     130     140
m229.pep      RQAVGGFRPASARKFNRFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRE----
                ||| ||||| ||||| ||||| ||||| : ||| : ||| : ||| : |||
g229      RQAVGGFRPASARKFNRFGRSVVYSGLTKIRTRRAAGSTDGTEPVRPVLGRLEPFPL
                120     130     140     150     160     170

                                150     160
m229.pep      -----SRSIFCSSLX
                : ||| |||||
g229      SRGGATRTGFCSSAILC
                180     190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

a229.seq (partial)

```

1  ATGGCTGTCG TATCGGGCGG CGGTGCGGTC TTCCTGATAA CGCTTCCACA
51 TATTGCCCAC GTTCAGCGTC AGCCGCCA.. GTTCGCTCAA GCGTCGGGAG
101 AAATCGGCAT TGAAGCCGCC GACGAAATTG TATCGGCTGC CGCCTAAGAG
151 GTTTTGCTCG ATAAACGGCA CGATGCCGAA TGAGCGCGTT ACTGAACGGT
201 TTTTATAGCC GAGCGACAGG CGCAGGCTCT GTTCGCTGAA ATCTTTGTTA
251 TCCTAATAGT GCACGCCGCC GCCGCTGATG TCTCCGTAGA GGAAATGATG
301 CCCGCCCGCA TTGATTTCGC GCGACACGCC CAAGCCGTAG CGCAAACCGT
351 GTGCCTTTTG CGGCAGGCTG TCGGCGGTTT TCGTCCAGCT TCTGCCGTGA
401 AATTCAATCG TTTTTCGGA CGAAGCGTTG TTTATAGCGG ATTAACAAAA
451 ATCAGGACAA GGCGACGAAG CGCAGACAGT ACAGATAGTA CGGAACCGAT
501 TCACTTGGTG CTTACGACC TTAGAGAATC GTCTCTTTGA GCTAAGCGCA
551 GGCAACGCCG TACTGGTTTT TGTCATCCA CTATA

```

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

a229.pep (partial)

```

1  MAVVSGGGAV FLITLPHIAH VQRQPPXFAQ ASGEIGIEAA DEIVSAAA*E
51  VLLDKRHDAE *ARY*TVFIA ERQAQALFAE IFVILIVHAA AADVSEEMM
101 PARIDFARHA QAVAQTVCLL RQAVGGFRPA SACKFNRFEG RSVVYSGLTK
151 ITRRRRSADS TDSTEPIHLV LQHLRESSL* AKARQRTGF CSSTI

```

m229/a229 85.6% identity in 167 aa overlap

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                ||| ||||| ||||| ||||| ||||| ||||| |||||
a229      MAVVSGGGAVFLITLPHIAHVQRQPPXFAQASGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFVIMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||| ||||| ||||| ||||| : ||||| : ||||| : ||||| : |||||
a229      XARYXTVFIAERQAQALFAEIVFVILIVHAAAADVSEEMMPARIDFARHAQAVAQTVCLL
                70      80      90      100     110     120

```

	100	110	120	130	140	149
m229.pep	RQAVGGFRPASARKFNRRFFGRSVVYSGLTkIRTRQRSADSTNSTEPIHLVLQHLRES---					
a229	RQAVGGFRPASACKFNRRFFGRSVVYSGLTkIRTRRRSADSTDSTEPIHLVLQHLRESSLX					
	130	140	150	160	170	180
	150	160				
m229.pep	-----RSLFCSSAILCX					
a229	AKARQRRRTGFCSSSTI					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

```

g230.seq
1  atgttccatt ccatcgaaaa atacagaaca cccgcccag tcttattagg
51  cctgattgca ttaacttttg tcggcttcgg cgtcagcacg gtttcccatc
101 cgggcgcgca ctacatcgtc caagtggcg acgaaaaaat cagcgagcac
151 tcaatcaaca acgccatgca gaacgagcag gcggacggcg gcagcccttg
201 gcgcgacgcg gtgttccaat ccctgctgca acgcgcctac ctgaaacagg
251 gcgcgaagct gatgggcatt tcggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccaattt ccacgacgca aacggcaaat tcagtcacgc
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtttg
401 tcgaagaaat ccgcgatcag ttgccttgcc agaatttggg aagcctcgtc
451 caaaacggcg tattggtcgg cgacgcgcag gcggaacagc tgatcaggct
501 gacgcaggtc aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcacgcgcca agtcaaaagc tctgaagccg atttgcagaa attttataat
601 gcgaacaaaa aagactatct gctgccgcag gcggtcaaat tgggaatatgt
651 cgccttgagt ctgaaggatt ttgcagacaa gcagaccgtc agtgaaacgg
701 aatgtaaaaa tgcgcttgaa gagcgcgtag cgcgcttgcc ggcacatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaag gcggttgccg acttcaacaa ggcaaaagaa aagctgggag
851 acgatgctgt caatcatccc tcctcgcttg ccgaagccgc caaaaacagc
901 gggttgaaag tggaaaccca agaaacttgg ctgagcaggc aggacgcaca
951 aatgtccggc atgcccgaac acctaataca tgccgtattc agcgacgagc
1001 tattgaagaa aaaacacaat tccgaagtcg tgaccatcaa cagcgaacc
1051 gcgtgggtcg tccgcgcaa agaagtccgc gaagaaaaaa acctactgtt
1101 tgaagaagcc aaagatgcgg tcggtcaggc ctatatccgt accgaagccg
1151 ccaaactttt gaaaacaatg taa

```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

```

g230.pep
1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAKLMI SVSSEIQKM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHME DQFVEIRDQ FALQNLVSLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFPN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRAKEVR EEKNLLFEEA KDAVRQAYIR TEAKLLKTM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

```

m230.seq (partial)
1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCC.GACGCG GTGTTCGAAT CCCTGCTGCA ACGCGCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC

```

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```

451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTCCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGAG GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGg
701 AAGTGAAAAA TGCATTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAGAA AAATTGGGCG
851 ACGATGC.GT CAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 CGGTGGGTGCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

m230.pep (partial)

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSDA VFQSLQRAY LKQGAALMGI SVSSEIQKI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSD QFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLITINSET
351 AWVVRAKEVR EEKTLFPAEA KDAVRQAYIR TEAAKL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

m230/g230

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
m230.pep	70	80	90	100	110	120
	ADGGGSPSDAVFQSLQRAYLKQGAALMGISVSSEIQKIIVDDPNFHDANGKFDHALLN					
g230	ADGGSPWRDAVFQSLQRAYLKQGAALMGISVSSEIQKQIMVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230.pep	130	140	150	160	170	180
	RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN					
g230	QYLSQRHMSDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN					
	130	140	150	160	170	180
m230.pep	190	200	210	220	230	240
	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
g230	PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
m230.pep	250	260	270	280	290	300
	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS					
g230	ERVARLPAHEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m23 0.pep	GLKQVETQETWLSRQDAQMSGMPENLINA VFSDDVLKKKHNSVLTINSETAWVVRKEVR					
g23 0	GLKQVETQETWLSRQDAQMSGMPENLINA VFSDDVLKKKHNSVLTINSETAWVVRKEVR					
	310	320	330	340	350	360
	370	380				
m23 0.pep	EEKTLPF AEAKDAVRQAYIRTEAAKL					
g23 0	EEKNLLFEEAKDAVRQAYIRTEAAKLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a23 0.seq (partial)

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGTCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTTCGA CACTTTC AACCCGCAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAACAAA AAGACTACCT GCTTCCCAA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGCAGGC AGGATGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTGG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT

```

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a23 0.pep (partial)

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51  SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGA LMG I SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELMKKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINA VFSDDVLKKKH NSVLTINSET
351 AWVVRKEVR EEKTLPF AEAKDAVRQAYIR TEAAKL

```

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m23 0.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a23 0	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m23 0.pep	ADGGGPSRDAVFQSLQRAYLKQGA LMG I SVSSEQIKQIIVDDPNFHDANGKFDHALLN					
a23 0	ADGGGPSRDAVFQSLQRAYLKQGA LMG I SVSSEQIKQIIVDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

522

```

m230.pep  RYLSQRHMSQDFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRITRSHTFN
a230      RYLSQRHMSQDFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRITRSHTFN
           130      140      150      160      170      180

           190      200      210      220      230      240
m230.pep  PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
a230      PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE
           190      200      210      220      230      240

           250      260      270      280      290      300
m230.pep  ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS
a230      ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS
           250      260      270      280      290      300

           310      320      330      340      350      360
m230.pep  GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR
a230      GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR
           310      320      330      340      350      360

           370      380
m230.pep  EEKTLPF AEAKDAVRQAYIRTEAAKL
a230      EEKTLPF AEAKDAVRQAYIRTEAAKL
           370      380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACA CCCGCCCAAG TCTTTATTAGG
51  CCTGATTGCA TTAACTTTTC TCGGCTTCGG CGTCAGCAGC GTTTCCTATC
101 CGGGCGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGGCG GCAGCCCTTG
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCTTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATG
301 ATTGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAGCCTCGTC
451 CAAACCGCGC TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTTCGA CACTTTC AACCCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GGA AAAAGGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAGCTGGGCG
851 ACGATGCGTT CAATCATCCC TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TGGAACCCCA AGAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCGGGC ATGCCCGAAA ACCTAATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAGATGCGG TGCGTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACCTGC CGAAAAACAAG GCAAAAGAAG TGCTTACCCA ACTGAACGGC
1201 GCGAAGGCAG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCGCA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAACCGGCG AAACGGCAAA CCCGCCTATG TCAGACTGAC CGGTCGCGCG
1351 GCACCCGTGA TTGTCGAGGC GCAGGCAGTC ACGCCTCCGG AGGATATTGC
1401 CGCACAGCTT CCTCTGCGA AACAGGCTTT GGCGCAACAG CAGTCTGCCA
1451 ATACTTTTCA CTGCTGATC CGCTATTTC ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGGCGAT GGTCACTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pap

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAKLMI SVSSESIKQM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHMSQ DQFVEEIRDQ FALQNLVSLV

```

```

151  QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201  ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251  AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301  GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLITINSET
351  AWVVRAKEVR EEKNLLFEEA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401  GKAVDVKWE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLTGLP
451  APVIVEAQAV TPPEDIAAQL PPAKQALAAQ QSANTFDLLI RYFNGKIKQT
501  KGAQSVDNQD GQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCGTATTGCA TTAACCTTCG TCGGCTTCGG GGTACGACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCCG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGA CACTTCAAC CCGGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 TCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAT TGGAAATATG
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACGG
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCCTCGAAA ACCGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCCGT ATGCCCGAAA ACCTGATCAA TGCCGTATTG AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCTGCGCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAACTTGC CGAAAACAAG GCAAAGACG TGCTTACCCA ACTGAACGGC
1201 GCGAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 CAGGCAAGG CAGTCCATGC CGCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTA TTGTGCAAGT ACAGGCTGTA ACCCGCCCG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GGCGCAACAG CAGTCTGCCA
1451 ATACTTTTCA CTTGTTGATA CGTTATTTC ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGGCGAC GGTCAAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51  SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAKLMI SVSSEIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLITINSET
351 AWVVRAKEVR EEKTLFPAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEQAV TPPDDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVDNQD GQ*

```

m230-1/g230-1 96.3% identity in 512 aa overlap

```

10      20      30      40      50      60
m230-1.pep MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHINNAIQNEQ
|||||
g230-1      MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ
10      20      30      40      50      60

70      80      90      100     110     120
m230-1.pep ADGGGPSRDAVFQSLQRAYLKQGAKLMI SVSSEIKQI IVDDPNFHDANGKFDHALLN
|||||
g230-1      ADGGSPWRDAVFQSLQRAYLKQGAKLMI SVSSEIKQI QMIVDDPNFHDANGKFSHALLS
70      80      90      100     110     120

130     140     150     160     170     180
m230-1.pep RYLSQRHMESEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN

```

a230-1.seq

1	ATGTTCCATT	CCATCGAAAA	ATACAGAACG	CCCGCCCAAG	TCCTTTTGGG
51	CCTGATGCGA	TTAACTTTCG	TCGGCTTCGG	GGTCAGCACG	GTATCCCATT
101	CGGGTGCCGA	CTACATCGTC	CAAGTGGCGC	ACGAAAAAT	CAGCGACCAT
151	TCCATCAACA	ACGCCATACA	GAACGAACAG	CGGGACGGCG	CGGCGCCCTT
201	GCGCGACGCG	GTGTTCCAAT	CCTGTCTACA	ACGCGCTTAC	CTGAACACGG
251	CGCGCAAGCT	GATGGGCATT	TCGGTTCCTT	CCGACAATA	CAACGACAGT
301	ATCGTGGACG	ATCCCAATTT	CCAGCAGCGA	AACGGCAAT	TCGACACGCT
351	GCTTTTAAAC	CGTCACTCTT	CCCAACGTCA	TATGTCGAA	GACCAAGTTG
401	TCGAAGAAAT	CCGCGATCAG	TTTGCTTTGC	AGGATTTGGT	AAACCTCGTC
451	CAAAACGGCG	TATTGGTCGG	CGACGCGCAG	CGGAACAGC	TGATCAGGCT
501	GACGCAGGTC	AACCGCACCA	TCCGTTCCGA	CACTTTCAAC	CCCGACGAA
551	TCATCGCCCA	AGTCAAAGTG	TCGGAAGCCG	ATTTCGAGAA	GTTTTATRAA
601	GCAACAAAA	AGAATACCT	GCTTCCCAA	CGCGTCAAT	TGGAATATGT
651	CGCCTTGAAT	CTGAAAGACT	TTGCAGACAA	ACAGACCGTC	AGCGAAACAG
701	AAGTGA AAAA	TGCGTTTGAA	GAGCGCGTGC	CGCGTTTGCC	GGCAAATGAA
751	GCCAAACCTT	CTTTCGAGCA	GGAAAAAGCC	GCGCTCGAAA	ACGAATTGAA
801	AATGAAAAAG	CGGGTTGCGC	ACTTCAATTA	GGCAAAGAA	AGCTGGGCGT
851	ATGACGCGTT	CAACCATCCT	TCCTCGCTTG	CCGAAGCCGC	CAAAAACAGC
901	GGTTTGAAGT	TCGAAACCCA	AGAAACTTGG	CTGACGAGGC	AGGATGCGCA
951	ATGTCTCGAA	ATGCCGAGAA	ACCTGATCAA	TGCCGTATTC	AGCGACGAGC
1001	TATTGAAGAA	AAAACACAAT	TCCGAAGTGC	TGACCATCAA	CAGCGAAACC
1051	GCGTGGGTCT	TCCGCGCCAA	AGAAGTCCGC	GAAGAGAAAA	CCCTGCGGTT
1101	TGCCGAAGCC	AAAGACCGCG	TACGTCAGGC	TTATATCCGT	ACCGAAGCCG
1151	CCAAACTTTC	GAAAAACAAG	GCAAAAAGAC	TGCTTACCCA	ACTGACACGC
1201	GGCAAGGCTG	TTGACGTGAA	ATGGTCGGAA	GTGTCCGTTT	TGGGCGCACA
1251	CGAGGC AAGG	CAGTCCATGC	CGCCCGAGGC	TTATGCGGAA	CTGCTGAAAG
1301	CAAAACCGCG	AAACGCCAAA	CCGCGCTACG	TCAGGCTGAT	CGGTCTGCCG
1351	GCACCCGTGA	TTGTCGAAGT	ACAGGCTGTA	ACCCGCGCGG	ATTGATATCG
1401	CGCACAGCTT	CCGCTTGCAA	AACAGGCTTT	GGCGCAACAG	CAGTCTGCCA
1451	ATACTTTTCA	CTTGTGTATA	CGTTATTTCA	ACGGCAACAG	CAACAGACCC
1501	AAAGGAGCGC	AATCGGTCGA	CAACGGCGAC	GCTCAGTAA	

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

a230-1.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51  SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAQMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRAKEVR EEKTLFPAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQQAQ QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPPDDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501          KGASVDNGD GQ*

```

a230-1/m230-1 99.8% identity in 512 aa overlap

a230-1.pep	10	20	30	40	50	60
	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
m230-1	10	20	30	40	50	60
	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230-1.pep	70	80	90	100	110	120
	ADGGGPSRDAVFQSLQRAYLKQGAQMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
m230-1	70	80	90	100	110	120
	ADGGGPSRDAVFQSLQRAYLKQGAQMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
a230-1.pep	130	140	150	160	170	180
	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRIRSHFTN					
m230-1	130	140	150	160	170	180
	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRIRSHFTN					
a230-1.pep	190	200	210	220	230	240
	PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE					
m230-1	190	200	210	220	230	240
	PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE					
a230-1.pep	250	260	270	280	290	300
	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
m230-1	250	260	270	280	290	300
	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
a230-1.pep	310	320	330	340	350	360
	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLINSETAWVVRAKEVR					
m230-1	310	320	330	340	350	360
	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLINSETAWVVRAKEVR					
a230-1.pep	370	380	390	400	410	420
	EEKTLFPAEAKDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVKWSEVSVLGAQQAQ					
m230-1	370	380	390	400	410	420
	EEKTLFPAEAKDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVKWSEVSVLGAQQAQ					
a230-1.pep	430	440	450	460	470	480
	QSMPEAYAE LLKAKPANGKPAYVRLIGLPAPVIVEVQAVTPPDDIAAQLPLAKQALAAQ					
m230-1	430	440	450	460	470	480
	QSMPEAYAE LLKAKPANGKPAYVRLIGLPAPVIVEVQAVTPPDDIAAQLPLAKQALAAQ					
a230-1.pep	490	500	510			
	QSANTFDLLIRYFNGKIKQTKGASVDNGDGQX					
m230-1	490	500	510			
	QSANTFDLLIRYFNGKIKQTKGASVDNGDGQX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 839>:

```
g231.seq
1  atgtcaaaac gaaaatccat aaaccgtccg tatcaaaaac cggcggaact
51  gccgcggttg caaataatc cgccatttta ccgtaaaaac cgccgcctga
101 acttttttat cgcggcagac ggcggttgcg cgtctccgca aaaatgcagg
151 gcgcgcggtt ttcagacggc atttgccgtt caaggccgtg cgggtgtcttt
201 accaaatgcc caaccattcg cccacggaat ccatccaatc cttattgccc
251 ccgcgcgtcc tgcctgcccg gcggtacgcc cacggcgctt gcggattttt
301 agctttccac aatcctttgc gtccctttc cgctgaatt tgagcgctcg
351 catagtcggc aaaatccgcc ttatcctgct gttcttttagc ataactttta
401 taatgccacg ccgcccgcgc ctgcacctgc atcagggttca aatcgggttt
451 gccggcggtt acctgcgcca cttcgcgctg atagcggtcg gtttcaaaca
501 cagtcacact gactttccta ccctccgcgc ccgcgcgcag gttgtcgcgc
551 gaacgtgtac cgtaagcctg tttcatctcc ggtgcgtcga tatacggcat
601 ccgaatttta tgtttcgcgc cgtcgccgct gatgacgtga agggatatcgc
651 cgtcatagac tttggacacc gtgcctgtgt agctgtggcc ggatttcgcc
701 gatgcccgtc ggcgaacggg cgcgtcgaaa cccacgtccc ctgcagtgcc
751 gagtacgtcg agtacggcaa ccgcgcgtcc caccgcctca ctgtcatatc
801 ccgtataacc caacgcgccc aaaagcgaca ggcgcagggg aagccatttc
851 atgatttttt taatctgcat atttttcaaa tgccgatgcc gtctgaacat
901 ctctga
```

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

```
g231.pep
1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVSGIVG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 AGGYLRHFAL IAVGFKHTYT DFPTLRRRAQ VVARTCTVSL FHLRCVDIRH
201 PNFMFRAVAV DDVKGIAVID FGHRACVAVA GFRRCPSANG RVETHVPCSA
251 EYVEYGNRRP HRLTVISRIT QRAQKRQGDG KPFHDFNLH IFQMPMPSEH
301 L*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

```
m231.seq (partial)
1  ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG GC....
```

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

```
m231.pep (partial)
1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFV QGRAVSLPNA QPFG.....
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng) from *N. gonorrhoeae*:

```
m231/g231
10      20      30      40      50      60
m231.pep  MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
          |||||
g231      MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
          10      20      30      40      50      60

70
m231.pep  QGRAVSLPNAQPFG
          |||||
g231      QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVSGIVG
          70      80      90      100     110     120
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

a231.seq (partial)

```

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGNGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCC GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTGTCGAACA
501 CCGGGACGCT GACTTCTCTG CTTCCGCGC CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACCCCAT
601 CCGGATTTTG TGTTTCGCGC CGTCGCGGTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GGCGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCGGTCG CACGCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

a231.pep (partial)

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRLNRHFAL VAVGVEHADA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRAVAVA GFRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 I

```

m231/a231 98.6% identity in 73 aa overlap

```

              10      20      30      40      50      60
m231.pep      MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
              |||||
a231           MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV
              10      20      30      40      50      60

              70
m231.pep      QSRVSLPNAQPFG
              |||||
a231           QSRVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVGIIG
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

g231-1.seq

```

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCC GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGGCGGAT ACCTGCGCCA CTTGCGCTG ATAGCGGTCG GTTTCAAACa
501 CaCgTaCaat gagtttcgta ccctccGCCG ccgcgcgcCAG GTTgtcgcGC
551 GAACgTGTAC CGTAagcgtg Ttcatctcc GGTGcgtcGA TATACGCCaT
601 cCgAATTtTa tGtttcgcgc cgtcgcCgtc gATGACGTGA AGGgtatcGC
651 CgtcATAGAC TTTGGACACC Gtgcctgcgt AGctGTGGCC GGAttctgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

g231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```

101 SFQSFAPFF RLNLVGIIVG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
 151 AGGYLRHFAL IAVGFKHTYN EFRTLRRRAQ VVARTCTVSV FHLRCVDIRH
 201 PNFMFRAVAV DDVKGIAVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
 51 GCCGCCGTTG CAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
 151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
 201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCC
 251 CCGCCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTT
 301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAAT TGAGCGTCGG
 351 CATATCGGC AAAATCCGCC TTATCTGCT GTTCTTTAGC ATAACTTTAA
 401 TAATGCCACG CCGCCCGTCT CTGCACCTGC ATCAGGTTCA AATCGGTTT
 451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCG GTATCGAACA
 501 CGCGCACGCT GACTTTCCTG CCTTCCGCGC CCGCGCGCAG GTTGTGCGCG
 551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GCGCGTCTGA TATACGCCAT
 601 CCGGATTTTG TGTTCGCGC CGTCGCGTCT GATAACGTGA AGGGTGTGCG
 651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
 701 GATGCTCGGC GCGGGCGGG GCGCTCGGAA CCCGCGTCCC CTGCCGCGCC
 751 GAGTACGTCG AGTACGGCAA CCGCCGTCGG CACCGCTCG CTGCCGTACC
 801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC
 851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
 901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep

1 MSKRKSNRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
 51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF
 101 SFQSFAPFF RLNLVGIIVG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
 151 ADRLNRHFAL VAVGIEHAHA DFPFRRRAQ VVARTRAVSL FHLRRVDIRH
 201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRCSAAGG RVGTRVPCRA
 251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLHI FQMPMPSEH
 301 IIGIFQTAS*

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSNRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCAS	PQKCRARGFQTAFV				
m231-1	MSKRKSNRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCAS	PQKCRARGFQTAFV				
	10	20	30	40	50	60
g231-1.pep	QGRAVSLPNAQPF	FAHGIHPILIAPAAPACPAVRPRRLRIFS	SFQSFAPFRLNL	SVGIIVG		
m231-1	QSRVSLPNAQPF	FAHGIHPILIAPAAPACSAVRPRRLRIFS	SFQSFAPFRLNL	SVGIIVG		
	70	80	90	100	110	120
g231-1.pep	KIRLILFFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFRTLRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVLHLHQVQIGFADRLNRHFALVAVGIEHAHADFPFRRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSVFHLRCVDIRHPNFMFRAVAVDDVKGIAVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNDVKGVAVIDFGHRACVAVAGFRRC	SAAGG				
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHI	FQMPMPSEH				
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
 51 GCCGCCGTTG CAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG


```

151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCC GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTC GTTCCCTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTA
401 TAATGCCAGC CGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 CCGGACAGAA ACCTGCCGCA CTTCCGCTG GTAGCGGTG GTGTCGAACA
501 GCGCGACGCT GACTTTCTG CCTTCCGCG CCGCGCGCAG GTGTGCGCGC
551 GAACGCGTGC CGTAAGCCTG TTTTCATCTC GCGCGGTCGA TATACGCCAT
601 CCGGATTTTG TGTTTCGCGC CGTCGCCGTC GATAACGTGA AGGGTGTCGC
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGGCGGG CGCGTCGGAA CCGCGCTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCGCTCC CACCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

a231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAACPAC AVRPRRLRIF
101 SFPQSFAFPF RLNLVGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRFAL VAVGVEHADA DFPFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRAVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

	10	20	30	40	50	60
a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a231-1.pep	QSRVSLPNAQPFAHGIHPILIAPAACPAPVPRRLRIFSFPQSFAFPFRLNLVGIIG					
m231-1	QSRVSLPNAQPFAHGIHPILIAPAACPACSAVRPRRLRIFSFPQSFAFPFRLNLVGIIG					
	70	80	90	100	110	120
	130	140	150	160	170	180
a231-1.pep	KIRLILFFSITFIMPRRPVHLHQVQIGFADRNLRHFALVAVGVEHADADFPFRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVHLHQVQIGFADRNLRHFALVAVGIEHADADFPFRRRAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
a231-1.pep	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNVKGVAIDFGHRACVAVAGFRRCSAAGG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNVKGVAIDFGHRACVAVAGFRRCSAAGG					
	190	200	210	220	230	240
	250	260	270	280	290	300
a231-1.pep	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300
	310					
a231-1.pep	IGIGFQTASX					
m231-1	IGIGFQTASX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

g232.seq

```

1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatactggt
51 tggtcagatt ttgggaacgg cggttgccgg cgcgcgcct tatattgtcg
101 ggatactggt tttgctggtc gccgtcggag gaacggccgg cagcctggtt

```

```

151 atgccgtccg taccgcgcaa ggctgccgat acccaaatcg agtggaaat
201 tgtccgtggt acaaaatccc tgctgcgtga aacgggtgagg cacaatcccc
251 tttttaccgc cattatcggc atctcgtggt tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg gcggcaacga
351 taatgttttt aacctgatgc ttgctttgtt ttccatcggg attgcccgg
401 gttcggtagt gtgtgccaa gggtgcaggg aacgggtgat gttggcttgg
451 gtaacgggtg gtgcgttggg ttgcacggtt tgcggcctgg ttttgggtg
501 gctgacgcac ggacaccggt ttgaagggct gaacggcatt ttttgggttt
551 tatcgcaagg atggggcatac cccgtgatgg cgggtgatgac gctgatcggc
601 tttttcggcg gatttttctc cgttccgctc tatacctggc tgcaaaccgc
651 cagcagcgag actttccgag cccgcgaggt tgcggccaac aatatcgtaa
701 acggcatctt tatggtttcc gccgcggtt tgagcgcggt attgctgttt
751 ttggttgaca gcatttccct gctgtatctg attgtcgcct tgggcaatat
801 tccgttggcg gtatttttga ttaagcgcga aaggcggttt ttaggcgcgg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

g23 2. pep

```

1  MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51  MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HNPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGLNGI FWFLSQGWAY PVMAVMTLIG
201 FFGGFFSVPL YTWLQTASSE TFRARAVAN NIVNGIFMVS AAVLSAVLLF
251 LFDSISLLYL IVALGNIPLA VFLIKRERRF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

m23 2. seq

```

1  ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTGTGTC CCATCCTGTT
51  CGGTCAGATT TTGGGAACGG CGGTGGCAGG TGTACCGCCT TATATTGTCG
101 GGATACTGGT TTTGCTGGTC GCCGTCGGAG GCACGTCGG CAGCCTGTTT
151 ATGCCGTCCG TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGGAAATAT
201 TGTCGGTGGC ACAAATCCC TGCTGCGTGA AACGGTGGCG CACAAGCCCG
251 TTTTACCGC CATTATCGGT ATTCGTGGT TTTGGTTTGT CCGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTT AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAKGG AACGCTGAT GTTGGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTTGACGGT TGC GGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CGGTGATGAC GCTGATCCGC
601 TTTTTCGGCG GATTTTCTC CGTCCGCTC TATACCT (g) TG CAAACCGCCA
651 TAGCGAGATT TCCGCGCCCg GCCGTTGCCG CCAACAATAT CGTTAACGGT
701 ATTTTATGG TTTCCGCTGC CGTTTGTAGC GCGGTGTTGC TGTTTTTGT
751 TGACAGCATT TCCTTGTGT ATCTGATTGT CGCTTGGGC AATATTCCGT
801 TGTCGGTATT TTTGATTAAG CGCGAAAGGC GGTTTTTAGG CGCGCGGCA
851 ATCAGGAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

m23 2. pep

```

1  MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51  MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HKPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGLNGI FXFLSQGWAY PVMAVMTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

```

              10      20      30      40      50      60
m23 2. pep  MMGNSLIESGTFVAILFGQILGTAAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g232        MMGNSLIESGTFVAILFGQILGTAAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```

531

	10	20	30	40	50	60
m232.pep	70	80	90	100	110	120
	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGA VYTTQLPTFTQIHLGGNDNVF					
g232	70	80	90	100	110	120
	TQIEWNIVRGTKSLLRETVRHNVPVFTAIIGISWFWFVGA VYTTQLPTFTQIHLGGNDNVF					
m232.pep	130	140	150	160	170	180
	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	130	140	150	160	170	180
	NLMLALFSIGIAAGSVLCAKFRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
m232.pep	190	200	210	220	230	
	FXFLSQGWAYPVMAMVMTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	190	200	210	220	230	240
	FWFLSQGWAYPVMAMVMTLIGFFGGFFSVPLYTWLQTASSETFRARAVAANNIVNGIFMVS					
m232.pep	240	250	260	270	280	289
	AAVLSAVLLFLFDSISLLYLIVALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	250	260	270	280	290	
	AAVLSAVLLFLFDSISLLYLIVALGNIPLAFLIKRERRFLGAAAIRKKP					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

a232.seq	1	ATGTACGCTA	AAAAAGGCGG	TTTGGGACTG	GTTAAAAGCC	GCCGTTTCGC
	51	ACCTCTTTTC	GCTACGCAGT	TTCTCGGCGC	GTTCAACGAC	AATGTGTTCA
	101	AAACCGCGCT	GTTTGTGATG	ATTGGGTTTT	ACGGTTTGGG	GCAAAACGGC
	151	TTCTGCGCTG	CCGGACAGAT	GTTGAACTTG	GGCGCGTTGC	TGTTTATTTT
	201	GCCGTATTTC	CTGTTTTCTT	CGCTGTCGGG	GCAGTTGGGT	AACAAATTCG
	251	ACAAGGCCGT	TTTGGCGCGT	TGGGCCAAGG	TGCTGGAAAT	GATCATTATG
	301	GCGGTGGCGG	CATACGGGTT	TTATATCCGG	TCTGCCCGCG	TGCTTTTGGC
	351	GTGTCTGTTT	TGCATGGGCG	CGCAATCGAC	GCTGTTCCGG	CCGCTGAAAT
	401	ACGCCATCCT	GCCCCATTAT	CTCGACGACA	AAGAGTTGAT	GATGGGCAAC
	451	AGCCTGATTG	AATCGGGTAC	GTTTGTGCGC	ATCCTGTTTC	GTCAGATACT
	501	GGGGACTGCG	GTGGCAGGTG	TACCGCCTTA	TATTGTCGGG	ATACTGGTTT
	551	TGCTGGTCCG	CGTAGGAGGC	ACGGTCGGCA	GCCTGTTTAT	GCCGTCCGTA
	601	CCCGCCAAGG	CTGCCGATAC	ACAAATTGAG	TGGAATATTG	TCCGGGGTAC
	651	AAAATCCCTG	CTGCGTGAAA	CGGTGCGGCA	CAAGCCCGTT	TTTACCGCCA
	701	TTATCGGTAT	TTCTGTGTTT	TGGTTTGTTC	GCGCGGTTTA	TACCACGCCA
	751	CTGCCGACCT	TTACCCAAAT	CCATCTAGGC	GGCAACGACA	ATGTTTTCAA
	801	CCTGATGCTT	GCCCTGTTTT	CCATCGGTAT	TGCCGCCGGT	TCGGTACTGT
	851	GTGCCAAGTT	CAGCAGGGAA	CGGCTGAGGT	TGGCTTGGGT	AACGGTTGGT
	901	GCGTTGGGTT	TGACGGTTTG	CGGCTTGGTT	TTGGTGTGGC	TGACGCACGG
	951	ACACCGTTTT	GAAGGGCTGA	ACGGCATTTT	TTGGTTTTTA	TCGCAAGGAT
	1001	GGGCATATCC	CGTGATGGCG	GTGATGACGC	TGATCGGCTT	TTTCGGCGGA
	1051	TTTTTCTCCG	TTCCGCTCTA	TACCTGGCTG	CAAACCGCCA	GTAGCGAGAC
	1101	TTTCCGCGCC	CGCGCCGTTG	CCGCCAACAA	TATCGTTAAC	GGTATTTTTA
	1151	TGGTTTCCGC	TGCCGTTTTG	AGCGCGGTGT	TGCTGTTTTT	GTTTGACAGC
	1201	ATTTCTTGTG	TGTATCTGAT	TGTCGCTTTG	GGCAATATTC	CGTTGTCCGT
	1251	ATTTTGTGAT	AAGCGCGAAA	GGCGGTTTTT	AGGCGCGGCG	GCAATCAGGA
	1301	AAAAACCTTG	A			

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

a232.pep	1	MYAKKGGGLGL	VKSRRFAPLF	ATQFLGAFND	NVFKTALFVM	IGFYGLGQNG
	51	FLPAGQMLNL	GALLFILPYF	LFSSLSGQLG	NKFDKAVLAR	WAKVLEMIIM
	101	AVAAYGFYIR	SAPILLACL	CMGAQSTLFG	PLKYAILPDY	LDDKELMMGN
	151	SLIESGTFFVA	ILFGQILGTA	VAGVPPYIVG	ILVLLVAVGG	TVGSLFMPSV
	201	PAKAADTQIE	WNIVRGTKSL	LRETVRHKPV	FTAIIGISWF	WFGAVYTTQ
	251	LPTFTQIHLG	GNDNVFNML	ALFSIGIAAG	SVLCAKFSRE	RLRLAWVTVG

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPVMA VMTLIGFFGG
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAVL SAVLLFLFDS
 401 ISLLYLIAL GNIPLSVFLI KRERRFLGAA AIRKKP*

m232/a232 95.9% identity in 290 aa overlap

m232.pep				10	20	30
				MMGNSLIESGTFVAILFGQILGTAVAGVPP		
a232	ACLFCMGAQSTLFGPLKYAILEDYDDKELMMGNSLIESGTFVAILFGQILGTAVAGVPP					
	120	130	140	150	160	170
m232.pep		40	50	60	70	80
		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG				
a232	YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
	180	190	200	210	220	230
m232.pep		100	110	120	130	140
		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMALFSIGIAAGSVLCAKFSXERLMLAW				
a232	ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMALFSIGIAAGSVLCAKFSRERLRLAW					
	240	250	260	270	280	290
m232.pep		160	170	180	190	200
		VTVGALGLTVCGLVVLVWLTHGHRFEGLNGIFWFLSQGWAYPVMAVMTLIGFFGGFFSVPL				
a232	VTVGALGLTVCGLVVLVWLTHGHRFEGLNGIFWFLSQGWAYPVMAVMTLIGFFGGFFSVPL					
	300	310	320	330	340	350
m232.pep		220	230	240	250	260
		YT-VQTAIARFPRP-AVAANNIVNGIFMVSAVLSAVLLFLFDSISLLYLIALGNIPLS				
a232	YTWLQTASSETFRARAVAANNIVNGIFMVSAVLSAVLLFLFDSISLLYLIALGNIPLS					
	360	370	380	390	400	410
m232.pep		270	280	289		
		VFLIKRERRFLGAAAIRKKPX				
a232	VFLIKRERRFLGAAAIRKKPX					
	420	430				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq

```

1  atgaaacgca aaaatatcgc gctgattccc gccgccggca tcgggggtgcg
51  tttcgggtgcg gacaaaccca agcaatatgt cgaaatcgga agcaaaacgg
101 ttttagaaca tgtacttggg atttttgaac ggcattgaggc cgtcgatttg
151 accgtcgttg tcgtctcgcc cgaagacacg ttgcccgata aggttcagac
201 ggcatttcca caggttcggg tgtggaaaaa cgggtggacag acccgcgccg
251 aaactgtccg caacggtgtg gcaaaactgt tggaaaccgg tttggcgggc
301 gaaaccgaca atattctggt acacgatgcc gcccgctgct gcctgccgtc
351 tgaagctctg gcgcggttga tagaacaggc gggcaacgcc gccgaaggcg
401 ggattttggc agttcccgtt gccgatacgc tcaagcgcgc agaaagcgga
451 caaatcagtg caactgtcga ccgttcgggg ctttggcagg cgaaacgcc
501 gcagcttttt caagcgggtt tgctgcaccg cgattggct gcggaaaact
551 tgggcggcat taccgatgaa gcgtccgccg tggaaaaact ggggtgtcgt
601 ccgctactga tacagggcga cgcgcgcaat ttgaaactga cgcagccgca
651 ggacgcatac atcgtcaggc tgctgctcaa tgccgtctga
```

This corresponds to the amino acid sequence <SEQ ID 858; ORF 233.ng>:

g233.pep

```

1  MKRKNIALIP AAGIGVRFGA DKPKQYVEIG SKTVLEHVLG IFRHEAVDL
51  TVVVVSPEDT FADKVTQAFP QVRVWKNGGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL ARLIEQAGNA AEGGILAVPV ADTLKRAESG
```

151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGVR
 201 PILLIQGDARN LKLTQPDAY IVRLLNNAV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)

1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTCAAGC
 201 GGCATTTCCT CAGGTTCCGG TGTGGAAAAA CGGCGGACAG ACCCGCGCG
 251 AAACCGTCCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTTGGCGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGGCG
 401 GGATTTTGGC AATTCCTATT GCCGATACGC TCAAGTGC GCACGGTGGG
 451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)

1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
 51 TVVVVSPEDT FADKVQTAFP QVRVWKNGGQ TRAEVTRNGV AKLLETGLAA
 101 ETDNIVHDA ARCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG
 151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
g233	MKRKNIALIP AAGIGVRFADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m233.pep	FADKVQTAFPQVRVWKNGGQTRAEVTRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
g233	FADKVQTAFPQVRVWKNGGQTRAEVTRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
	70	80	90	100	110	120
	130	140	150			
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
g233	ARLIEQAGNA AEGGILAVPVADTLKRAESQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq

1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTCAAGC
 201 GGCATTTCCT CAGGTTCCGG TGTGGAAAAA CGGCGGACAG ACCCGCGCG
 251 AAACGTCCG CAACGGTGTG GCAAAATTGT TGGAAACCGG TTTGGCGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG
 401 GGATTTTGGC AATTCCTATT GCCGATACGC TCAAGTGC GCACGGTGGG
 451 AACATTAGTG CAACCGTCGA GCGGACGAGC CTTTGGCAGG CGCAAACGCC
 501 GCAGCTTTTC CGCGCCGGGC TGCTGCACCG CGCATTGGCT GCGGAAAAC
 551 TGGACGGCAT TACCGATGAA GCGTCCGCCG TGGAAAAATT GGGCATCCGC
 601 CCTTTGCTGG TGCAGGGCGA CGCGCGCAAT TTGAACTGA CGCAGCCGCA
 651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51 TVVVVSPEDT FADKVQTAFP QVRVWKNNGGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAI PV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDVAV*
```

m233/a233 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m233.pep	MKRKNIALIPAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
a233	MKRKNIALIPAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
m233.pep	FADKVQTAFPQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
a233	FADKVQTAFPQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
m233.pep	FADKVQTAFPQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
a233	FADKVQTAFPQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
a233	TRLIEQAGNA AEGGILAI PVADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA					
	130	140	150	160	170	180
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
a233	TRLIEQAGNA AEGGILAI PVADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA					
	130	140	150	160	170	180
a233	AENLDGITDEASAVEKLGIRPLLVQGDARNLKLTQPQDAYIVRLLLDVAVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1 atgaaaaccg ttccgcgcgc catcgctttt gccgcgcgctg ccgtttcact
51 gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat caggtgttc gcaccccgat ttccgtcgga
151 acattcgaca accgctccag cttccaaaaa ggcattttct ccgacagtga
201 agaccgtctg ggcagccagg caaaaacccat cctggtaaca cacctgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaatccg gcatttcgag caaagcgcag aacctgaaag gcgcagatta
351 tgtcggtacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggtcgcggca aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctattc
501 cacacagggc gcgggcgaat acgcacttcc caaccgcgaa atcatcggtt
551 tcggcgccac ttccggctac gatgcgactt tgaacggcaa agttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaacgg
651 cgcattggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1 MKTVSAAIAF AAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
51 TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRFN V LNRTNLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALS NRE IIGFGGTSY DATLNGKVL D
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1 ...GGCGCGGGCG AATACGCACT TTCCAACCGT GAAATCATCG GTTTCGGCGG
51 CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTGA GACTTGGCAA
101 TCCGCGAAGC .gTCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

536

```

1  atgaaacctt tgatttttagg gcttgccgcc gtggtggctc tgtctgcctg
51  ccaagttcga aaagctcccc acctcgacta cacgtcattc aaagaaagca
101 aaccggcttc aattttggtg gttccgccgc tgaacgagtc gcctgatgtc
151 aacggcactt gggggatgct ggcttcgacc gccgcgccga ttccgaagc
201 cggctattac gtctttcccg ccgcagtcgt ggaggaaacc ttcaaagaaa
251 acggcttgac caatgccgcc gatattcacg ccgtccggcc ggaaaaactg
301 catcaaattt tcggcaatga tgcggttttg tacattacgg ttaccgaata
351 cggcacttca tatcaaattt tagacagcgt gacgaccgta tccgccaaag
401 cacggctggg cgattcccgc aacgggaaag agttgtggtc ggggttcggcc
451 agcatccgcg aaggcagcaa caacagcaac agcggcctgt tgggggcttt
501 ggtcggcgca gtggtcaatc agattgcaa cagcctgacc gaccgcggtt
551 atcaggtttc caaaaccgcc gcatacaacc tactgtcgcc ctattccgcc
601 aacggtatct tgaaagggtc gagattcgtc gaagagcagc ccaaataa

```

This corresponds to the amino acid sequence <SEQ ID 870; ORF 235.ng>:

g235.pep

```

1  MKPLILGLAA VLALSACQVR KAPDLDTYSF KESKPASILV VPPLNESPDV
51  NGTWGMLAST AAPISEAGYY VFPAAVVEET FKENGLTNAI DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTG YQILDVSTTV SAKARLVDSR NGKELWGSQA
151 SIREGSNNSN SGLLGLALVGA VVNQIANSLT DRGYQVSKTA AYNLLSPYSR
201 NGILKGPRFV EEQPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 871>:

m235.seq

```

1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGTTTTG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAGAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTGAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC CAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAAGGTCC GAGATTCGTT GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 872; ORF 235>:

m235.pep

```

1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAI DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTG YQILDVSTTV SAKARLVDSR NGKELWGSQA
151 SIREGSNNSN SGLLGLALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng) from *N. gonorrhoeae*:

m235/g235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST					
g235	MKPLILGLAAVLALSACQVRKAPDLDTYSFKESKPASILVVPPLNESPDVNGTWGMLAST					
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTG					
g235	AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTG					
	70	80	90	100	110	120
	130	140	150	160	170	180

537

```

m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
g235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           130      140      150      160      170      180

           190      200      210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
           |||||||||||||||||||:||||||||||||||
g235      DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPKX
           190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTCGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GAAAAACTG
301 CATCAGATT TCGGCAATGA TCGGTTTTG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAG
401 CACGCTGGT CGATTCCCGC AACGGAAGAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGCCTGT TGGGGGCTTT
501 GGTACGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAAGGTCC GAGATTCGTC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

           10      20      30      40      50      60
m235.pep  MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
           10      20      30      40      50      60

           70      80      90      100     110     120
m235.pep  AAPLSEAGYYVFPAAVVEETFKQNLTNAAADIHAVRPEKLHQIFGNDAVLVYITVTEYGTS
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      AAPLSEAGYYVFPAAVVEETFKQNLTNAAADIHAVRPEKLHQIFGNDAVLVYITVTEYGTS
           70      80      90      100     110     120

           130     140     150     160     170     180
m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           130     140     150     160     170     180

           190     200     210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
           |||||||||||||||||||:||||||||||||||
a235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq

```

1 ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGACAG
51 CGGTTTCATA ACCTGCAACC GCGCCACAT CGCGGGTGTG ATGCCAGCAG
101 CGTTCGCATT TTTCGCCGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTACAGATG CCGGCCATTT CTTCGGGCGC GGTAATTTCTG
251 GCTTCCGCCT GCAAaggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcg9cg gTTACTGCTT CGCGCGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAGTTC GGCTTCGGCT TTTTCGTTGA TGGCCGGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGTCCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTCGCCGC TCGCGCGGGC GCGGCTGTCTG
551 GCTTTGGTGG TGTAGAGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGGAAAG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTCTTGACG CCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCCACC ATATCCGCCT GTTGACGGC
751 ATCTTCAATC GGATTAAAGT CGCTCAAATT GGCAAAcagG AAGCTCAAGG
801 TATTGCGGAT GCGGCGGTAG CTTTCGGTAA CGCGTTTGAG GATTTCTTTG
851 GAAatcgCCA Attcgccgct gTAATCGGTG GATGCGCGCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTCGT TATAGACTTC CTGCGGCGCG ACGACGTTGC
951 CGATGGATTT CGACATTTTG CGGCCGTTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TCGCGTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1 MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAFAFFAV AGFGNGKFI
51 TDFHFCFRHQ QGKAQFFAQS IQIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGLLRAAG AAVGFGVEA VFQDVEVERA
201 QVFRAERNV FHGEVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAG
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1 ..TGACCGGAC GAACCGACGG TTTTGTCCGC GCGCAAAGGC TCGATGGCGG
51 CGGTTACCGC TTCGCGGGCT TCGCGGATTG CCGTCCATTT TTTCACCAGT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCTCTTCGC CGCCGCCGwT GAYGTCCCAC GCTTCTTCGC
201 CGGTGAAGCA CAAAATCGGT GCAATCAAGA GAACCAAACT GCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGGTCTTTCA GGATGTCGAG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACAATG TCTTTTACGG CAAAGTGGaA kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG ACACTCTTGC AGCTGACGTG CCAATACCAC
451 GGCGTAGCGG TCGATTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTTG AGGATTTCTT TGGAAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCGC CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCGGTG CAACGACGTT GCCGATGGAT
701 TCGACATTT TTTTGCCTTC GCCGTCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1 ..LHGRTDGFVG AQRLDGGGYR FAGFADCRPF FHQFGFGFFV DGRELVPSME
51 EDAVXFAAAX DVPRFFAGEA QNRCNQENQT ACDVIQGS LC AAACMAVCFG
101 GVEAVFQDVE VERTQVFRAE RNXYFYGKVE XITRIVIAQ TLLQLTCQYH
151 GVAVDFHHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQQ
251 LFIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng) from *N. gonorrhoeae*:

m236/g236

539

m236.pep						10	20	30
						LHGR	TDGFVGAQRLDGGGYRFAGFADCRPF	
g236	FRHQQGKAQFFAQSIQIAGHFFRRGNFGFRLOGR	TDSFVGAQRLDSSGGYCFARFADCRPF						
	60	70	80	90	100	110		
m236.pep		40	50	60	70	80	90	
	FHQFGFGFFVDGRELVP	SMEEDAVXFAAAXDVPRFFAGEAQNRCNQENQTACDVIQSLC						
g236	FHQFGFGFFVDGRELVP	SMEEDAVFFAAADDVPRFFAGEAQNRCNQENQAARDVVQGLR						
	120	130	140	150	160	170		
m236.pep		100	110	120	130	140	150	
	AAACMAVCFGGVEAVFQDVEVERTQVFRAERNXVFYGVKVEITRIVIA	CQTLLQLTCQYH						
g236	AAAGAAGVFGGVEAVFQDVEVERAQVFRAERNNVFHGEVEGIARIVTACQ	TLLQPPROYQ						
	180	190	200	210	220	230		
m236.pep		160	170	180	190	200	210	
	GVAVDFHHIRLLHGIFNRIKVAQVGKQKAQGIADTAVAFGYAFEDFFGNRQFAAVIGRCR							
g236	GVAVDFHHIRLLHGIFNRIKVAQIGKQEAQGIADA AVAFGNAFEDFFGNRQFAAVIGGCR							
	240	250	260	270	280	290		
m236.pep		220	230	240	250	259		
	PQAQDVCAEFVINLLRCNDVADGFRHFFAFVDNETMGQQLFIRRATHX							
g236	PQAQDVRAEFVIDFLRRDDVADGFRHFAAVLVNHETVGQQLFIRCASHG							
	300	310	320	330	340			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 879>:

a236.seq

1	ATGGCGCGTT	TCGCCTTCTC	CGCCGACATT	CTCTGCACAG	CGTTTGCAGA
51	CGGTTTCATG	GCCTGCAACC	GCGCCACAT	CGCGGGTGTA	GTGCCAGCAG
101	CGTTCGCATT	TTTCAACATC	ACTGGCTTTA	GCGGCAACGG	CAAGTTCGCT
151	GCCTACTTTC	ACTTCTGCTT	TAGACACCAG	CAAAGCAAAG	CGCAATTCTT
201	CGCCCAAAGC	ATTGAGATAG	CCGGCCATTT	CTTCCGGGCG	GGTAATTTCG
251	GCTTCGGCTT	GCAAGGACGA	ACCGACGGTT	TTGTTCGGCG	GCAAAGGCTC
301	GATGGCGGCG	GTTACCGCTT	CGCGGGCTTC	GCGGATTGCC	GTCCATTTT
351	TCACCAAGTC	GGCTTCGGCT	TTTTCGTTGA	TGGTCGGGAA	CTCGTGCCAA
401	GTATGGAAAA	GCACGCTGTC	TTCTGCGCCG	CCGCCGATGA	TGTCCCACGC
451	TTCTTCGCGG	GTGAAGCACA	AAATCGGTGC	AATCAAGAGA	ACCAGGCTGC
501	GCGTGATGTG	GTACAGGGCG	GTTTGCAGCG	TGCGGCGGGC	GCGGCTGTGC
551	GCTTTGGTGG	TATAGAGGCG	GTCTTTCAGG	ATATCGAGGT	AGAACGCGCC
601	CAAGTCTTCC	GAGCAGAAAG	AAACCATTTT	TTTACGGCA	AAGTGGGAAG
651	CATAACGCGG	ATAAAAATCA	CCGGCAACGC	GTTCTTGCG	CCGCCTTGCC
701	AACACCAAGG	CATAGCGGTC	GATTTCCACC	ATATCCGCCT	GTTGCACGGC
751	ATCTTCAATA	GGATTGAAGT	CGCTCAAGTT	GGCAAACAAA	AAGCTCAAGG
801	TATTGCGGAT	ACGGCGGTAG	CTTTTCGGTTA	CGCGCTTGAG	GATTTCTTTG
851	GAAATCGCCA	ATTGCGCGCT	GTAATCGGTG	GATGCCGCCC	ACAGGCGCAG
901	GATGTCCGCG	CCGAACGCT	TATACACTTC	TTGCGGCGCG	ACGACGTTGC
951	CGATGGATTT	CGACATTTTG	CGCCCGTTTT	GATCCACCAC	GAAACCATGG
1001	GTCAGCAGCT	GTTGTACGG	CGCGCGACCC	ATTGA	

This corresponds to the amino acid sequence <SEQ ID 880; ORF 236.a>:

a236.pep

1	MARFAFSADI	LCTAFADGFM	ACNRAHIAGV	VPAAFAFTTI	TGFSNGNKFA
51	AYFHF CFRHQ	QSKAOFFAQ	IQIAGHFFRR	GNFGFGLQGR	TDGFVGAQRL
101	DGGGYRFAGF	ADCRPFFHQ	GFGFFVDGRE	LVPSMEKHAV	FCAAADDVPR
151	FFAGEAQNRC	NQENQAARDV	VQGLRAAAG	AAVGFGGIEA	VFQDIEVERA
201	QVFRAERNHF	FHGKVEGTR	IKITGNAFLQ	PPCQHQGI	AVDFHHIRLLHG
251	IFNRIEVAQV	GKQKAQGIAD	TAVAFGYALE	DFFGNRQFAA	VIGGCRPQAG
301	DVRAELVIHF	LRRDDVADGF	RHFAPVLIHH	ETMGQQLFVR	RATH*

540

m236/a236 81.0% identity in 258 aa overlap

m236.pep					10	20	30
					LHGRTDGFVGAQRLDGGGYRFAGFADCRPF		
a236	FRHQSKAQFFAQSIQIAGHFFRRGNFGFGLQGRTDGFVGAQRLDGGGYRFAGFADCRPF						
	60	70	80	90	100	110	
m236.pep		40	50	60	70	80	90
	FHQFGFGFFVDGRELVP	SMEEDAVXFAAAXDVPRFFAGEAQNRCNQENQTACDVIQGS	LC				
a236	FHQFGFGFFVDGRELVP	SMEKHAVFCAAADDVPRFFAGEAQNRCNQENQAARDVVQGG	LR				
	120	130	140	150	160	170	
m236.pep		100	110	120	130	140	150
	AAACMAVCFGGVEAVFQDVEVERTQVFRAERNXVFYGVKEXITRIVIA	CQTLLQLTCQYH					
a236	AAAGAAVGFGGIEAVFQDIEVERAQVFRAERNHFFHKGVEGITRIKITG	NAFLQPPCQHQ					
	180	190	200	210	220	230	
m236.pep		160	170	180	190	200	210
	GVAVDFHHIRLLHGI	FNRIKVAQVGKQKAQGIADTAVAFGYAFEDFFGNRQFAAVIGR	CR				
a236	GIAVDFHHIRLLHGI	FNRIEVAQVGKQKAQGIADTAVAFGYALEDDFFGNRQFAAVIGG	CR				
	240	250	260	270	280	290	
m236.pep		220	230	240	250	259	
	PQAQDVCAEFVINLLRCNDVADGFRHFFAFVAVDNETMGQQLFIRRATHX						
a236	PQAQDVRAELVIHFLRRDDVADGFRHFAPVLIHHEHETMGQQLFVRRATHX						
	300	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 881>:

g237.seq

```

1  atgctgggaca aggttgccgg taatatcgca ctccccgcc caccgaatatt
51  cgattctaac atcggaagc tgcggaaaaa ctttaagcat atcttgccgg
101 acaagctcgg tcatacgcg aggattgtcg ataaattcgt tacccttacc
151 gccgaaaagc agcctgccgt ccgcgctgag gcggaataa tccaaaatat
201 ggctgtgttc gcatactgcc atattgtgtc ggataagccc tttgtgctgc
251 gcgcccgaag gttcgggtgc aataataaag gtgctgacgg caatcgctt
301 gcgttccaaa ggccggaata tcgggttcaa accgacataa gtattgacgg
351 catagaccac atttttacac tcgacgctgc cttcgggcgt gtaaacaccg
401 caaccgtttt gatacgggtc gatgcgctgc atcggggatt gctcgaaaat
451 ctgcgcgcgc gtttcggcag cggcgctggc aacacccaac gtgtaattga
501 gcggatgaag atgcccggac aagggatcga actgtgcgcc ttggtacata
551 tcgctgtcaa gctgtgttt caactcggct ttatcccaa gttgataatg
601 actcgacccg taatgccgtt gggcgtgttc atgccactgc tgcaactctt
651 cccaatgctg cggacggacg gcaaccgttg cataaccgct ctgccaatcg
701 caatcgatgg catgtttgct gacgcgttcg tccaccagtt cgaccgctg
751 caaagactgt tgccaaaacc attgcgcctg ctccaagcgg acctgttttt
801 caatttcccc cataccgcag gcgtagtcgc tgataacctg cccgccactc
851 ctgccggacg cgccgaagcc gatacgtgcg gttccaaaa cgacggcttc
901 atgtccgtgt tccgccagcg gcaatgcggt acacaaaccg ctcaaaccgc
951 cgccgataat gcaggtttcg gctttcagac ggcattggag tttcggataa
1001 acagtatgct gattaaccga actaaaataa taagaaggca gatattcttg
1051 aaaatcaggg cgaatcattg tgtttgcttt atcgggtata tttcggacg
1101 gaatgataca gactgtcggg ccatatcgtc caaacagaaa atcgggtga

```

This corresponds to the amino acid sequence <SEQ ID 882; ORF 237.ng>:

g237.pep

```

1  MRDKVGGNIA LPAPRIFDSN IGKLRKNFKH ILADKLGHTR RIVDKFVILT
51  AEQPAVRAE AVIIQNMAVV AYCHIVADKP FCARAQGGG NNGADGNRL

```

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNOPTVLIRF DARHRGLEN
 151 LRAGFGSGAG NTQVIERMK MPQGIELCA LVHIAVKLLF QLGFIKPLIM
 201 TRTVMLPLGVF MPLLQLFPML RTDGNRGITA LPIAIDGMFA DAFVHQFDRL
 251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRABA DTCGFQNDGF
 301 MSVFRQRQCG TQTAQTAADN AGFGFQTALE FRINSMRINR TKIIRRQIFL
 351 KIRANHCVCF IGYIFGRNDT DCRAISSKQK IG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m23 7.seq
 1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT
 51 CGATTTTGAC ATCGGCAAGC TCGGAAAAA CTTTAAGCAT ATCTGGCGG
 101 ACAAGCTCGG TCATaCGCTC AGGATTGTCG ATAAACTCGT TATCCTTACC
 151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT
 201 GGCGGTGTC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTTGGCGCG
 251 GCCCCAAGG GTTCGGTCCG AATAATAAAG GTGCTGACAG CAATCGCCTT
 301 GCGTTCCAAA GGCCGGAATA TCGGGTTCAA ACCTGCATAA GTATTGACAG
 351 CATAGACCAC ATTTTTCAC TCGACGCTGC CTTGCGGCGT GTAAACCAGC
 401 CAACCGTTTT GATGCGGTTT GATGCACGTC ATCGGGGATT GCTCGAAAAAT
 451 CTGCGCACCG GCTTCGGCAG CGGCACGAGC GATGCCCCAA GTGTAAGTGA
 501 GCGGATGCAG GTGTCCGGAT AAGGGGTCGA ATTGTGCCCC TTGGTACATA
 551 TCGCTGTCAA GCTGCTGTTT CAACTCGGCT TTATCCCAA GTTGATAATG
 601 ACTCGCACCG TAATGCCGTT GGGCGTGTTT ATGCCACTGC TGCAACTCTT
 651 CCCAATGCTG CGGACGGACG GCAACCGTGG CATAACCGCG CTGCCAATCA
 701 CAATCGACCG CATGTTTTCG GACGCGTTTC TCCACCAGTT CGACCGCCTG
 751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT
 801 CAATTTCCCC CATAACCGAG nCGTAATCGC TGATAACCTG CCCGCCACTC
 851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
 901 ATGTCCTGCG TCCGCCAAGG GCAATGCAGT GCACAAACCA CCCAATCCGC
 951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTTCGGATAA
 1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
 1051 AAAATCAGGG CGAATCATTG TGTTTGCTTT ATCAGGTGTA TTTTCGGACG
 1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAWACAGAAA ATCGGTTGA

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m23 7.pep
 1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGHTL RIVDKLVILT
 51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NNGGADSNRL
 101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNOPTVLMRF DARHRGLEN
 151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFIKPLIM
 201 TRTVMLPLGVF MPLLQLFPML RTDGNRGITA LPIAIDGMFA DAFVHQFDRL
 251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPSRAET DTRGFQHNRF
 301 MSLRQGCQS AQTTQSAADD TGIGFQTALE FRINSMRINR TEIIRRQIFL
 351 KIRANHCVCF IRCIFGRNDT GCRAISSKQK IG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m23 7/g237

	10	20	30	40	50	60
m23 7.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE					
g23 7	MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGHTRIVDKFVILTAEKQPAVRAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m23 7.pep	AVIIQNMAVVAYCHIVTDKPF CARPQGFGRNNGGADSNRLAFQRPEYRVQTCISIDSIDH					
g23 7	AVIIQNMAVVAYCHIVADKPF CARAQGFGRNNGGADGNRLAFQRPEYRVQTDISIDGIDH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m23 7.pep	IFALDAAFGRVNOPTVLMRFDARHRGLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					

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a237.seq
1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCTCGCCC CACGAATATT
51 CGATTTTGAC ATCGGCAAGC TCGGGAAAAA CTTTAAGCAT ATCTTGGCGG
101 ACAAGCTCGG CTATACGCGC GGGATTGTGC ATAAACTCGT TATCCTTACC
151 GCCGAAAAGC AGTCTGCCGT CGCGCTGAG CGGGTAATAA TCCAAAATAT
201 GACGGTTGTC GCATACTGCC ATATTGTTGC GGATAAGCCC TTTTGCACGC
251 GCGCCCAAGG GTTCTGTGGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGCTCCAAa GGCTTGAATA TCGGATTCAA ACCGGCATA GTATTGACGG
351 CGTACACAG ATTTTGCAT TCGACGCTGC CTTCGGGATG GTAAACCAGC
401 CAACCGTTTT GATAAGGTTT AATGCGTATC ATCGGGAGAAT GCTCAAAAAT
451 CTTGTAACCA GCTTCGGCAG CGGCGCGGGC GATGCCAAC GTGTAATTGA
501 GCGGATGGAG AGTCGCGGAC AAGGGATCGA ACTGTGCGCC TTGGTACATA
551 TCGCTGTCAA GCTGCTGCTT CAGTTCAAGT TTATCCCGA GTTGATAATG
601 AGTTGCACCG TAATATTTTT GGGCGTGCTC ATGCCATTGT TGCAATTCTT
651 CCAATGCTG CGAACGGATG GCAACCGTGG CATAACCGCG CTGCCAATCG
701 CAATCAATGG CATGTTTGC GACGCGTTCG TCCACCAGTT CGACCGCCTG
751 CAAAGACTGT TGCCAAAACC ATTGCGCTTG CTCCAAACCG ACCTGTTTTT
801 CAATTTCCTC CATACCGCAG GCGTAATCGC TGATAAACCTG CCCCGCACTC
851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAAACGGTTT
901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CTCAATCCGC
951 GCGCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTTCGGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGG CGAATCATTT TGTTTGCTTT ATCGGGTATA TTTTCCGACG
1101 GAATGATACA GGCTGTCGAG CCATATCGTC CAAACAGAAA ATCGGTTGA

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a237.pep

1	MRDKVGGNVA	LPAPRIFDFD	IGKLRKNFKH	ILADKLGHTR	GIVDKLVILT
51	AEKQSAVRAE	AVIIQNMTVQ	AYCHIVADKP	FCTRAQGFQCG	NNKGADSNRL
101	ALQRLEYRIQ	TGISIDGVHQ	IFAADFAAFGG	VNQPTVLIRF	NAYHGRMLKN
151	LRTSFGSGAG	DAQRVIERME	MPGQGIELCA	LVHIAVTKLL	QFSVIPELIM
201	<u>SCTVIFLGLV</u>	<u>MPLLQFFPML</u>	<u>RTDGNRGITA</u>	<u>LPIAINGMFA</u>	<u>DAFVHQFDRL</u>
251	QRLLPKPLRL	LOTDLFFNFL	HTAGVIADNL	PATPSRRAET	DTRGFQHNRF
301	MSLLRQGQCS	AQTTSQAADD	TGIGFQTALK	FRNSMRINR	TEIIRRQIFL
351	KIRANRHQVCF	IGYIFGRNDT	GCAISSKOK	IG*	

m237/a237 85.6% identity in 382 aa overlap

m237.pep	10	20	30	40	50	60
	MRDKVGGNVALPAPRI	FD	DIGKLRKNFKHILADKLGHTLRIVDKLVILTAEQSAVRAE			
a237	10	20	30	40	50	60
	MRDKVGGNVALPAPRI	FD	DIGKLRKNFKHILADKLGHTRGIVDKLVILTAEQSAVRAE			
m237.pep	70	80	90	100	110	120
	AVIIQNMVAVYCHIVTDKPF	CAR	PQGFGNNKGADSNRLAFORPEYRVQTCISIDSIDH			
a237	70	80	90	100	110	120
	AVIIQNMVAVYCHIVADKPF	CTRA	QGF	CGNNKGADSNRLALQRL	EYRIQTGISIDGVHQ	
m237.pep	130	140	150	160	170	180
	IFALDAAFGRVNQPTVLMR	FDARH	RGLLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP			
a237	130	140	150	160	170	180
	IFAFDAAFGRVNQPTVLI	RFNAYHGRMLKNLRTS	FGSGAGDAQRVIERMEMPGQGI	ELCA		
m237.pep	190	200	210	220	230	240
	LVHIAVKLLFQLGFIPKLI	MTRTMPLGVFMP	LLQLFPMLRTDGNRGIT	ALPITIDGMFA		
a237	190	200	210	220	230	240
	LVHIAVKLLQFSVIP	ELIMSC	TVIFLGVLMPL	LQFFPMLRTDGNRGIT	ALPIAINGMFA	
m237.pep	250	260	270	280	290	300
	DAFVHQFDRQLRLLPKPL	RLLQADLFFNF	PHTAXVIADNLPATPS	RR	ETDTRGFQHNRF	
a237	250	260	270	280	290	300
	DAFVHQFDRQLRLLPKPL	RLLQD	LFFN	FLHTAGVIADNLPATPS	RR	ETDTRGFQHNRF
m237.pep	310	320	330	340	350	360
	MSLLRQGQCSAQT	TQSAAD	TGIGFQTALKFRIN	SMRINRTEI	IR	QIFLKIRANHC
a237	310	320	330	340	350	360
	MSLLRQGQCSAQT	TQSAAD	TGIGFQTALKFRIN	SMRINRTEI	IR	QIFLKIRANHC
m237.pep	370	380				
	IRCI	FG	RNDTGCRAISSXQKIGX			
a237	370	380				
	IGYI	FG	RNDTGCRAISSXQKIGX			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctggtggcag cggcaatatt
51  gatgctgcat atccccatta gtcattgcga cgggttggat gcccgtttgc
101 gcatgatgat gcaggcaaaa cactacgaac cgggttggca ataccatctg
151 tttggtaatg ctgcgcgcag tgtaaaaaat cgggttggcg ccgtccaaac
201 atttgatgca actgcggtcg gcccataact gcctattaca cacgaacgga
251 caggatttga aggtgttatc ggctatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtcggtt cgataatcat gattcaaaaa gcacttctga
351 tttcagcggc ggcgtagacg gcggttttac cgtttaccaa cttcatcgga
401 cagggtcgga aatacatccc gcagacggat atgacggggc tcaaggcggc
451 ggttatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaacaa agataaacac tgttccgcaa gcccttttt
551 cagaccgctg gctaaaagaa aatgccggtg ccgcttcagg tttctcagc
601 cgtgcgggat aagcaggaaa actgatattg gaaaacgacc ccgataaaaa
651 ttggcgggct aaccgtatgg atgatattcg cggcatcgtc caaggtgcgg
701 ttaatccttt ttaacgggt tttcaagggt tagggattgg ggcaattaca
751 gacagtgcgg taagcccggt cacagatata gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtcc ggaagcacia cttgccgcgg

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544

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851 cgagcctatt acaggacagt gcctttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgccttgccc gtagcagagg ccgcaggtac ggtttgccgc ggtaaaaaag
1001 tagaacttaa ccgacccaaa tgggattggg ttaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcgga aggaaaagct aatgctgcaa
1151 cctatcctaa gttgggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggtcctaa atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atgggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacattt
1401 tgcaactaca ggtattcaag caaattttga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1 MNLPIQKFMM LLAAAIISMLH IPISHANGLD ARLRDDMQAK HYEPPGKGYHL
51 FGNARGSVKN RVCVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGS TKTKINTVPQ APFSDRWLKE NAGAASGFSL
201 RADEAGKLIW ENDPKNWRA NRMDDIRGIV QGAVNPFLTQ FQGVGIGAIT
251 DSAVSPVTDI AAQQTLOGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGINS
301 ARQWADAHPN ITATAQTALA VAEAAGTVWR GKVELNPTK WDWVKNTGYK
351 KPAARHMQTV DGENAGGNRP PKSITSEGKA NAATYPKLVN QLNEQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEGA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYI IDSNEKRNKI KNHGLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGGTTTGA AGGTGTTATC GGTATGAAA CCCATTTTTC AGGGCACGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAAA GCACCTCTGA
351 TTTCAGCGGC GGTGTAGACG CCGGTTTAC TGTTTACCAA CTTTCATCGAA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCGGAGG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAACCTCA ACAAACAAAG AGACTAATAT TGTCCTCAA GCCCCATTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCCGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTTTG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTAGGAA AATTAAGTCC GGAAGCACAA CTTGTGCGCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGCAG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCAAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAAAAAAG
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TAAAAAATAC CGGTTATAAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAATCTT TACCAAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAACTGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTCACG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAAATTTAC AAGGTAAAGCA
1401 AGCAAAAGAT TATTTACAAC AACAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPPGKGYHL
51 FGNARGSVK RYVAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

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151 DYPPPGGARD IYSYYVKGTS TKTKTNIVPQ APFSDRWLKE NAGAASGFFS
 201 RADEAGKLIW ESDPNKNWWA NRMDDVRGIV QGAVNPFLMG FQGVGIGAIT
 251 DSAVSPVTD TAAQQTLOGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGINS
 301 AKQWADAHNP ITATAQTALS AAEAAGTVWR GKKVELNPTK WDWVKNTGYK
 351 KPAARHMOTL DGEMAGGNKP IKSLPNSAAE KRKQNFKEFN SNWSSASFDS
 401 VHKTLPNAP GILSPDKVKT RYTSLDGKIT IIKDNENNYF RIHDNSRKQY
 451 LDSNGNAVKT GNLOGKQAKD YLQQQTHIRN LDK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 238 shows 86.0% identity over a 401 aa overlap with a predicted ORF (ORF 238.ng) from *N. gonorrhoeae*:

m238/g238

m238.pep	10	20	30	40	50	60
	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
g238	MNLPIQKFMMLLAAASMLHIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
m238.pep	70	80	90	100	110	120
	RVYAVQTFDATAVSPVLPITHERTGFEVIGYETHFSGHGHEVHSPFDHSDSKSTSDFSG					
g238	RVCAVQTFDATAVGPILPITHERTGFEVIGYETHFSGHGHEVHSPFDNHDSDSKSTSDFSG					
	70	80	90	100	110	120
m238.pep	130	140	150	160	170	180
	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYYVKGTS TKTKTNIVPQ					
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGYEPQGGARDIYSYHIKGTSTTKINTVPQ					
	130	140	150	160	170	180
m238.pep	190	200	210	220	230	240
	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDDVRGIVQGAVNPFLMG					
g238	APFSDRWLKENAGAASGFLSRADEAGKLIWENDPKNWRANRMDDIRGIVQGAVNPFLTG					
	190	200	210	220	230	240
m238.pep	250	260	270	280	290	300
	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGKLSPEAQ LAAASLLQDS AFAVKDGINS					
g238	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGKLSPEAQ LAAASLLQDS AFAVKDGINS					
	250	260	270	280	290	300
m238.pep	310	320	330	340	350	360
	AKQWADAHNPITATAQTALSAAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMOTL					
g238	ARQWADAHNPITATAQTALAVAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMOTV					
	310	320	330	340	350	360
m238.pep	370	380	390	400	410	420
	DGEMAGGNKPIKSLPNSAAEKRKQNFKEFNSNWSSASFDSVHKTLPNAPGILSPDKVKT					
g238	DGEMAGGNRPPKSI-TSE GKANAATYPKLVNQLNEQNLNNIAAQDPRLSLAIHEGKKNFP					
	370	380	390	400	410	
m238.pep	430	440	450	460	470	480
	RYTSLDGKITIIKDNENNYFRIHDNSRKQYLDNSNGNAVKTGNLOGKQAKDYLQQQTHIRN					
g238	IGTATYEEADRLGKIWVGEGARQTS GGGWLSRDGTRQYRPPTEKKSQFATTGIQANFETY					
	420	430	440	450	460	470

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

a238.seq (partial)

```

1 ATGAATTGTC CTATTCAAAA ATTCATGATG CTGTTTGCGAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCCAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAT CGGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTCG GCCCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTGTA AGGCATTATC GGTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACCTCTGA
351 TTTCAGCGGC GCGGTAGACG GTGGTTTAC CGTTTACCAA CTTATCGGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCAGGAGG AGCAAGGGAT ATATACAGCT ACTATGTCAA
501 AGGAACCTCA AAAAAACAA AGAGTAATAT TGTCCCGCA GCCCCATTTT
551 CAGACCGCTG GCTAAAAGAA AATGCCGCTG CCGCCTCTGG TTTTTCAGC
601 CGTGCTGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATATCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACAA CTTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTTGGCG TAAAAGACGG TATCAATTC
901 GCCAGACAAAT GGGCTGATGC CCATCCGAAT ATAACGCAA CAGCCCAAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTTGGGGC GGTAAAAAAG
1001 TAGAACTTAA CCCGACCAA TGGGATTGGG TAAAAATAC CGGTATATAA
1051 ACACCTGCTG TTCGCACCAT GCATACTTG GATGGGAAA TGGCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA

```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

a238.pep (partial)

```

1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPPGGKYHL
51 FGNARGSVKN RVYAVQTFDA TAVGPILPIT HERTGFEGII GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS
151 DYPPPGGARD IYSYVKGTS TKTKSNIVPR APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDIRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQOTLQGIN HLGNSPEAQ LAAATALQDS AFAVKDGIN
301 ARQWADAHPN ITATAQTALA VAEAAATVWG GKKVELNPTK WDWVKNTRYK
351 TPAVRTMHTL DGEMAGGNRP PKSITSNSKA DASTQ

```

m238/a238 91.9% identity in 385 aa overlap

	10	20	30	40	50	60
m238.pep	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYEPPGGKYHL	FGNARGSVKK
a238	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYEPPGGKYHL	FGNARGSVKN
	70	80	90	100	110	120
m238.pep	RVYAVQTFDA	TAVSPVLPIT	HERTGFEGV	IGYETHFSGH	GEVHSPFDN	HDSKSTSDFSG
a238	RVYAVQTFDA	TAVGPILPIT	HERTGFEGV	IGYETHFSGH	GEVHSPFDN	HDSKSTSDFSG
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYVKGTS	TKTKTNIVPQ
a238	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYVKGTS	TKTKSNIVPR
	190	200	210	220	230	240
m238.pep	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDVRGIV	QGAVNPFLMG
a238	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDIRGIV	QGAVNPFLMG
	250	260	270	280	290	300
m238.pep	FQGVGIGAIT	DSAVSPVTD	TAAQOTLQGI	NDLGKLSPEAQ	LAAASLLQDS	AFAVKDGIN

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a238      |||||  

          FQGVGIGAITDSAVSPVTDTAQQTLQGINHLGNLSPEAQLAAATALQD$SAFAVKDGINS  

           250       260       270       280       290       300  

m238.pep   310       320       330       340       350       360  

          AKQWADAHPNITATAQTALSAAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARMHQT  

          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  

a238      ARQWADAHPNITATAQTALAVAEAAATTWGGKKVELNPTKWDWVKNTGYKTPAVRTMHTL  

           310       320       330       340       350       360  

m238.pep   370       380       390       400       410       419  

          DGEMAGGNPKPIKSLP-NSAAEKRKQNFEFNSNWSSASFDSVHKLTLPNAPGILSPDKVK  

          |||||:|:||:|:|:|:|:  

a238      DGEMAGGNRPPKSITSNSKADASTQ

```

g239.seq

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

g239.ppt

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

m239.seq

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

m239.pep

```

1 MLHHKGXARN RXMEVLFFCR RPDRFVVRQT RLLQPHLR II LLQGDFLFFR
51 LIQSCEIEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPT IFRGSSGKSA SLTAAQGRGR
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
201 MRTANKVRVA GSCPRSRVRT FCATICASLR VVSIIGLSARC ATMARAIRRL
251 NRSSP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 239 shows 93.7% identity over a 255 aa overlap with a predicted ORF (ORF 239.ng) from *N. gonorrhoeae*:

m239/g239

	10	20	30	40	50	60
m239.pep	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLR I ILLQGDFLFRL LIQSCEIEPV					
	:					
g239	MFHHKGIARNRMEVLFFCRRPDRFVIQTRLLQPHLR I ILLQGDFLFRL LVQSCEIEPV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m239.pep	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRK TALLALGLAAIS					
g239	LVLLHHNGKSGNAHRKQOKEIRFVHCRSDVFLCYYSIGIGPAVRSATRK TALLALGLAAIS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m239.pep	ASPGFNALPTIFRGSSGKSASLTAAQGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
g239	ASPGFNALPTIFRGSSGKSASLTAAQLGRGSCCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m239.pep	RRHMTGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIIGLSARC					
g239	RRHMTGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIIGLSARC					
	190	200	210	220	230	240
	250					
m239.pep	ATMARAIRRLNRSSPX					
	:					
g239	ATMARTIWRRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 897>:

a239.seq

```

1 ATGCTCCACC ATAAAGGTAT TGCCCGAAAC CGGCGGATGG AGGTTTTGTT
51 TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCTT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAGT TGAGCCTGTA CTGGTTTTGC TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTCACCCG GCTTTAATGC CCTGCCCGCG ATTTTCAGGG
401 GCGGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCCAGCG CGGCAGGGGC
451 GCGTGTTCGC AATATTTTTT GACAACTGC TTCACAATGC GGTCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CCTACTTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGATTG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGGACG TTTTGTGCCA CGATCTGCGC CAGCTTGCGG GTTGATCGA
701 TTGGACTTTC CGCCGTTGCG GCAACAATGG CGCGCGCAAT CTGGCGGCTA
751 AACCGCTCTT CACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
1  MLHHKGIARN RRMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFLFFR
51  LIQSCEVEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKTAL LALGLAAIS ASPGFNALPA IFRGGSGKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIWRL
251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

	10	20	30	40	50	60
m239.pep	MLHHK	GXARNR	XMEVLFF	CRRPDR	FVVRQT	RLLQPHLRRI
a239	MLHHK	GIARNR	RRMEVLFF	CRRPDR	FVVRQT	RLLQPHLRRI
	10	20	30	40	50	60
	70	80	90	100	110	120
m239.pep	LVLLH	HNGKSG	NAHRKQ	OKEIQF	VHCHSD	VFLCDCSG
a239	LVLLH	HNGKSG	NAHRKQ	OKEIQF	VHCHSD	VFLCDCSG
	70	80	90	100	110	120
	130	140	150	160	170	180
m239.pep	ASPGF	NALPTI	FRGSSG	KSASLT	AAQRGR	GACCEY
a239	ASPGF	NALPAI	FRGSSG	KSASLT	AAQRGR	GACCEY
	130	140	150	160	170	180
	190	200	210	220	230	240
m239.pep	RRHMT	CGNTA	PTSSSS	RLIKM	RTAWK	VRVAGS
a239	RRHMT	CGNTA	PTSSSS	RLIKM	RTAWK	VRVAGS
	190	200	210	220	230	240
	250					
m239.pep	ATMAR	AIIRLN	NRSSPX			
a239	ATMAR	AIWRLN	NRSSPX			
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
1  atgatagaag tcatacattt cttcggcgcc gaaacgcgca gacagtttgc
51  ttgtgccgac gttggacgat ttctgcataa tgccgcgcac atccaaagag
101 gggtaaacat gggatcatc gcgcacggga gacggtccga tttataagg
151 ctgcgtattc agcgcgttcg tcaaatcggg ttgcccgcga tccaatgcct
201 tcgcaatcac gaacggtttg attgccgaac caggttcgat catatcggtt
251 acggcacggt tgcgcgcgtg ttcgctgtct gcccgcccg gtctgttggg
301 atcgtaggcg ggcgtattgg ccaaggcgag gatttcccc gtgcgggcat
351 ccaaaaccac caccgttcg gcttttgct gatggtatc gaccgccttg
401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
451 gatgtctttg ccggttttgc gtgctttatt gcgcggggag tccaagctgt
501 ccacaatatt gccctgcggg tcccgcaaaa caacttcgc gccgtcttcg
551 ccatacaggc tgtcttcaag cgaaagtcc aaaccttct gacctttgcc
601 gtcaatatcg gtaaatccga tgacgtgtgc aaacaggtt cccatcggtt
651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
1  MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
51  LRIQPFVQIG FARIQCLRNH ERFDCRTRFD HIGYGTVAPL FAVCPAGSVG
101 IVGGRIGQGE DFPRAGIQNH HRSGLMVF DRLVQLFIGQ GLNPLIEGKD
151 DVFAVLRCFI ARGVQAVHNI ALPVPQNNFR AVFAIQAVFK RKFQTFITFA
```

550

201 VNIGKSDDVC KQVAHRVMAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 901>:

m240.seq

```

1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATGCC CTGCCGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCC ATCGGGTAAT
651 GGCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 902; ORF 240>:

m240.pep

```

1 MIEVIHFFGT ETRRQFACAD VGRFLHDAH IQRGVNMGIA HGRRSDFIRL
51 RIQPFVQIGF ARIQCLRNHK RFD CRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIQGQED FPRAGIQXHH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFXA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTFLTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

m240/g240

	10	20	30	40	50	59
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAHIQRGVNMGIAHGRRSDFIRLRIQPFVQIG					
g240	MIEVIHFFGAETRRQFACADVGRFLHNAHIQRGVNMGIIAHGRRSDFIRLRIQPFVQIG					
	10	20	30	40	50	60
m240.pep	60	70	80	90	100	119
	FARIQCLRNHKKRFD CRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIQGQEDFPRAGIQXH					
g240	FARIQCLRNHERFD CRTGFDHIGYGTVAPLFAVCPAGSVGIVGGRIQGQEDFPRAGIQNH					
	70	80	90	100	110	120
m240.pep	120	130	140	150	160	179
	HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFR					
g240	HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVLRFCFIARGVQAVHNIALPVPQNNFR					
	130	140	150	160	170	180
m240.pep	180	190	200	210	220	
	AVFAMQAVFKRKQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
g240	AVFAIQAVFKRKQTFLTFAVNIGKSDDVCKQVAHRVMAF					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 903>:

a240.seq

```

1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG

```

551

```

251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 AAACCACCAC CGTCCGGCT TTTGCCTGAT GGTATTGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
1 MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRSDFIRL
51 RIQPFVQIGF ARIQCLRNHK RFD CRTGFDH IGYGTVA PLF AVCPAGVGI
101 VGGRIGQGED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFIA RGVQAVHNIA LPVPQNDFRA VFAMQAVEFKR KFQTFLTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

	10	20	30	40	50	60
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAHIQRGVNMGIAHGRSDFIRLRIQPFVQIGF					
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAHIQRGVNMGIAHGRSDFIRLRIQPFVQIGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m240.pep	ARIQCLRNHKRFDCRTGFDHIGYGTVA PLF AVCPAGVGI VGGRIGQGED FPRAGIQXHH					
a240	ARIQCLRNHKRFDCRTGFDHIGYGTVA PLF AVCPAGVGI VGGRIGQGED FPRAGIQNH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFKARGVQAVHNIALPVPQNDFRA					
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFARGVQAVHNIALPVPQNDFRA					
	130	140	150	160	170	180
	190	200	210	220		
m240.pep	VFAMQAVEFKRKFTFLTFAVNIGKSDDVCKQVAHRVMAFX					
a240	VFAMQAVEFKRKFTFLTFAVNIGKSDDVCKQVAHRVMAFX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 AACCACCAC CGTCCGGCT TTTGCCTGAT GGTATTGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
1 MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS

```

552

```

51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCDL IGCIAHAFNR SFKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

m241.seq (partial)

```

1  ..CGGCAATCAG TGGTGGTGAT GACCGTGCGG GCCGTGGACA TGACCGTGTG
51  CGATTTCTC ATCGGATGCA TCGCGCACGC TTTCAACTGT AGCCTTAAAG
101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151 GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201 CGTCGGCTTC AAACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251 GCATCTTCGA TACGGACCAA CTCCGGATCC TGCTCGCCGA ACGCATCGTC
301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGAACG
351 CCTCTTCAC CAAAGGGAAA ATGCCGTCGT AACCGCCGTG CAGATACGCA
401 ATCGGTTCTT CGGTTTGTG CAAAAGCTGA TTGTGGCAT CATACTCTC
451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGTCTTT
501 CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

m241.pep (partial)

```

1  ..RQSVVMTVR AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVVHRLA
51  VGNIGYTIDD NIAGFRIVGF KKHADFDNR EHARIFDQD LRILLAERIV
101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

m241/g241

m241.pep				10	20	30
				RQSVVMTVR	AVDMTVCDL	IGCIAHAFNC
g241						
	70	80	90	100	110	120
m241.pep		40	50	60	70	80
		SLKADFHACQ	RMVAVVHRLA	VGNIGYTIDD	NIAGFRIVGF	KKHADFDNR
g241						
	130	140	150	160	170	180
m241.pep		100	110	120	130	140
		LRILLAERIV	GRQRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFV
g241						
	190	200	210	220	230	240
m241.pep		160	170			
		IMQRNHGIFH	DSHICPFRNS	RLITGAFX		
g241						
	250	260				
		IMQRNHGIFC	NSHICPFRNS	RLITGAFX		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

a241.seq

```

1  ATGCCAACAC GTCCAACTCG CGCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCACG GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC

```



```

251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 910; ORF 241.a>:

```

a241.pep
1  MPTRPTRA AK HTPPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRRENPHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPS C RQSVVVM TVR
101 TVDMTVCD FL IGCIHTFNR SLKADFHACQ RMVAVHRLT VGNIGYTID D
151 NIAGFRIVGF KHHADFDFNR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241/a241 96.0% identity in 177 aa overlap

```

m241.pep                                10      20      30
                                RQSVVVM TVRAVDM TVCD FLIGCIAHAFNC
a241                                |||||:|||||:|||||:|||||:
0PTYYLLHPSNKMPSEMEQTLFRRHQIPPSCRQSVVVM TVRTVDM TVCD FLIGCIAHTFNR
70      80      90      100     110     120

m241.pep                                40      50      60      70      80      90
SLKADFHACQRMVAVHRLAVGNIGYTID DNIAGFRIVGFKHHADFDFNREHARIFD TDQ
a241                                |||||:|||||:|||||:|||||:|||||:
SLKADFHACQRMVAVHRLTVGNIGYTID DNIAGFRIVGFKHHADFDFNREHARIFNTDQ
130     140     150     160     170     180

m241.pep                                100     110     120     130     140     150
LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
a241                                |||||:|||||:|||||:|||||:|||||:
LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
190     200     210     220     230     240

m241.pep                                160     170
IMQRNHGIFHDSHICPFRNSRLITGAFX
a241                                |||||:|||||:|||||:|||||:
IMQRNHGILHDSHICPFRNSRLITGAFX
250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 911>:

```

g241-1.seq
1  ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTT GCCCGCATCC AATGCCTTCC
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGCGGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCCGGCT TTTGCCTGAT GGTATTCGAC CGCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTTAKTCCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTCCGGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GGC GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

g241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCDL IGCIAHAFNR SFKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFEDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

m241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCTGCAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCCG GCAAAATCA
151 GCGAACCGAC GGGAAAATTC TCATAATGCC CAACCGCAT ACCTTCTCCA
201 TCCATCAAAAC AAAATGCCGT CTGAAACGGA ACAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 GCGGTGGACA TGACCGGTG CGATTTCCTC ATCGGATGCA TCGCGCACGC
351 TTTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCGA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACC GCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACATCTC ATAATGCAGC GAAACCACGG AATTTTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

m241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVMTVR
101 AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVGF KHADFDLDFNR EHARIFDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFH
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTTWLQTAYCPRPYPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPYPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pep	70	80	90	100	110	120
g241	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSQSVVMTVRVAVDMTVCDLIGCIAHAFNC					
	70	80	90	100	110	120
m241-1.pep	130	140	150	160	170	180
g241	SLKADFHACQRMVAVHHRLAVGNIGYTIDDNIAGFRIVGFKHADFDNREHARIFDQ					
	130	140	150	160	170	180
m241-1.pep	190	200	210	220	230	240
g241	SFKADFHACQRMVAVHHRLAVGNIGYTIDDNIAGFRIVRFKHHTDLDLDFNRERARIFDQ					
	190	200	210	220	230	240
m241-1.pep	250	260				
g241	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
	250	260				
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

a241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```

555

```

101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCCG GGC AAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTCCTC TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACATCTC ATAATGCAGC GAAACACGG AATTCTTAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1 MPTRPTRAAK HPTPTWLQT AYCPRPYR PSVQTHPHE PASSTCAAKS
51 ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSC RQSVVMTVR
101 TVDMTVCDFL IGCIAHTFNR SLKADFHACQ RMVAVHHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADDFNR EHARIFNTDQ LRILLAERIV GRKRHDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFGEV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

```

          10      20      30      40      50      60
m241-1.pep MPTRPTRAANPPTPTWLQTAYCPRPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a241        MPTRPTRAAKHPTPTWLQTAYCPRPYRPPSVQTHPHEPASSTCAAKSANRRENFHNA
          10      20      30      40      50      60

          70      80      90      100     110     120
m241-1.pep QPTYLLHPSNKMPSETEQLFRRHQIPPSCRQSVVMTVRVDMTVCDFLIGCIAHAFNC
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a241        QPTYLLHPSNKMPSEMEQLFRRHQIPPSCRQSVVMTVRTVDMTVCDFLIGCIAHTFNR
          70      80      90      100     110     120

          130     140     150     160     170     180
m241-1.pep SLKADFHACQRMVAVHHRLAVGNIGYTIDDNIAGFRIVGFKHHADDFNREHARIFDTDQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a241        SLKADFHACQRMVAVHHRLTVGNIGYTIDDNIAGFRIVGFKHHADDFNREHARIFNTDQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m241-1.pep LRILLAERIVGRQRHDRIA GILTVQRLFHQRENAVVTAVQIRNRFGEVQKLIVGIIHL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a241        LRILLAERIVGRKRHDRIA GILTVQRLFHQRENAVVTAVQIRNRFGEVQKLIVGIIHL
          190     200     210     220     230     240

          250     260
m241-1.pep IMQRNHGIFHDSHICPFRNSRLITGAFX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a241        IMQRNHGILHDSHICPFRNSRLITGAFX
          250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1 atgatcggcg aacttggtgt tttgttcgtg atcgagcact tcaagcaacg
51 cgctggcggg atcgccccga aagtcgctgc ccaatttgc gatttcgtcg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccg cggatttcgc
201 tttcgtcgcg cacgccgccc aaggccatac ggacataatt ccgccccgtt
251 gctttggcga tggattcgcc caaagagggt ttgccacgc ccggaggggc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt tttggacgg
351 cgaggtattc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcatccagca ccagtcggc tttggcgatg tctttgctga cgcgggattt
451 tttctccac ggcagtcgga gcagggtgtc gatgtagttg cgtacgacgg

```

556

```

501 tggattcggc agacatcggc ggcattcat ttagtttttt cagttcggac
551 aggcattttt cttccgcttc tttggtcata cccgcctttt tgatgcctgc
601 ctccaaggca tccagttcgc cgttttcgtc ttcttcgccc aattctttgt
651 gtatcgcttt aatctgttcg ttcagataat attcgcgttg ggatttttcc
701 atttggcgtt tgacgcgtcc gcgtatgcgt ttttcggcct gcataatgtc
751 gagttcggat tccagctttg ccagcaggaa ttccatccgt ttgccgattt
801 cgggaatctc caaaatctgt tggcgttcgc ccagtttcaa ctgcaaatgc
851 gctgcgaccg tatcggttag

```

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

```

g242.pep
1 MIGELVVLFV IEHFKQRAGG IAPKVAAQFV DFVEQEQRVS YACFCHILQN
51 LAGHRADIGT AVPADFAFVA HAAQGHDTIF PPRCFDGF A QRGFAHARRA
101 DQTQNRTEFEL VHTFLDGEVF QNPFFDFFQA VVVGIOHQSG FGDVFADAGF
151 FLPRQSEQGV DVVAYDGGFG RHRRHHFEFF QFGQAFFFRF FGHTRLFDAC
201 LQGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNH
251 EFGFQLCQOE FHPFADFGNL QNLLALRQFQ LQMRCDRIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

```

m242.seq
1 ATGATCGGCA AACTTGTTGT TTTGTTCCGGG ATCGAGCACT TCGAGCAACG
51 CGCTGGCGGG ATCGCCTCGG AAGTCGTTAC CCAATTTGTC GATTTTCGTCG
101 AGCAGGAACA AGGGGTTTTT CACGCCGGCT TTTGCCATAT TCTGCAAAAT
151 CTTACCGGGC ATAGAGCCGA TATAGGTGCG GCGGTGTCCC CTGATTTTCGC
201 TTTTCGTCGC CACGCCGCCC AAAGCCATGC GGACATATTT CCGCCCCGTT
251 GCTTTGGCGA TGGATTCCGC CAAAGAGGTT TTGCCACGC CCGGAGGGCC
301 GACCAGGCAC AGAATCGGGC CTTTGAGTTT GTCCATACGT TTTTGGACGG
351 CGAGGTATTC CAAAATCCGT TCTTTGACTT TTTCCAGGCC GTAGTGGTCG
401 GCATCCAGCA CCAGTCCGGC TTTGGCGATG TCTTTGCTGA CGCGGGATT
451 TTTCTTCCAC GGCAGCTCGA GCAAAGTGTC GATGTAGTTG CGTACGACGG
501 TGGATTCCGC AGACATCGGT GGCATCATTT TGAGCTTTTT CAGTTCGGAC
551 AGGCATTTTT CTTCGCTTC TTTGGTCATA CCCGCCTTTT TGATATCTGC
601 TTCCAAGGCA TCCAGTTCGC CGTTTTCGTC TTCTTCGCCC AGTCTTTTGT
651 GTATCGCTTT AATCTGTTTC TTCAGATAAT ATTCGCGCTG GGATTTTTC
701 ATTTGGCGTT TGACGCGTCC GCGTATGCGT TTTTCGGCCT GCATAATGTC
751 GAGTTCGGAT TCCAGCTGTG CCAGCAGGAA TTCCATCCGT TTGCCGATT
801 CGGGAATTC CAAAATCTGT TGGCGTTGCG CCAGTTTCAA CTGCAAATGC
851 GCTGCGACCG TATCGGTTAG

```

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

```

m242.pep
1 MIGKLVVLFV IEHFQQRAGG IASEVVTQFV DFVEQEQQVF HAGFCHILQN
51 LTGHRADIGA AVSPDFAFVA HAAQSHADIF PPRCFDGF A QRGFAHARRA
101 DQAQNRFAEF VHTFLDGEVF QNPFFDFFQA VVVGIOHQSG FGDVFADAGF
151 FLPRQLEQSV DVVAYDGGFR RHRWHHFEFF QFGQAFFFRF FGHTRLFDIC
201 FOGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNH
251 EFGFQLCQOE FHPFADFGNF QNLLALRQFQ LQMRCDRIG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

m242/g24290.3% identity in 289 aa overlap

	10	20	30	40	50	60
m242.pep	MIGKLVVLFVIEHFQQRAGGIASEVVTQFVDFVEQEQQVFHAGFCHILQNLTGHRADIGA					
	: : : : : : :					
g242	MIGELVVLFVIEHFKQRAGGIAPKVAAQFVDFVEQEQRVS YACFCHILQNL LAGHRADIGT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGF A QRGFAHARRADQAQNRFAEFVHTFLDGEVF					
	: : : : : : : : : : :					
g242	AVPADFAFVAHAAQGHDTIFPPRCFGDGF A QRGFAHARRADQTQNRTEFELVHTFLDGEVF					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m242 . pep	QNPFDFDFFQAVVVGIIHQSGFGDVFADAGFFLPRQLEQSVDDVVAYDGGFRRHRWHHFELF					
g242	QNPFDFDFFQAVVVGIIHQSGFGDVFADAGFFLPRQSEQGVDDVVAYDGGFRRHRWHHFELF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m242 . pep	QFGQAFFFRFFGHTRLFDCIQGIIQFAVFVFFAQFFVYRNFVQIIIFALGFFHLAFDAS					
g242	QFGQAFFFRFFGHTRLFDCIQGIIQFAVFVFFAQFFVYRNFVQIIIFALGFFHLAFDAS					
	190	200	210	220	230	240
	250	260	270	280	290	
m242 . pep	AYAFFGLHNVEFGFQLCQQEFHPPFADFGNLFQNLALRQFQLQMRCDRIGX					
g242	AYAFFGLHNVEFGFQLCQQEFHPPFADFGNLFQNLALRQFQLQMRCDRIGX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 921>:

a242 . seq

1	ATGATCGGCG	AACTTGTGT	TTTGCTCGGG	ATCAAGCACT	TCGAGCAACG
51	CGCTGGCGGG	ATCGCCCCGG	AAGTCGCTAN	CCAATTTGTC	GATTTCGTCG
101	AGCAGGAACA	ATGGGTTTTT	TACGCCGGCT	TTTGCCATAT	TCTGCAAAAT
151	CTTACCGGGC	ATGGAGCCGA	TATAGGTGCG	GCGGTGTCCC	CGGATTTTCG
201	TTTCGTGCGC	CACGCCGCC	AAAGCCATGC	GGACATATTT	CCGCCCCGTT
251	GCTTTGGCGA	TGGATTCGCC	CAAAGAGGTT	TTGCCACGC	CTGGAGGGCC
301	GACCAGGCAC	AGAATCGGGC	CTTTGAGTTT	GTCCATACGT	TTTGGACGG
351	CGAGGTATTC	CAAATCCCGT	TCTTTGACTT	TTTCCAGGCC	GATGTGGTCG
401	GTATCCAGCA	CCAATCCGGC	TTTGGCGATG	TCTTTGCTGA	CGCGGGATT
451	TTTCTTCCAC	GGCAGTTTCA	GCAGGTGTC	GATGTAGTTG	CGTACGACGG
501	TGGATTCGGC	AGACATCGGC	GGCATCATTT	TGAGCTTTT	CAGTTCGGAC
551	AGGCATTTT	CTTCCGCTTC	TTTGGTCATA	CCCGCCTTT	TGATATCTGC
601	TTCCAAGGCA	TCCAGTTCGC	CGTTTTCGTC	TTCTTCGCCC	AGTCTTTTGT
651	GTATCGCTTT	AATCTGTTCG	TTCAGATAAT	ATTCGCGCTG	GGATTTTTC
701	ATTTGGCGTT	TGACGCGTCC	GCGTATGCGT	TTTTCGGCCT	GCATAATGTC
751	GAGTTCGGAT	TCCAGCTGTG	CCAGCAGGAA	TTCCATCCGT	TGCCCATT
801	CGGGAATTT	CAAAATCTGT	TGGCGTTGCG	CCAGTTTCAA	CTGCAATGC
851	GCTGCGACCG	TATCGGTTAG			

This corresponds to the amino acid sequence <SEQ ID 922; ORF 242.a>:

a242 . pep

1	MIGELVLLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQWVF	YAGFCHILQN
51	LTGHGADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFDGF	QRFHAWRA
101	DQQRNRAFEF	VHTFLDGEVF	QNPFDFDFFQ	VVVGIIHQSG	FGDVFADAGF
151	FLPRQFEQGV	DVVAYDGGFG	RHRRHHELF	QFGQAFFFRF	FGHTRLFDC
201	FGIIQFAFV	FFAQFFVYR	NLFVQIIIFAL	GFFHLAFDAS	AYAFFGLHN
251	EFQFQLCQQE	FHPFADFGNF	QNLALRQFQ	LQMRCDRIG*	

m242/a242 95.2% identity in 289 aa overlap

	10	20	30	40	50	60
m242 . pep	MIGKLVVLFGLIEHFEQRAGGIASEVVTFQVDFVEQEQQGVFHAGFCHILQNLTGHRADIGA					
a242	MIGELVLLGLIKHFEQRAGGIAPEVAXQFVDFVEQEQQWVFYAGFCHILQNLTGHGADIGA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242 . pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGFQRFHARRADQAQNRFAEFVHTFLDGEVF					
a242	AVSPDFAFVAHAAQSHADIFPPRCFGDGFQRFHAWRADQAQNRFAEFVHTFLDGEVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m242 . pep	QNPFDFDFFQAVVVGIIHQSGFGDVFADAGFFLPRQLEQSVDDVVAYDGGFRRHRWHHFELF					

g243.seq

```
1 ATGGTaatcg tctGGTTGcC cgAGTTaccg CCGATGCCGG CGACGATGGG
51 CATCAGCGCG GCGAGTGCGA CGATTTTTC gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGGCGGTGC AGAGGTGAC GGCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCCAACA GGTCTTCCTC
201 TTCCTGCAAA CACTGCCATGT TCAACATATC CGGTCGGAAT TCTTCGCGGA
251 TCAGCTCCAC CATCTCGTCG ATGGTAATCc tgCCGATGAG CTTTTTGTTT
301 TCATCAACGA CGGGCGCGGT AACCAAGTCG TAG
```

g243.pgp
1 MVIWLPPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51 IQFLTESKT GANRSSSSCK PAMFNISASD SSRTSTISS MVILPMSFLF
101 SSTTGAVTKS *

```
m243.seq
1 ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51 CATCAGCGCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGCGGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGyGGT TTTTCACCGA ATCCCACACG GGGGCGAAyA GGTCTTCCTC
201 TTCCTGCAAA CCCGCCATAT TCAGCATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTTGTTT
301 TCACGACGCA CGGGCGCGGT AACCAAGTCG TAG
```

```
m243.ppe
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51 IQXFFTESHT GANRSSSSCK PAIFSISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *
```

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m243.pep	MVIVWLP	ELPPMPATMGIS	SAXSATIFSML	PSNAPITRL	LARKAVQRLT	ASHIQXFFT
g243	MVIVWLP	ELPPMPATMGIS	AASATIFSIL	PSNAPMTRL	LARKAVQRLT	ASHIQRFL
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANR	SSSSCKPAIF	SISADSSRIT	STISSMVIL	PMSFLF	SSTTGAVTKSX
q243	GANR	SSSSCKPAMF	NISADSSRIT	STISSMVIL	PMSFLF	SSTTGAVTKSX

70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTC GATGCTGCC TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAA CCCGCCATAT TCAACATATC CGCTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCGTCA ACGGTCACCC TGCCGATGAG CTTTTGTTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPMSEFLF
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANKSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSTVTLPMSEFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1  atgccgcttg aagcccggcc ggccgggttca gacggcattg ccgctttact
51  tcgatcggtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcacgccttg atggatattc
251 ggatcgagct tatcgccgcg tttaggattg atttccttga tttgctggc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcacgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acattttcac ggcaaacttc tgtccggcga acttggtcgt
451 atcggcaatt tctgctggtt ggccggcgcg caggttttgc tegtgtgcca
501 aagcgcgcag ttgttctgct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggtcggcg gcagcctgtt cctgtacacc
601 gtccgcattt cctactgtct cgacggtttc caccgcctcc acattttcaa
651 ccgcttcttc actgttttgc tgctgtgtct gttcgctcat atogtatccc
701 tcaaaacaaa ttggaaatca aaatccggtt attacccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgccgcc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1  MPPEARPAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LPCHRNHRA
51  QHTVGGITL LHHTNHGIGF LLTGHLRLHRL MDIRIELIAR FRIDFLDLRG
101 IKRLLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRLQILIS RLGGSFLFLYT
201 VRISYCLDGF HLRHIFNRFF TVLLLCFLFAH IVSLKTNWKS KSGYYPKIR
251 TFSRNFQKQK EISHPPNTL PQPKYK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

m244.seq

560

```

1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCTT CTTTCATACA CCCACCACGG
201 TATTCGGCTC CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGGTTG ATTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAACCTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TyCTGCTGGT GCGGGCGGCG CAGGTTTTGC TCGTTTGCCA
501 AAGCGCGCTG CTCGTCTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAAATCCT CATAAGCCGG CTCTGCGGCA GCCTGTTTCT GCACACCGTC
601 CGCATTTTCT ACTGTTTCGA CGGTTTCCAC CGCTCCACA TTTTCAACCG
651 CTTCTTCACT GTTTTGCTGC TGTGTCTGTT CGCTCATATC GTATCCCTTA
701 AAACAAATTG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGGACA
751 TTTTCAAGAA ACTTCAAKCA AAACAGAGA ATTTCAAATT CATTTTCAAA
801 TCCCTACCG AAAAAATAAT ATAGACGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 932; ORF 244>:

```

m244.pep
1  MPSEARQAGS DGIAALLRSV YTONALQBIN QIIPQTPSGF LLRHRNHSRA
51  QHAVGORITL LHHTHHGIRL LFACHRLHRL MDIRIELIAR FRVDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAL LVFQLRFQLG NPRLQILISR LCGSLFLHTV
201 RISYCFDGFH RLHIFNRFET VLLCLFAHI VSLKTNWKS SYYPRKIRT
251 FSRNFXQQR ISNSFSNPLP KXYRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 244 shows 86.3% identity over a 277 aa overlap with a predicted ORF (ORF 244.ng) from *N. gonorrhoeae*:

M244/G244

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTONALQBINQIIPQTPSGFLLRHRNHSRAQHAVGORITL					
g244	MPPEARPAGSDGIAALLRSVYTONALQBINQIIPQTPSGFLPCHRNHSRAQHTVGGGITL					
	10	20	30	40	50	60
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244.pep	IAALIQKRHFQIILDRQHFHKGKLLSGELVRIRNFLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQKRHFQIILDRQHFHKGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVQLRFQL					
	130	140	150	160	170	180
m244.pep	IAALIQKRHFQIILDRQHFHKGKLLSGELVRIRNFLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQKRHFQIILDRQHFHKGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVQLRFQL					
	130	140	150	160	170	180
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFETVLLCLFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSLFLYTIVRISYCLDGFHRLHIFNRFETVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFETVLLCLFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSLFLYTIVRISYCLDGFHRLHIFNRFETVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244.pep	KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKXYRRX					
g244	KSGYYPSKIRTFSRNFKQQRQEISHPPNTLPQKPYKRX					
	250	260	270			
m244.pep	KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKXYRRX					
g244	KSGYYPSKIRTFSRNFKQQRQEISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCTT CTTCATCAGC CCCACCACGG
201 TATTGGGTTT CTGTTGCTT GCCACCGCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATT CTACTGTCT CGACGGTTC CACCGCTCC ACATTTTCAA
651 CCGCTTCTC ACTGTTTTC TGCTGTGCT GTTCGCTCAT ATCGTATCCC
701 TTAAACAAA TTGGAAATCA AAATCCAGT ATTACCCGC CAAGATAAGG
751 ACATTTTCAA GAACTTCAA GCAAAGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAT AATATAGAC GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1  MPSEARQAGS DGIAALLRSV YTONALQEI QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAFORIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAQ LLVFQLRFL GNPRQLILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

m244.pep	10	20	30	40	50	60
a244	10	20	30	40	50	60
m244.pep	70	80	90	100	110	120
a244	70	80	90	100	110	120
m244.pep	130	140	150	160	170	179
a244	130	140	150	160	170	180
m244.pep	180	190	200	210	220	239
a244	190	200	210	220	230	240
m244.pep	240	250	260	270		
a244	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1  atgccgcctg aagcccgcc gccgggttca gacggcattg ccgctttact
```

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```

51  tgcgacgggt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccggggc
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcacgcctg atggatattc
251 ggatcgagct taccgcccgc tttaggattg atttcctga ttgctgggc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcatcgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acatttcacac ggcaaaacttc tgcggcgca acttgctgct
451 atcgcgcaatt tctgctgggt ggcgggcgcg caggttttgc tcgtttgcca
501 aagcggcgag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctgtt cctgtacacc
601 gtccgcattt cctactgtct cgacgggttc caccgcctcc acattttcaa
651 ccgcttcttc actggtttgc tgcgtgtct gtctgctcat atcgatccc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccggag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgcgcgc
801 gaatacccta ccgcaaaaac catataaacg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

g244-1.pep

```

1  MPPEARPAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LPCHRNHSRA
51  QHTVQGQITL LHHTNHGIGF LLTGHRHLRL MDIRIELIAR FRIDFLDLRG
101 IKRLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFF GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFFVQLRFQL GNPRLQILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSGYYPKIR
251 TFSRNFKQRQ EISHPPNTL PQKPYKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

m244-1.seq

```

1  ATGCCGTCTG AAGCCCGACA GCGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCT CTTTCATACA CCCACCACGG
201 TATTCGGCTC CTGTTGCTT GCCACGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGGTTG ATTTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACCTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TyCTGCTGGT GCGCGCGCGC CAGGTTTTGC TCGTTTGCCA
501 AAGCGCGCTG CTCGTCTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAAAATCCT CATAAGCCGG CTCTGCGGCA GCCTGTTCTT GCACACCGTC
601 CGCATTTCTT ACTGTTTCGA CGGTTTCCAC CGCTCCACA TTTTCAACCG
651 CTTCTTCACT GTTTTGCTGC TGTGTCGTT CGCTCATATC GTATCCCTTA
701 AAACAAATTG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGGACA
751 TTTTCAAGAA ACTTCAAKCA AAACAGAGA ATTTCAAATT CATTTTCAAA
801 TCCCTACCG AAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

m244-1.pep

```

1  MPSEARQAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LLRHRNHSRA
51  QHAVGQRIITL LHHTNHGIRL LFACHRLHRL MDIRIELIAR FRVDFDLRS
101 IKCFQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFF GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAL LVFQLRFQLG NPLQILIS LCGSLFLHTV
201 RISYCFDGFH RLHIFNRFFT VLLCLFAHI VSLKTNWKSK SSYYPRKIRT
251 FSRNFXQXR ISNSFSNPLP KK*

```

m244-1/g244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRIITL					
g244-1	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLPCHRNHSRAQHTVQGQITL					
	10	20	30	40	50	60
m244-1.pep	LHHTNHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFQLVQSHLHAHFQRIE					
g244-1	LHHTNHGIGFLLTGHRHLRLMDIRIELIARFRIDFLDLRGIKRLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m244-1.pep	IAALIQRHFQIILDRQHFHGKLLSGELVRIRNFFLVAAAQVLLVCQSAALLVFQRLRFQL					
g244-1	ITALIQRHFQIILDRQHFHGKLLSGELVRIGNFFLVAAAQVLLVCQSAQLFVFQRLRFQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLLCFAHIVSLKTNWKS					
g244-1	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLLCFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKKX					
g244-1	KSGYYPSKIRTFSRNFKQRQEI SHPPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

```

1  ATGCCGCTCG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGGC
151 CAACACGCGG TCGGACAGCG TATAACCCTT CTTATCAGC CCCACCACGG
201 TATTGGGTTT CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTAGGATTG ATTTCCTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCAG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAACTTC TGTCGGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGCGGCGC CAGGTTTGC TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TCAACTGCG CTTCAGCTC GGCAATCCGC
551 GCCTGCAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATT CCTACTGTCT CGACGGTTTC CACGCGCTCC ACATTTTCAA
651 CCGCTTCTT ACTGTTTTC TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTAACAACAA TTGAAATCA AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCTTA CCGAAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

```

1  MPSEARQAGS DGIAALLRSV YTONALQEI QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQRHF QIILDRQHFH GKLLSGELVR
151 IRNFFLVAAA QVLLVCQSAQ LLVFQRLRFQ GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLLCFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFRQQR RISNSFSNPL PKK*

```

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTONALQEIQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244-1	MPSEARQAGSDGIAALLRSVYTONALQEIQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
a244-1	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244-1.pep	IAALIQRHFQIILDRQHFHGKLLSGELVRIRNFFLVAAAQVLLVCQSA-LLVFQRLRFQ					
a244-1	IAALIQRHFQIILDRQHFHGKLLSGELVRIRNFFLVAAAQVLLVCQSAQLLVFQRLRFQ					
	130	140	150	160	170	180
	180	190	200	210	220	239
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLLCFAHIVSLKTNWKS					
a244-1	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLLCFAHIVSLKTNWKS					
	190	200	210	220	230	240

g246.seq

1	atgtacgggc	ggaacggtag	tactcaagcg	gccgttgcc	tcgttttcga
51	ccagacacag	cgtgccggt	tcggcaacgg	cgaagtttac	gccgctcaag
101	ccgacatcgg	cagtgcgtga	aatatcgcgc	agggctttgc	gggcgaatcc
151	ggtcagttgg	tccacgtcgt	ctgtaagcgg	tggtccgagg	ttttggtgga
201	acagttcgc	gacctgttct	ttggttttat	tgattgcggg	catcacgata
251	tgggtcgggt	tttcgcctgc	catttggaag	ataaactcgc	ccaagtcgct
301	ttccaccgcc	ttaatgcctt	ttgcttcaag	ataatggttc	agctcgattt
351	cttcgctgac	catggatttg	cctttgacca	tcagcttgcc	gtttttggct
401	gtgatgatgt	cgtggataat	ttggcaggct	tcggcagggg	tttcgcgccca
451	gtgtactttc	acgccaact	tagtcagggt	ttcttccaac	tgctccagca
501	qcgcgggttaa				

g246.pep

1	MYGRNGSTQA	AVAFVFDQTO	RARFGNGEVY	AAQADIGSAV	NIAQGFAGES
51	GQLVHVCKR	CAEVLVEQFA	DLFFGFMDCG	HHDMGRFFAC	HLDDKLAQVA
101	FHRLNAFCFK	IMVQLDFAD	HGFAFDHQLA	VFGCDVVDN	LAGFGRGFRP
151	VYFHAOLSOV	FFOLLQORG*			

```
m246.seq (partial)
1 ATGCACGGGC GGTACGGTGG TACTCAAGCG ACCGTTgCTT CGTTTTCCAC
51 CAGACACAGC GTACCTGTTT CAGCAACGGC AAAGTTTACG CCACTCAAAC
101 CGACATCGGC AGTGCTGTAA ATATCGCGCA GTGCTTTACG GGCGAAGCCG
151 GTCAGTTGGT CTACATCGTC TGTCAGCGGC GTACCGAGGT TTTGGTGGAA
201 CAGTTCGCTA ACCTGTTCTT TGGTTTTGTG GATAGCAGGC ATCACGATAT
251 GGGTCGGTTT TTCGCCTGCC ATTTGGACGA TGAACTCGCG CAAGTCGCTT
301 TCTACCGCTT TAATGcyTTT TGCTTCAAGA TAATGrTTCA GCTCGATTTC
351 CTCGCCGACC ATCGATTGTC CTTTGACCAT CAGCTTGGCG TTTTTGGCTG
401 TGATGATGTC ATCGATAATT CTTGAGGCTT CGGTCTGGGGT TTCTGCCCG...
```

m246.pep (partial)

1	MHGRYGGTQA	TVAFVFHQIQ	RTCFSNGKVV	ATQTDIGSAV	NIAQCFTGEA
51	GQLVYIVCQR	RTEVLVEQFA	NLFFGFVDSR	HHDGMRFFAC	HLDDLAQVA
101	FYRFNAFCFK	IMXQDFLAD	HRFAFDHQLA	VFGCDVVDN	LAFGRGFCP...

Homology with a predicted ORF from *N. gonorrhoeae*

m246/q246

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQ	TQRTCF	SGNKVYATQTD	IGSAVNIAQCFT	GEAGQLVYIV	CQR
	:	: : :	: :	: : : : :	: : : : :	: :
g246	MYGRNGSTQA	AVAFVFDQ	TQRRARFGNG	EVYAAQADIG	SAVNIAQGF	FAGESGQLVHV
	:	: : :	: :	: : : : :	: : : : :	: :
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGF	VD	SRHHDMGRFF	ACHLDDELAQ	VAFYRFNAFC	KIMXQLD
	: :	: : :	: :	: :	: : : : :	: :
g246	CAEVLVEQFADLFFGF	MDCGHDMGRFF	ACHLD	DDKLAQVAF	HRLNAFC	KIMVQLD
	: :	: : :	: :	: :	: : : : :	: :

565

	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
g246	HGFAFDHQLAVFGCDDVVDNLAGFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246.seq (partial)

```

1 ATGCACGGGC GGAACGGTGG TACTCAAGCG ACCGTGCGCT TCGTTTTCCA
51 CCAGACACAG CGTACCTGTT TCAGCAACGG CGAAGTTCAC GCCACTCAAA
101 CCGACATCGG CAGTGTCTGTA AATATCGCGC AGTGCTTTAC GGGCGAAGCC
151 GGTCAGTTGG TCTACGTCGT CCGTTAACGG TGTGCCGAGG TTTTGGTGGA
201 ACAGTTCGCT AACCTGTTCT TTGGTTTTAT GGATTGCGGG CATCACCATA
251 TGGGTCGGTT TTTACCTGCG CATTGAGCG ATGAAGTCGC CCAAGTCGCT
301 TTCCACCGCT TTAATGCCTT TTGCTTCAAG ATAATGGTTC AGCTCGATTT
351 CCTCGCTGAC CATCGATTG CCTTTGACCA TCAGCTTGCC GTTTTGGCT
401 GTGATGATGT CGTGGATGAT TTCGCAGGCT TCGGCCGGTG TTTCCGCCCA
451 GTGTACTTTT ACGCCCAACT TGGTCAGGTT TTCTCCAGC TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246.pep (partial)

```

1 MHGRNGGTQA TVAFVEHOTQ RTCFSNGEVH ATQTDIGSAV NIAQCFTGEA
51 GQLVYVVR*R CAEVLVEQFA NLFFGFMDCG HDMGRFFTC HLDDELAQVA
101 FHRFNAFCFK IMVQLDFLAD HRFAFDHQLA VFGCDDVDD FAGFGRCFRP
151 VYFYAQLGQV FFQLLQQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQTQRTCFNSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQTQRTCFNSNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHDMGRFFTCCHLDELAQVAFHRFNAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
a246	HRFAFDHQLAVFGCDDVDDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247.seq

```

1 atgaaacgta aaatgctaaa cgtaccaaag ggcgggttatg atggtatgaa
51 ggggtttacc attgttgaat ttctggttgc gggcctgctc agtataattg
101 tcctgatagc ggtcgtatcg agttacttta catcccgga attaaatgat
151 gtggcaaacg agcgtcttgc cattcaacag gatttgcgga atgcggcaac
201 attaattgtc cgcgatgcaa gaatggcggg gagcttcggt tgtttcaata
251 tgtccgagca tactaaagac gatattgttg attcaagtaa tcaaactcaa
301 tctaaccctg caaaacccgg tgccaaacaa gaaaatcccc ttttttcctt
351 aaaaaggagc ggcattgata aacaactgat tcccggtgct gaatccatag
401 atattaaata tccgggtttt atccagcgcc ttaacgcatt ggtttttcaa
451 tacggtatcg atgatcttga tgcgagtgtc gagactgttg tagtcagcag
501 ctgttccaaa atagcaaac cgggtaagaa aatatctacc ttgcaagaag
551 caaagagtgc attacagatt actaatgatg ataaacaaaa tggaaatatc

```

```

601 acccgtcaga aacatgtggt caatgcctat gcggtcggca ggtttggcaa
651 taatgaggaa agtttgttcc gcttccaatt ggatgataag ggcaagtggg
701 gtaatcctca gttgtctcgtg aaaaagggtta aacgtatgga tgtgcggtat
751 atttatgttt ccggttgtcc tgaagatgaa gatgccggca aagaggaaaa
801 attcagatat acgaataaat tcgacaaatc caaaaatgct gttacgcctg
851 ccgggggtgga ggttttattg gatagcggcc ttaatgccaa gattgccgct
901 tcttcagaca atagtattta tgcttaccgt atcaatgcga caatacgcgg
951 gggaaatgta tgcgcaaaaca gaacactttg a

```

This corresponds to the amino acid sequence <SEQ ID 948; ORF 247.ng>:

g247.pep

```

1 MKRKMLNVPK GGYDGMKGFT IVEFLVAGLL SIIVLIAVVS SYFTSRKLND
51 VANERLAIQQ DLRNAATLIV RDARMAGSFG CFNMSEHTKD DIVDSSNQTS
101 SNLAKPGAKQ ENPLFSLKRS GMDKQLIPVA ESIDIKYPGF IQRLNALVFQ
151 YGIDDLASA ETVVSSCSK IAKPGKKIST LQEAKSALQI TNDDKQNGNI
201 TRQKHVVNAY AVGRFGNNEE SLFRFQLDDK GKWGNPQLLV KKVKRMDVRY
251 IYVSGCPEDE DAGKEEKFRY TNKFDKSKNA VTPAGVEVLL DSGLNAKIAA
301 SSDNSIYAYR INATIRGGNV CANRTL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 949>:

m247.seq (partial)

```

1 ATsAGACGTA AAATGCTAAA CGTwsyArAA GGCAGTTATG ATGGTATGAA
51 AGGTTTITACC ATTATTGAAT TTTTGGTTGC GGGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCGGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAAACG AGCGTCTTGC CGCGCAACAG GATTTCGCGA ATGCGGCAAC
201 ATTGATGTGC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTCATAA
251 TGTCCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAAT
301 TCTCCTTTT CCTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTTC AATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTGAGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AAGTTTGTTC CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAACTCTC AGTTGC...

```

This corresponds to the amino acid sequence <SEQ ID 950; ORF 247>:

m247.pep (partial)

```

1 XRRKMLNVXX GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51 AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPTTQON
101 SPFSLKRNGI DKLIPIAESS NINYQNFFQV GSALIFQYGI DDVNASTATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEESLF RFQLDDKQKW GNPQL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng) from *N. gonorrhoeae*:

m247/g247

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTIIEFLVAGLLSMIVLMAVGSSYFTSRKLND AANERLAAQQ					
	: : : : : : :					
g247	MKRKMLNVPKGGYDGMKGFTIVEFLVAGLLSIIVLIAVSSYFTSRKLNDVANERLAIQQ					
	10	20	30	40	50	60
	70	80	90	100		
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQONS PFSLKRN					
	: : : : : :					
g247	DLRNAATLIVRDARMAGSFGCFNMSEHTKDDIVDSSNQTSNLAKPGAKQENPLFSLKRS					
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	GIDK-LIPIAESSNINYQNFFQVGSALIFQYGIDVDVNASTATTVVSSCAAISKPGKQIPT					
	: : : : : : : : :					

```

g247      GMDKQLIPVAESIDIKYPGFIQRLNALVFQYGIDDLASAEYVVVSSCSKIAKPGKKIST
           130      140      150      160      170      180

m247.pap  170      180      190      200      210      220
LEDKAKELKIPDQDKQNGNIARQRHVVNAYAVGRIAD-EESLFRFQLDDKKGKGNPQL
|::||:|:|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
g247      LQEAKSALQITNDDK-QNGNITRQKHVVNAYAVGRFGNNEESLFRFQLDDKKGKGNPQLL
           190      200      210      220      230

g247      VKKVKRMDVRYIYVSGCPEDEDAGKEEKFRYTNKFDKSKNAVTPAGVEVLLDSGLNAKIA
           240      250      260      270      280      290

```

```

a247. seq
1 ATGAGACGTA AAATGCTAAA CGTACCAAAA GGCAATTATG ATGGTATGAA
51 GGGTTTTACC ATTATTGAAT TTTTGGTTGC GGGCATGCTC AGTATGATTG
101 TCCTGATGGC GGTCGGATTC AGTTACTTCA CATCCCGGAA ATTAATATGAT
151 GCGGCAAAACG AGCCTCTTTC CGCGCAACAG GATTTGGCGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCAA AGGTGGCAGG GGGCTTCGGT TGTTTCAATA
251 TGTCCGAGCA TACTAAAAAT GATATTATTG TTGATCCAAG TAAGCAAACT
301 CAACATGTCC CTGTAAAACC CGGTGCCAAA CAAGAAAATC CCCTTTTTTC
351 TTTAGAGTGG GCTAATACTA ATAATACTAA TAATAATACA GCTAAATTGA
401 TTCCTATTGC TGAATCCACA GATATTAATAT ATCCGGGTTT TGCCCAGGCT
451 CGTCCGGCAT TGATTTTCCA ATACGGCATC GATGATCTTG ATCCGAGTGC
501 TGAGACTGTT GTAGTCAGCA GCTGTCCAA AATAGCAAAA CCGGTAAGA
551 AAATATCTAC CTTGCAAGAA GCAAAGAGTG CATTACAGAT TACTAATGAT
601 GATAACAACA ATGGAATATC CACCCGTCAA AGGCATGTGG TCAATGCCTA
651 TGCGGTCGCG AGGATTGCCG GTGAGGAAGG TTGTTCGCGC TTCCAATTGG
701 ATGATAAGGG CAAGTGGGGT AATCCTCAGT TGTCTGTAAG AAAGATTAGA
751 CATATGAAAG TGCGGTATAT CTATGTTTCC GACTGTCTG AAGATGACGA
801 TGCCGGCAAA GAGGAAAAAT TCAAATATAC GGGTACATTC GACAGCTCCA
851 CAAATGCTGT TACGCCCCGC GGGGTGGAGG TTTTATTGAG TANCGGTACT
901 GATACCAAGA TTGCGCTTTC TTGACACAAT CATATTATG CTTACCGTAT
951 CGATGCGACA ATACGCGGGG GAAATGTATG CGCAAAACA ACACCTTGA

```

a247.pap

1	<u>MRRKMLNVPK</u>	<u>GNYDGMKGFT</u>	<u>IIIEFLVAGML</u>	<u>SMIVLMAVGS</u>	<u>SYFTSRKLN</u>
51	<u>AANERLSAQ</u>	<u>DLRNAATLIV</u>	<u>RDARMAGGFG</u>	<u>CFNMSEHTKN</u>	<u>DIIVDPSKQT</u>
101	<u>QHVPVKPGAK</u>	<u>QENPLESLEW</u>	<u>ANTNNTNNNT</u>	<u>AKLIPIAEST</u>	<u>DIKYPGFAQA</u>
151	<u>RPALIFQYGI</u>	<u>DDLDAEAETV</u>	<u>VVSSCSKIAK</u>	<u>PGKKISTLQE</u>	<u>AKSALQITND</u>
201	<u>DKQNGNITRQ</u>	<u>RHVVNAYAVG</u>	<u>RIAGEEGLFR</u>	<u>FQLDDKGKWG</u>	<u>NPQLLVKKIR</u>
251	<u>HMKVRYIYVS</u>	<u>DCPEDDDAGK</u>	<u>EEKFKYTGTF</u>	<u>DSSTNAVTPA</u>	<u>GVEVLLSXGT</u>
301	<u>DTKIAASSDN</u>	<u>HIYAYRIDAT</u>	<u>IRGGNVCANR</u>	<u>TL*</u>	

```

      10      20      30      40      50      60
m247.pep  XRRKMLNVXXGSYDGMKGFTTIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAANERLAAQQ
          ||||| |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a247      MRRKMLNVPKGNYDGMKGFTTIEFLVAGMLSMIVLMAVGSSYFTSRKLNDAANERLSAQQ
          10      20      30      40      50      60

      70      80      90      100
m247.pep  DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQONSPFSLK-
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a247      DLRNAATLIVRDARMAGGFGCFNMSEHTKNDIIVDPSKQTQHVVPVKPGAKQENPLFSLEW
          70      80      90      100      110      120

      110     120     130     140     150     160
m247.pep  -----RNGIDKLIPIAESSNINYQNFFQVGSALIFQYGIDVDNASTATTVVSSCAAISK
          |:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a247      ANTNTNTNNTAKLIPIAESTDIKYPGFAQARPALIFQYGIDDLDAETAETVVVSSCSKIAK
          130     140     150     160     170     180

```

```
g247-1.seq (partial) ..
1      CCCGGTGCCA AACAGAAAAA TCCCCTTTT TCCTTAAAAA GGAGCGGCAT
51     GGATAAACAA CTGATCCCG TTGCTGAATC CATAGATATT AAATATCCGG
101    GTTTTATCAA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATGAT
151    CTTGATCGGA GTGCTGAGAC TGTTGTAGTC AGCAGCTGTT CCAAATATGC
201    AAAACCGGGT AAGAAATAT CTACCTTGA CAAGACAAGG AGTGCAATTAC
251    AGATTACTAA TGATGATAAA CAAATGGAA ATATCACCCG TCAGAAAGAT
301    GTGGTCAATG CCTATCGCGT CGGAGGTTT GGCAATAATG AGGAAGAGTTT
351    GTTCGCGTTC CAATTGGATG ATAAAGCGAA GTGGGGTAAT CCTCAAGTTGC
401    TCGTGAAAAA GGTTAACGTT ATGGATGTGC GGTATATTAT TGTTCGCGGT
451    TGCTCTGAAG ATGAAGATGC CGGCAAGAGG GAAAAATTCA GATATACGAA
501    TAAATTCGAC AAATCAAAAA ATGCTGTTAC CGGCTCGCGG GTGGAGGTTT
551    TATTGGATAG CGGCCTTAAT GCCAAGATTG CCGCTTCTTC AGACAATAGT
601    ATTTATGCTT ACCGTATCAA TGCGACAATA CGCGGGGGAA ATGTATCGCG
651    AAACAGAAAC CTTTGA
```

g247-1.pap (partial) ...

1	FGAQRQETLV	SLKRSQMDKQ	LIPVAESIDI	KYPGFIQRLN	ALVFQYGIDD
51	LDASAENPVF	SSCKSIAPKG	KKISTLQEAK	SALQITNDCK	QNGNITROKH
101	VVNAYAVGRF	GNNEESLFRF	QLDDRGKWN	PQLLVKKVVR	MDVRIYVSG
151	CPEDEDAGKE	EKFRTYNKDF	KSKNAVTPAG	VEVLLDSGLN	AKIAASSDNS
201	IYAYRINATI	RGGNVCANRT	L*		

```
m247-1.seq
1   ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAGTTATG  ATGGTATGAA
51  AGGTTTACC  ATTATGAAT  TTTTGGTTGC  GGGCTGCTC  AGTATGATTG
101 TCCTGATGCG  GTCGGATCG  AGTTACTTCA  CATCCCGGAA  ATTAATGAT
151 GCGGCAACG  AGCGTCTTGC  CGCGCAACAG  GATTTCGGGA  ATCGGGCAAC
201 ATTGATTGTC  CGCGATGCGA  GAATGGCAGG  CGGCTTCGGT  TGTTTCAATA
251 TGTCCGAGCA  TCCTGCAACT  GATGTTATTC  CCGATACGAC  GCAACAAAT
301 TCTCCTTTT  CCTTAAAAAG  GAACGGTATA  GATAAACITA  TTCCATAGC
351 GGAATCTTCA  AATATCAATT  ATCAGAATT  TTTCCAGGTT  GGTAGCGCAT
401 TGATTTTTC  ATACGGAAAT  GATGATGTTA  ATCGAAGCAC  CGCGCATACC
451 GTCGTCAGCA  GCTGTGCCGC  AATATCGAAA  CCGGGCAGC  AAATCCCTAT
501 TTTAGAAAG  GCAAAAAAAG  AATGAAGAT  TCCGGATCAG  GATAAGGAGC
551 AAAATGGCAA  TATAGCCGCT  CAAAGCGATG  TGGTCAATGC  CTATCGCGTC
601 GCGAGGATTG  CCGATGAGGA  AGGTTTGTT  CGCTTCCAAT  TGGATGATAA
651 GGGCAAGTGG  GGTAACTCT  AGTTGCTCGT  GAAAAGAGTT  AGACATATGA
701 AAGTGCGGTA  TATCTATGTT  TCCGGCTGTC  CTGAAGATGA  CGATGCCCGC
751 AAAGAGGAAA  CATTCAAAT  TACGGATAAA  TTCGACAGCG  CCCAAATGCG
801 TGTTACGCC  GCCGGGGTGG  AGGTTTATT  GAGTAGCGGT  ACTGATACCA
851 AGATTGCCCG  TTCTTCAGAC  AATCATATTT  ATGCTTACCG  TATCGATGCG
901 ACAATTACCG  GGGGAAATGT  ATGCGCAAC  AGAACACTTT  GA
```

```
m247-1.pap
  1 MRRKMLNVPK GSYDGMKGFT IIEFLVAGLL SMIVLMVGS SYFTSRKLLND
51 AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIDPTTQQN
101 SPFSLKRNGI DKLPIAESS N1NYONLFQV GSALIFYOGI DDVNASTATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEEGLF RFQLDDKGKW GNPQLLVKKV RHMVRYIYV SGCPEDDDAG
251 KEETFKYTDK FDSAQNAVPT AGVEVLLSSG TDTKIAASSD NHIYAYRIDA
301 TIRGGNVCAN RTL*
```


569

m247-1 / g247-1 72.1% identity in 222 aa overlap

```

      70      80      90      100      110      120
m247-1.pep  NAATLIVRDARMAGGFGCFNMSEHPATDVIPDTTQONSFPFLKRNIGDK-LIPIAESSNI
g247-1      | : | : | | | | : | | | | | : |
              PGAKQENPLFSLKRSQMDKQLIPVAESIDI
              10      20      30

      130      140      150      160      170      180
m247-1.pep  NYQNFQVGSALIFQYGIDVDNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDK
g247-1      : | : | : | | | | | : | : | : | : | : | : | : | : | : | : |
              KYPGFIQRLNALVFQYGIDDLASAETVVVSSCSKIAKPGKKISTLQEAKSALQITNDDK
              40      50      60      70      80      90

      190      200      210      220      230      240
m247-1.pep  EONGNIARQRHVVNAYAVGRIAD-EEGLFRFQDDKKGWGNPQLLVKKVRHMKVRYIYVS
g247-1      | | | | : | : | : | : | : | : | : | : | : | : | : | : |
              -QNGNITRQKHVVNAYAVGRFGNNEESLFRFQDDKKGWGNPQLLVKKVRHMDVRYIYVS
              100      110      120      130      140

      250      260      270      280      290      300
m247-1.pep  GCPEDDDAGKEETFKYTDKFDKSAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDAT
g247-1      | | | | : | : | : | : | : | : | : | : | : | : | : | : |
              GCPEDDAGKEEFKRYTNKFDKSKNAVTPAGVEVLLDGLNAKIAASSDNIYAYRINAT
              150      160      170      180      190      200

      310
m247-1.pep  IRGGNVCANRTLX
g247-1      | | | | | | | |
              IRGGNVCANRTLX
              210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

a247-1.seq (partial)

```

1  AATAATACAG CTAATTGAT TCCTATTGCT GAATCCACAG ATATTAAATA
51  TCCGGGTTTT GCCCAGGCTC GTCCGGCATT GATTTTCCAA TACGGCATCG
101 ATGATCTTGA TCGGAGTGCT GAGACTGTTG TAGTCAGCAG CTGTTCCAAA
151 ATAGCAAAAC CGGGTAAGAA AATATCTACC TTGCAAGAAG CAAAGAGTGC
201 ATTACAGATT ACTAATGATG ATAAACAAAA TGGAAATATC ACCCGTCAAA
251 GGCATGTGGT CAATGCCTAT GCGGTGCGCA GGATTGCCGG TGAGGAAGGT
301 TTGTTCCGCT TCCAATTGGA TGATAAGGGC AAGTGGGGTA ATCCTCAGTT
351 GCTCGTGAAA AAGATTAGAC ATATGAAAGT GCGGTATATC TATGTTTCCG
401 ACTGTCTGA AGATGACGAT GCCGGCAAAG AGGAAAAATT CAAATATACG
451 GGTACATTGC ACAGCTCCAC AAATGCTGTT ACGCCCCCGG GGGTGGAGGT
501 TTTATTGAGT AGCGGTACTG ATACCAAGAT TGCCGCTTCT TCAGACAATC
551 ATATTTATGC TTACCGTATC GATGCGACAA TACGCGGGGG AAATGTATGC
601 GCAAAACAGAA CACTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 958; ORF 247-1.a>:

a247-1.pep (partial)...

```

1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDLASA ETVVVSSCSK
51  IAKPGKKIST LQEAKSALQI TNDDKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQDDKKG KWGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEKFKYT
151 GTFDSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIYAYRI DATIRGGNVC
201 ANRTL*

```

m247-1 / a247-1 80.6% identity in 206 aa overlap

```

      10      20      30
a247-1.pep  NNTAKLIPIAESTDIKYPGFAQARPALIFQ
m247-1      | : | | | | | | : | : | : | : | : | : |
              GFGCFNMSEHPATDVIPDTTQONSFPFLKRNIGDKLIPIAESSNINYQNFQVGSALIFQ
              80      90      100      110      120      130

      40      50      60      70      80      89
a247-1.pep  YGIDDLASAETVVVSSCSKIAKPGKKISTLQEAKSALQITNDDK-QNGNITRQRHVVNAY
m247-1      | | | | : | : | : | : | : | : | : | : | : | : | : | : |
              YGIDVDNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDKEONGNIARQRHVVNAY
              140      150      160      170      180      190

      90      100      110      120      130      140      149
a247-1.pep  YAVGRIAGEEGLFRFQDDKKGWGNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEKFKY
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

m247-1      YAVGRIADEEGLFRFQLDDKKGWNPQLLVKKVRHMKVRYIYVSGCPEDDDAGKEETFKY
            200      210      220      230      240      250

a247-1.pep  150      160      170      180      190      200
            TGTFDSSSTNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            | |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m247-1      TDKFDSAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            260      270      280      290      300      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 959>:

```

g248.seq
1   atgcgcaaac agaacacttt gacaggaatc cgcacttctg acggacagag
51  ggggtccgca ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 tggttgtaac tgccgcccag tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cggctttgcg
201 ggagggcgaa tttcagggtt tggatttggg atatgctgcg gacagtaagg
251 ttacgtttag cgaaaactgt gaaaaaggtc tgtgtaccgc agtgaatgtg
301 cggacaaata ataatggtag tgaagaggct tttggcaata tcgtggtgca
351 aggcaagccc gccgttgagg cggtgaaacg ttctgacct gcaaagtctg
401 gcaaaaattc taccgacctg tgcattgaca ataaagggat ggaatataat
451 aaaggcgctg caggcgctag caaaatgccg cgctatatta tcgaatatatt
501 aggcgtgaag aacggacaaa atgtttatcg ggttactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcaataat
601 gatgagcaat aa

```

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

```

g248.pep
1   MRKQNTLTGI PTSDGQRGSA LFIVLMVMIV VAFLVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE FQVLDLEYAA DSKVTFSENC EKGLCTAVNV
101 RTNNGSSEEA FGNIVVQGKP AVEAVKRSCP AKSGKNSTDL CIDNKGMEYN
151 KGAAGVSKMP RYIIEYLGVK NGQNVYRVTA KAWGKNANTV VVLQSYVGN
201 DEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 961>:

```

m248.seq (partial)
1   ..GGGTTTGAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.TyWT
51  gGwTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAGTkCCA
101 ACGAATCAGA CAGGAAATTG GCTwTGTCTT TGGCCGAGkC GkCTwTGCGG
151 GAAGGCGAAC TTCAGGTTTT GGATTTGGAA TATGATACGG ACAGTAAGGT
201 TACATTTAGC GAAAACGTGT GAAAAGGTCT GTsTGCCGCA GTGAATGTGC
251 GGACAAATAA TGATAATGAA GAGGCTTTTG ACAATATCGT GGTGCAAGGC
301 AAGCCCACCG TTGAGGCGGT GAAGCGTCT TGCCCTGCAA ATTCTACCGA
351 CCTGTGCATT GACAAGAAAG GwTGGAATA TAAGAAAGGC ACGAGAAGCG
401 TCAC.AAAAT GCCACGTTAT ATTATCGAAT ATTTGGGCGT GwAGAACGGA
451 GAAATGTTT ATCGGGTTAC TGCCAAGGCT TGGGGtAAGA ATGCCAATAC
501 CGTGGTCGTC CTTCAATCTT ATGTAAGCAA TAATGATGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 962; ORF 248>:

```

m248.pep (partial)
1   ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISKNESDRKL AXSLAEXXXR
51  EGELQVLDLE YDTSKVTFS ENCGKGLXAA VNVRTNNDNE EAFDNIVVQG
101 KPTVEAVKRS CPANSTDLCI DKKGXKEYKKG TRSVTKMPRY IIEYLGvXNG
151 ENVYRVTAKA WgKNANTVVV LQSYVSNND *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

m248/g248

```

m248.pep      10      20      30      40
              GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISKNESDRKLAXS
              | |||: |||| | ||||| ||||| ||||| ||||| |||||

```

571

```

g248      MRKQNTLTGIPTSDGQRGSALFIVLMVMIVVAFVLTAAQSYNTEQRI SANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTDSKVTFSENCGLXAAVNVRTNND-NEEAFDNIVVQGKP
           |||  |||:||||| :||||||| ||| :||||| :|||
g248      LAEAAALREGEFQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNGSEEAFFGNIVVQGKP
           70      80      90      100     110     120

           110     120     130     140     150
m248.pep  TVEAVKRSCPA----NSTDLCIDKKGXEYKKGTRSVTKMPRYII EYLGVKNGENVYRVTA
           :||||||| |||:|:| ||:|:| :|:||||| :|:|
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYII EYLGVKNGQNVYRVTA
           130     140     150     160     170     180

           160     170     180
m248.pep  KAWGKNANTVVVLQSYVSNINDEX
           |||:||||| :|||
g248      KAWGKNANTVVVLQSYVGNINDEX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```

a248.seq
1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTACAGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAAAGGTC TGTGTACCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

```

a248.pep
1  MRKQNTLTGI PTSDGQGFALFIVLMVMIV VAEFLVVTAQ SYNTEQRI SA
51  NESDRKLALS LAEAAALREGE LQVLDLEYDT DSKVTFSENC GKGLCTAVNV
101 RTNNDNEEAF DNIVVQGKPT VEAVKRSCTA KSTGLCIDNK GMEYKKGTS
151 VSKMPRYIIE YLGVKNGENV YRVTAKAWGK NANTVVVLQS YVSNINDEX*

```

m248/a248 89.4% identity in 180 aa overlap

```

m248.pep      10      20      30      40
               GFALLIVLMVXIVVAFXXVTAAQSYNTEQRI SXNESDRKLAXS
a248          10      20      30      40      50      60
MRKQNTLTGIPTSDGQRFALFIVLMVMIVVAFVLTAAQSYNTEQRI SANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTDSKVTFSENCGLXAAVNVRTNNDNEEAFDNIVVQGKPT
           |||  |||:||||| :||||||| ||| :||||| :|||
a248      LAEAAALREGEFQVLDLEYDTDSKVTFSENCGLCTAVNVRTNNDNEEAFDNIVVQGKPT
           70      80      90      100     110     120

           110     120     130     140     150     160
m248.pep  VEAVKRSCPANSTDLCIDKKGXEYKKGTRSVTKMPRYII EYLGVKNGENVYRVTA KAWGK
           |||:||||| :||| |||:|:| ||:|:| :|:||||| :|:|
a248      VEAVKRSCTAKSTGLCIDNKGMEYKKGTSVSKMPRYII EYLGVKNGENVYRVTA KAWGK
           130     140     150     160     170     180

           170     180
m248.pep  NANTVVVLQSYVSNINDEX

```

a248

|||||
NANTVVVLQSYVSNINDEX
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq

```

1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCITTGTCT TTGGCCGAGG CGGCTTTGCC
201 GGAAGGCGAA CTTCAAGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAGAGTTC TGTGTGCCG AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCAAC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep

```

1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVLVTTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV
101 RTNNDNEEAF DNIVVQKPT VEA VRSCPA NSTDL CIDKK GMEYKKGTRS
151 VSKMPRYIE YLGVKNGENV YRVTA KAWGK NANTVVVLQSYVSNDE*

```

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS					
g248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	119
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNND-NEEAFDNIVVQKPT					
	: : : : :					
g248	LAEALREGE LQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNNGSEAFGNIVVQKPT					
	70	80	90	100	110	120
	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA----NSTDL CIDKKGMEYKKGTRSVSKMPRYIEYLGVKNGENVYRVTA					
	: : : : : :					
g248	AVEAVKRSCPAKSGKNSTDL CIDNKGMEYNKGAAGVSKMPRYIEYLGVKNGENVYRVTA					
	130	140	150	160	170	180
	180	190				
m248-1.pep	KAWGKNANTVVVLQSYVSNINDEX					
g248	KAWGKNANTVVVLQSYVGNINDEX					
	190	200				

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS					
a248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNNDNEEAFDNIVVQKPT					
	: : : :					
a248	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCTAVNVRTNNDNEEAFDNIVVQKPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDL CIDKKGMEYKKGTRSVSKMPRYIEYLGVKNGENVYRVTA KAWGK					
	: : : :					
a248	VEAVKRSCPAKSTGL CIDNKGMEYKKGTSVSKMPRYIEYLGVKNGENVYRVTA KAWGK					
	130	140	150	160	170	180

```

                190
m248-1. pep  NANTVVVLQSYVSNDEX
              |||||
a248         NANTVVVLQSYVSNDEX
                190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 967>:

```

g249.seq
1   atgaagaata atgattgctt gcgcctgaaa aatccccagt ccggtatggc
51  gttgatagaa gtcttggtcg ctatgctcgt tctgaccatc ggtattttgg
101 cattgctgtc cgtacagttg cggacagtcg cttccgtcag ggaggcggaa
151 acgcaaacca tcgtcagcca aatcacgcaa aacctgatgg aaggaatggt
201 gatgaatccg accattgatt tggacagcaa caagaaaaac tatagtcttt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgcttgat
301 gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351 tcatgagctg aaaaatgcct tgccggatgc ggtagctatt cattacgccg
401 tctgcaagga ttcgtcgggt gacgcgccga cattgtccga cagcggtgct
451 ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501 attgtgggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551 ttgaagtgag cggcgacaat atcgtatata cctatcaggc aagggtcggg
601 ggtcgtgaat ga

```

This corresponds to the amino acid sequence <SEQ ID 968; ORF 249.ng>:

```

g249.pep
1   MKNNDCLRLK NPQSGMALIE VLVAMLVLT I GILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDLSNKKY YSLYMGKQTL SAVDGEFMLD
101 AEKSKAQLAE EQLKRFSHEL KNALPDAVAI HYAVCKDSSG DAPTLSDSGA
151 FSSNCDNKAN GDTLIKVLWV NDSAGDS DIS RTNLEVSGDN IVYTYQARVG
201 GRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 969>:

```

m249.seq
1   ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CCGACAGTCN NNNNNNNNNN NNNNNNNNNN
151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CCGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATTT TGCGATTGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTTAG
351 TTATGAGCTG AAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTGCGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAAACGGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTCGGCAG GGGATTCCGA TATTTCCCGT ACGAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTCCGAGGT
601 CGGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 970; ORF 249>:

```

m249.pep
1   MKNNDCFRLK DSQSGMALIE VLVAMLVLT I GILALLSVQL RTVXXXXXXXX
51  XXXXXXXXXXX XLMEGMLMNP TIDSDSNKKY YNLYMGNHTL SAVDGFDAID
101 AMKTKGQLAE AQLKRFSYEL KNALPDAAAI HYAVCKDSSG NAPTLSGNAF
151 SSNCDNKANG DTLIKVLWVN DSAGDS DISR TNLEVSGDNI VYTYQARVGG
201 RE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 249 shows 81.3% identity over a 203 aa overlap with a predicted ORF (ORF 249.ng) from *N. gonorrhoeae*:

m249/g249

```

                10      20      30      40      50      60
m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX
           |||||:||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

574

```

g249      MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     120
m249 . pep XLMEGMLMNPTIDSDSNKKNYNLYMGNHTLSAVDGDFAIDAMKTGQLAEQKRFYSYEL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      NLMEGMLMNPTIDLDSDNKKNYSLYMGKQTL SAVDGEFMLDAEKSQAQLAEQKRFSSHLL
           70      80      90      100     110     120

           130     140     150     160     170     179
m249 . pep KNALPDAAAIHYAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLIKVLWVND SAGDS DIS
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      KNALPDAAAIHYAVCKDSSGDAPTLSDSGAFSSNCDNKANGDTLIKVLWVND SAGDS DIS
           130     140     150     160     170     180

           180     190     200
m249 . pep RTNLEVSGDNIVYTYQARVGGREX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      RTNLEVSGDNIVYTYQARVGGREX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 971>:

```

a249.seq
1  ATGAAGAATA ATGATTGCTT CCGCCTGAAA AACCCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGGTCG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTTCAGTTG CGGACAGTCG CTTCCGTCAG GGAGGCAGAG
151 ACGCAAACCA TCGTCAGTCA AATCACGCAA AACCTGATGG AAGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATCATGCA CTATCAGTTG TGGATGGCGA TTTTCAGGTT
301 GATGCCATAA AACTAAGAC GCAGTTGGCA GAGGCACAAT TGAAGAGATT
351 TAGTTATGAG CTGAAAAATG CCTTGCCGGA TCGCGCAGCC ATCCATTACG
401 CCGTCTGCAA GGATTCGTCG GGTGTTGCGC CGACATTGTC CGCCGGCAGT
451 ACTTTTCTT CAAATTGCGA TGGTAGTGCA AATGGGGATA CTTTGATTAA
501 AGTATTGTGG GTAAATGATT CGGCAGGGGA TTCGGATATC GCCCGTACGA
551 ATCTTGAGAC GAACGGCAAC AATATCGTAT ATACCTATCA GGC AAGGGTC
601 GGAGGTCGGG AATGA

```

This corresponds to the amino acid sequence <SEQ ID 972; ORF 249.a>:

```

a249.pep
1  MKNNDCFRLK NPQSGMALIE VLVAMLVLTIGILALLSVQL RTVASVREAE
51  QTIVSQITQ NLMEGMLMNP TIDSDSNKKN YNLYMGNHHA LSVVDGDFQV
101 DAIKTKTQLA EAQLKRFSYE LKNALPDAAA IHYAVCKDSS GVAPTLSAGS
151 TFSSNCDGSA NGDTLIKVLW VND SAGDS DI ARTNLETNGN NIVYTYQARV
201 GGRE*

```

m249/a249 81.9% identity in 204 aa overlap

```

           10      20      30      40      50      60
m249 . pep MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      MKNNDCFRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     119
m249 . pep XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAEQKRFYSYE
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      NLMEGMLMNPTIDSDSNKKNYNLYMGNHHSVVDGDFQVDAIKTKTQLAEQKRFYSYE
           70      80      90      100     110     120

           120     130     140     150     160     170
m249 . pep LKNALPDAAAIHYAVCKDSSGNAPTLS-GNAFSSNCDNKANGDTLIKVLWVND SAGDS DI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      LKNALPDAAAIHYAVCKDSSGVAPTLSAGSTFSSNCDGSANGDTLIKVLWVND SAGDS DI
           130     140     150     160     170     180

```


576

D + M G A + T L +A +L ++ ++KN LP A
 Sbjct: 72 LYDVKDQ-----MATQSDFFKAKGSAFPTAPSSCTPLPDAIKDRLGCVAEQVKNELEFGAG 126
 Query: 130 AI---HYAVCKDSSGVAPTLASGSTFSSNCDGSANGDTL-IKVLWVNDSAGDSDIARTNL 185
 + Y +C+ S +CDG G L I++ W + A ++
 Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSMLLEIRLAWRGKQACVNAADSSA 172
 Query: 186 ETN 188
 +T+
 Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLK	DSQSG	MALIE	VLVAM	LVLTIG
a249	MKNND	CFRLK	NPQSG	MALIE	VLVAM	LVLTIG
	10	20	30	40	50	60
m249-1.pep	NLM	EGMLM	NPTID	SDSNK	KNYNLY	MGNH-TL
a249	NLM	EGMLM	NPTID	SDSNK	KNYNLY	MGNH-HA
	70	80	90	100	110	119
m249-1.pep	SAVDG	DFAID	AMKTK	GQLAE	AQLKR	FSYE
a249	SAVDG	DFAID	AMKTK	GQLAE	AQLKR	FSYE
	70	80	90	100	110	120
m249-1.pep	LKNAL	PDAAAI	HYAVCK	DSSGN	APTL	S-GNAF
a249	LKNAL	PDAAAI	HYAVCK	DSSGV	APTL	S-GNAF
	130	140	150	160	170	180
m249-1.pep	SRTN	LEVSG	DNIVY	TYQAR	VGGRE	X
a249	ARTN	LETNG	NNIVY	TYQAR	VGGRE	X
	180	190	200			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1  atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51  aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggta
101 tgcagggcgg gcaaaaaggt atgggcccgc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacgtca acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataacctt atgattaatt
251 cgcgccatat cctgatgggg ggcggcgctt gccacgcaca tgaaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1  MHTASPRDE FIRIKESSP MLIGLLPWAL ILGMOGGQKG MGRLEMLLMT
51  GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAHERN
101 TAEKSRARAV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1  ATGCACACCT TCCCCGCATA ACGAATTAT ACGCGGCATC AAAGAAAGTT
51  CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAATACT CCGTATGCAG
101 GGCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCAAGTAT
151 GAACTTCGCC GCGGCTCCG AGTTTGCCAC GGTCAACCTG TGGGCGAAGC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTTATGAT TAATTCTCGG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAaTACCGC
301 TGAAAAAAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1  MHTPSPHNEF IRGIKESSPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51  MNFAGGSEFA TVNLWAEPLP ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRARTVF YV*
  
```



```

1  atgcctgacc caatagggat tcttttcgct gccgtcgggg ttgatttttt
51  tgccgttggt ttgagggggc gttttcaacg aataggcgcg gttggcatgt
101 tgataataat aatcctgatg gcggagggtc gaaccaaaac ggtcgtaac

```

578

```

151 gaggttgacg ctcaggttgt ggcggatttt ggcggatcgc aaggattttt
201 tgaatgccgc ctgcaagagc ctgtggcttt ccccgtaa at cagcggtcg
251 gatttgtagt aggaagacgg cttgtcggca ctcggcgccg aatatttgc
301 cgaaccgctc gcggaacagt gcgtctgctg aaaatgattg tccaaaccga
351 tgccctgccg gtcgtaagag agggcgccat aatccgccc aagtgtctta
401 tcggcattgg tatagacata ttccaaaccg tagcggcttt tgggtgctg
451 ctcgtcgtaa aacacgccc gaccgtattc cgcgcccacc tccgcaccgt
501 tttcaccgtt ggtaatcagc ccgctgtatt tgcggccgcc cgcgtatttg
551 ccgtagcctc ttatcgatcc gtatttttta ttttcatcaa aaaccgcctt
601 ggtcaggaat gccggaaccg tcatatcgcg cgtgtcgaaa gtttgcgtcg
651 tgcgttcgag tatgcccgcg atgtagtgcc gtttgttttc aaaacgaaaa
701 cccggcgga acagccacga cgggctttcg tatga

```

This corresponds to the amino acid sequence <SEQ ID 982; ORF 251.ng>:

g251.pep

```

1 MPDPGILFA AVGVDFFAV LRGRFORIGA VGMLIIIIIM AEVGTKTVVT
51 EVDAQVVADF GGIEGFFECR LQEPVAFPVN HAVGFVVGR LVGTRAAIFV
101 RTVGGTVRL KMIQTDALP VVREAGIIRP SVFIGIGIDI FQTVAAFGVR
151 LVVKHARTVF RAHLRTVFTV GNQPAVFAAA RVFAVASYS VFFIFIKNRL
201 QQECRNRIA RVESLLRAFE YAADVVPFV KTKTRAEQPR PAFV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 983>:

m251.seq

```

1 ATGCGTGCTG CCGTAGTCGT AGCGCAAGCC CGCGCCGACA TCCGCCACCC
51 TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTACCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCGGTA ACGACATTTC CCCTGCCTAT GGTGACCCAA TAGGGGCTGG
201 TTCACTGCC GTTGGGGCTG ATTTTTTTGC CGTGTGTTT AGGGGGCGTG
251 TTCGACGAAT AGGCGCGGTT GGCATGTTGA TAATAATAAT CCTGATGGCG
301 GAGATTAGAG CCAAAGCGGT CAAACCCGAG ATTCACGCTC AGGTTGTGGC
351 GGATTTTGGC GGTATCGAAG GATTTTTTGA ATGCGCGCTG CAAGAGCCTG
401 TGGCTTTCCC CGTAAATCAC GCGATCGGAT TTGTAATAGG AAAACGGCTT
451 GTCGGCACTC GGGCGGCAAT ATTTGTCCGA ACCGTCGGCA GAACAGTGCG
501 TCTGCTGAAA ATGATTATCC AAACCGATGC CCTGCCGGTC GTAAGAGAGG
551 CGGCATAAT CCGCCCAAGT GTCTTTATCG GCATTGGTAT AGACATATTC
601 CAAACCGTAG CGGCTTTTGG TGTGCGTCTC GTCGTAAAC ACGCCCGTAC
651 CGTATTCGCG GCCCACCAGC GCACCGTTTT CGCCGTTGGT AAACAGTCCG
701 CCGTATTTGT GGTGCCCCG GTATTGCGG TTACCGGGCA AAGAACCCGC
751 CTGTTTTTTA TTTGCATCAA AAACCGCCTT GGTGAGGAAT GCCGGAACCG
801 TCATATCGCG CGTGTGCGAA GTTTGTTGCG TGTGTTGAG TATGCCCGCG
851 ATGTAGTGCC GCTTATCTC AAAACGAAAA CCCGGCGGGA ACAGCCACGA
901 CCGGCTTTTC TATGA

```

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

m251.pep

```

1 MRAAVVVAQA RADIRPPAQT DIVPNCRVIA FTVDAARRAV RISIVAQAAD
51 LPRNDISPAY GDPGAGFTA VGADFFAVVL RGRVRRIGAV GMLIIIIIMA
101 EIRAKAVKPE IHAQVADFG GIEGFFECRL QEPVAFPVNH AIGFVIGKRL
151 VGTRAAIFVR TVGRTVRLK MIIQTDALPV VREAGIIRPS VFIGIGIDIF
201 QTVAAFGVRL VVKHARTVFR AHQRTVFAVG QSAVFVVAR VFAVTGQTR
251 LFFICIKNRL QQECRNRIA RVESLLRVFE YAADVPLIL KTKTRAEQPR
301 PAFV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/g251

```

          40      50      60      70      80      90
m251.pep  TVDAARRAVRISIVAQAADLPRNDISPAYGDPGAGFTAVGADFFAVVLGRVRRIGAVG
          |||| |::||:|||||||:|||||
g251      MPDPGILFAAVGVDFFAVVLGRGRFORIGA
          10      20      30

```


580

a251	ADPIGLVLAAVGVGGF----RGRFRRIGAVGMLIIIIILMAEIRVKAVKTEIHAQVVA	70	80	90	100	110
m251.pep	GIEGFFECRLQEPVAFPNHAIGFVIGKRLVGTAAIFVRTVGRTVRLKMIQTALPV	130	140	150	160	170
a251	GIEGFFECRLQEPVAFPNHAGFVVGKRLVGTAAIFVRTVGRTVRLKMIQTALPV	120	130	140	150	160
m251.pep	VREAGIIRPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVFAVGKQSAVFVVAR	190	200	210	220	230
a251	VREAGIIHPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVFAVGKQTAVFVVAR	180	190	200	210	220
m251.pep	VFAVTGQTRLFFICIKNRLGQECRNRIARVESLLRVFEYAADVPLILKTKTRAEQPR	250	260	270	280	290
a251	VFAVASYSR-VFSIFIKNRLGQECRNRIARVESLLRVFEYAADVFPVFKTKTRAEQPR	240	250	260	270	280
m251.pep	PAFVX					
a251	SAFVX					
	300					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 987>:

g253.seq

```

1  atgatcgaca gggaccgtat gttgcgggac acgttgaac gtgtgctgac
51  ggggtcgttc tggttatggg tgggtggtggc atcgatgatg tttaccgcgc
101 gatttttcagg cacttatctt ctgatggaca atcaggggct gaatttcttt
151 ttagttttgg cgggagtgtt gggcatgaat acgctgatgc tggcagtatg
201 gttggcaacg ttgttcctgc gcgtgaaagt gggacggttt ttcagcagtc
251 cggcgacgtg gtttcggggc aaaggccctg taaatcaggc ggtgttgagg
301 ctgtatgcgg accagtggcg gcaaccttcg gtacgatgga aaataggcgc
351 aacggcgcac agcttgtggc tctgcacgct gctcggatg ctggtgtcgg
401 tattgctgct gcttttggtg cggcaatata cggtcaactg ggaaagcacg
451 ctgttgagca atgcccgttc ggtacgcgcg gtggaaatgt tggcatggct
501 gccgtcgaaa ctcggtttcc ctgtccccga tgcgcgggag gtcacgaag
551 gtcgtctgaa cggcaatatt gccgatgcgc gggcttggtc ggggctgctg
601 gtcggcagta tcgtctgcta cggcatcctg ccgcgcctct tggcttggtg
651 agtgtgtaaa atccttttga aaacaagcga aaacggattg gatttgaaa
701 aaacctatta tcaggcggtc atccgcgcgt ggcagaacaa aatcaccgat
751 gcggatacgc gtcgggaaac cgtgtccgcc gtttcgccga aaatcgtctt
801 gaacgatgcg ccgaaatggg cgctcatgct ggagaccgag tggcaggacg
851 gccaatgggt cgagggcagg ctggcgaggc aatggctgga taaggcgctt
901 gccgccaatc gggaacaggt tgccgcgctg gagacagagc tgaagcagaa
951 accggcgcaa ctgcttatcg gcgtacgcgc ccaaactgtg ccggaccggg
1001 gcgtgctgcg gcagattgtg cggctttcgg aagcggcgca gggcggcgcg
1051 gtggtgcagc ttttggcgga acaggggctt tcagacgacc tttcggaaaa
1101 gctggaacat tggcgtaacg cgctgaccga atgcggcgcg gcgtggcttg
1151 agcctgacag ggtggcgagc gaaggccgtt tgaagacca ataa

```

This corresponds to the amino acid sequence <SEQ ID 988; ORF 253.ng>:

g253.pep

```

1  MIDRDRMLRD TLERVAGSF WLWVVASMM FTAGFSGTYL LMDNQGLNFF
51  LVLAVGLGMN TLMLAVLAT LFLRVKVGFR FSSPATWFRG KGPVNQAVLR
101 LYADQWRQPS VRWKIGATAH SLWLCTLLGM LVSLLLLLV RQYTFNWEST
151 LLSNAASVRA VEMLAWLPSK LGFPVPDARA VIEGRLNGNI ADARAWSGLL
201 VGSIVCYGIL PRLLAWVVK ILLKTSENGL DLEKTYQAV IRRWQNKITD
251 ADTRRETUSA VSPKIVLND PKWALMLETE WQDGQWFEGR LAQEWLDKGV

```

m253.seq

This corresponds to the amino acid sequence <SEQ ID 990; ORF 253>:

m253.pcp

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 253 shows 94.7% identity over a 397 aa overlap with a predicted ORF (ORF 253.ng) from *N. gonorrhoeae*:

m253/g253

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLEVRAGSFWLWVVAATFAFFTGSVTYLLMDNQGLNFFLVLAGVLGMN					
	: : : : :					
g253	MIDRDRLRDTLERVRAGSFWLWVVVASMMFTAGFSGTYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMFLRVKVGRRFSSPATWFRGKDVPVNAQAVLRLYADEWRQPSVRWKIGATSH					
	: :					
g253	TLMLAVWLATLFLRVKVGRRFSSPATWFRGKGPNVNAQAVLRLYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSLLLLLVRQYTTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
g253	SLWLCTLLGMLVSLLLLLVRQYTTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m2 53 . pep	VIEGR	LNGNIADAR	AWSGLLVGS	IACYGILP	RLLA	VVCKILLKTS
g2 53	VIEGR	LNGNIADAR	AWSGLLVGS	IVCYGILP	RLLA	VVCKILLKTS
	190	200	210	220	230	240
	250	260	270	280	290	300
m2 53 . pep	IRRWQ	NKITDAD	TRRET	VS	SAVSPKI	ILNDAPK
g2 53	IRRWQ	NKITDAD	TRRET	VS	SAVSPKIV	LNDA
	250	260	270	280	290	300
	310	320	330	340	350	360
m2 53 . pep	ATNRE	QVA	ALET	ELKQK	PAQL	LLIGVRA
g2 53	AANRE	QVA	ALET	ELKQK	PAQL	LLIGVRA
	310	320	330	340	350	360
	370	380	390			
m2 53 . pep	SDDL	SEKLEH	WRNAL	AECGA	AWLEP	DRAAQ
g2 53	SDDL	SEKLEH	WRNAL	TECGA	AWLEP	DRVAQ
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

```

a2 53 . seq
1  ATGATCGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC
51  GGGGTCGTC TGGTTGTGGG TGGCGGCGGC GACGTTTGCG TTTTTCACCG
101 GTTTTTCAGT TACTTATCTT CTAATGGACA ATCAGGGTCT GAATTTCTTT
151 TTGGTTTTGG CGGGCGTGTT GGGCATGAAT ACGTGATGC TGGCAGTATG
201 GTTGGCAATG TTGTTCTGCG GCGTGAAAGT GGGGCGTTTT TTCAGCAGTC
251 CGGCGACGTG GTTTCGGGGC AAAGACCGTG TCAATCAGGC GGTGTTGCGG
301 CTGTATGCGG ACGAGTGGCG GCAACCTTCG GTACGTTGGA AAATAGGCGC
351 AACGTCGCAC AGCCTGTGGC TCTGCACGCT GCTCGGAATG CTGGTGTGCG
401 TATTGTTGCT GCTTTTGGTG CGGCAATATA CGTTCAACTG GGAAAGCAGC
451 CTGTTGGGCG ATTCTGCTTC GGTACGGCTG GTGGAATGT TGGCATGGCT
501 GCCTGCGAAA CTGGGTTTTT CCGTGCCCTGA TGC GCGGGCG GTCATCGAAG
551 GTCGTCTGAA CCGCAATATT GCCGATGCGC GGGCTTGGTC GGGGCTGCTG
601 GTCGGCAGTA TCGCCTGCTA CGGCATCCTG CCGCGCCTCT TGGCTTGGGC
651 GGTATGCAAA ATCCTTTTGA AAACAAGCGA AAACGGCTTG GATTTGGAAA
701 AGCCCTATTA TCAGGCGGTC ATCCGCCGCT GGCAGAACAA AATCACCGAT
751 GCGGATACGC GTCGGGAAAC CGTGTCGCCG GTTTCGCCGA AAATCGTCTT
801 GAACGATGCG CCGAAATGGG CGGTCATGCT GGAGACCGAA TGGCAGGACG
851 GCGAATGGTT CGAGGGCAGG CTGGCGCAGG AATGGCTGGA TAAGGGCGTT
901 GCCGCCAATC GGGAACAGGT TGCCGCGCTG GAGACAGAGC TGAAGCAGAA
951 ACCGGCGCAA CTGCTTATCG GCGTGCGCGC CCAACTGTG CCCGACCGCG
1001 GCGTGTTCG GAGATCGTC CGACTTTCGG AAGCGGCGCA GGGCGGCGCG
1051 GTGGTGCAGC TTTTGGCGGA ACAGGGGCTT TCAGACGACC TTTTCGAAAA
1101 GCTGGAACAT TGGCGTAACG CGCTGACCGA ATGCGGCGCG GCGTGGCTGG
1151 AACCCGACAG AGCGGCGCAG GAAGGCCGTC TGAAAACCAA CGACCGCACT
1201 TGA

```

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

```

a2 53 . pep
1  MIDNRNRLRE TLERVVAGSF WLWVAAATFA FFTGFSVTYL LMDNQGLNFF
51  LVLAVGLGMN TLMLAVWLAM LFLRVKVGRF FSSPATWFRG KDPVNQAVLR
101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSLLLLLLV RQYTFNWEST
151 LLGDSSSVRL VEMLAWLPAK LGFPVPDARA VIEGRNLNGNI ADARAWSGLL
201 VGSIAACYGIL PRLLA
```

m253/a253 97.2% identity in 395 aa overlap

m253.pep	10	20	30	40	50	60
	MIDRNRMLRETLEVRAGSFWLVVAAATFAFFTGFSTVYLLMDNQGLNFFLVLAGVLGMN					
a253						
	10	20	30	40	50	60
	MIDRNRMLRETLEVRAGSFWLVVAAATFAFFTGFSTVYLLMDNQGLNFFLVLAGVLGMN					
m253.pep	70	80	90	100	110	120
	TLMLAVWLAMFLRVKVGRRFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
a253						
	70	80	90	100	110	120
	TLMLAVWLAMFLRVKVGRRFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
m253.pep	130	140	150	160	170	180
	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRRAVEMLAWLPKLGFPVPDARA					
a253						
	130	140	150	160	170	180
	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLGSSSVRLVEMLAWLPKLGFPVPDARA					
m253.pep	190	200	210	220	230	240
	VIEGRNLNGNIADARAWSGLLVGSIAICYGILPRLAWVCKILLKTSENGLDLEKPYQAV					
a253						
	190	200	210	220	230	240
	VIEGRNLNGNIADARAWSGLLVGSIAICYGILPRLAWVCKILLKTSENGLDLEKPYQAV					
m253.pep	250	260	270	280	290	300
	IRRWNQKITDADTRRETSAVSPKIIINDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
a253						
	250	260	270	280	290	300
	IRRWNQKITDADTRRETSAVSPKIVLNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
m253.pep	310	320	330	340	350	360
	ATNREQVALETELKQKPAQLLIGVRAQTVPDGRVLRQIVRLSEAAQGGAVVQLLAEQGL					
a253						
	310	320	330	340	350	360
	AANREQVALETELKQKPAQLLIGVRAQTVPDGRVLRQIVRLSEAAQGGAVVQLLAEQGL					
m253.pep	370	380	390			
	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRLKDQX					
a253						
	370	380	390	400		
	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGRLKTDNRTX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcagggttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg tttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gcactgggtt ctttgagaaa cgggccgggc
301 tggacgggat tttcactgtc ctggctgctg gcggtgcgag gaatcgcaca
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggtcttgg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtattgg gcggcagcat aaccctaatt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLLLKT IGHGDGYRIF SVSVYGISLL

```

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51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMY VLIAGSYTPF ALVSLRNGPG
 101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLS SIAIYVMGW MVLAVMKSLT
 151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
 201 VSVYGYVI*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

m254.seq (partial)
 1 ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTTGA GTTCCTGGCT
 51 GTACCACGGA ATTGCAGCCG GAAAAC TGAA AAGCATTTTG AAAAAAACC
 101 ACCACTGCAT GATTATATGTG CTGATTGCCG GAAGCTACAC ACCGTTTGCA
 151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG
 201 GCTGCTGGCG GCTGCAGGAA TCGCACAAGA ACTCACCATC GGACGGAAAA
 251 GCGAAAAACG TCTGCTGTCT ATTGTGATTT ATGTCGTCAT GGGTTGGATG
 301 GTCTTGCGCG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT
 351 GGCTTGCGTG GCGGCAGGCG GTATGCTGTA CAGTGTGGC ATTACTGGT
 401 TTGTAAACGA TGAAAAATC CGACACGGGC ACGGAATCTG GCATCTGTTC
 451 GTATTGGGCG GCAGCATCAC CCAATTTGTC AGCGTGTACG GTTACGTAAT
 501 CTGA

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

m254.pep (partial)
 1 ..VSVYGISLLL LYLSSWLYHG IAAGKLKSI LKKTDHCMYV LIAGSYTPFA
 51 LVSLRNGPW TVFSLSWLLA AAGIAQELTI GRKSEKRLS IYIYVMGWM
 101 VLAVMKSLTA SLPSAGLAWL AAGGMLYSV GIYWFVNDEKI RHGHGIWHLF
 151 VLGGSITQFV SVYGYVI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng) from *N. gonorrhoeae*:

m254/g254

m254.pep				10	20	30
				VSVYGISLLL	LYLSSWLYHG	IAAGKLKSI
g254	HL	SL	GL	IL	AA	AG
	20	30	40	50	60	70
m254.pep		40	50	60	70	80
		KK	TD	HC	MI	YV
g254		80	90	100	110	120
		IV	IY	VM	GW	ML
m254.pep		100	110	120	130	140
		IV	IY	VM	GW	ML
g254		140	150	160	170	180
		IA	IY	VM	GW	ML
m254.pep		160				
		VL	GS	IT	QF	VS
g254		200				
		VL	GS	IT	QF	VS

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

a254.seq
 1 ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTTGA GCGGTTTGAT
 51 TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAAACC ATAGGACACG
 101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT
 151 CTGCTCTATT TGAGTTCTTC GCTGTACCAC GGAATTGCAG CCGGAAAAC
 201 GAAAAGCATT TTGAAAAA CCGACCACTG CATGATTAT GTGCTGATTG
 251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CGGGCCGGGC

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```

301 TGGACGGTAT TTCTACTGTC CTGGCTGCTG GCGGCTGCAG GAATCGCACA
351 AGAACTCACC ATTGGACGGA AAAGCGAAAA ACGACTGCTG TCTATTGCGA
401 TTTATATCGT AATGGGCTGG ATGGTCTTGG CCGTAATGAA ATCCCTGACA
451 GCCTCACTCC CGCCGGCAGG ACTGGCTTGG CTGGCGGCAG GCGGTATGCT
501 GTACAGCGTC GGCATTACT GGTTTGTAAG CGATGAAAAA ATCCGACACG
551 GGCACGGAAT CTGGCATCTG TTCGTATTGG GCGGCAGCAT CACCCAATTT
601 GTCAGCGTGT ACGGTTACGT AATCTGA

```

This corresponds to the amino acid sequence <SEQ ID 998; ORF 254.a>:

a254.pep

```

1  MYTGERFNTY SHLSGLILAA AGLALMLLKT IGHGDGYRIF SVSVYGISLL
51  LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIAIYIVMGW MVLAVMKSLT
151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
201 VSVYGYVI*

```

m254/a254 97.6% identity in 167 aa overlap

```

30                                     10                                     20
m254.pep
VSVYGISLLLLLYLSSWLYHGIAAGKLKSIL

|||||
a254
HLSGLILAAAGLALMLLKTIGHGDGYRIFSVSVYGISLLLLLYLSSSLYHGIAAGKLKSIL
20          30          40          50          60
70
40          50          60          70          80
90
m254.pep
KKTDHCMYIVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
|||||
a254
KKTDHCMYIVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
80          90          100          110          120
130
100          110          120          130          140
150
m254.pep
IVIYVVMGWMVLAVMKSLTASLPSAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF
|:|:|
a254
IAIYIVMGWMVLAVMKSLTASLPPAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF
140          150          160          170          180
190
160
m254.pep
VLGGSITQFVSVYGYVIX
|||||
a254
VLGGSITQFVSVYGYVIX
200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

g255.seq

This corresponds to the amino acid sequence <SEQ ID 1000; ORF 255.ng>:

g255.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1001>:

m255.seq

This corresponds to the amino acid sequence <SEQ ID 1002; ORF 255>:

m255.pcp

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

m255/g255

[illegible]

587

	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
	:					
g255	AALVGVADX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```

a255.seq
1   GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCCG TGTTGCGTGC
51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCACG GCCTTTGACG
101 GCGTTGATGC CCATCATGGC GTAGGCGATT TCGGCATCGA GCGGGTCGAA
151 TACGGGTTTCG CCAAGCCGA CGGGACGTT GCGGGCTTCA ATATGCAGCT
201 TCGCGCCGAC GGAATCCAAG GATTGCGCA CGCTGTCCAT ATAGTTTCC
251 AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
301 GTGTTGCGAG CCTTCAAACC GGATTCTTTT TTCGCCGACT TGGGTAACGT
351 AGGCGGTGAT TTCCGTGCCG AATTTTCTT TCAACCATTT TTTGGCAACG
401 GCTCCGGCGG CAACGCGGGC GCGGTTTCG CGGGCGGAAC TCCTGCCGCC
451 GCCCGGCTAG TCGCGCGTGC CGTATTTGTG CCAATAGGTA TAGTCGGCGT
501 GGCCGGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
551 TCGGTATTGC GGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

```

a255.pep
1   VVGQEALRGE FVAVFAAALR YAVKTCADFH AFDGVDAAHG VGDFGIEAVE
51  YGFAQADGDV GGFNMQLRAD GIQGFHAVH IVFQLGNLAM VGGKKRILGN
101 VFAAFKPDEF FADLGNVGGD FRAEFFFQPF FGNGSGGNAG GGFAGGTPAA
151 APVVARAVFV PIGIVGVAGA EAGGDVAVVF AALVGIAD*

```

m255/a255 93.1% identity in 188 aa overlap

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDFGIEAVKNRFAQADRDI					
	:					
a255	VVGQEALRGEFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDFGIEAVEYGFAQADGDV					
	10	20	30	40	50	60
m255.pep	GCFDMLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDEFFADLGNVGGD					
	:					
a255	GGFNMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDEFFADLGNVGGD					
	70	80	90	100	110	120
m255.pep	FRAEFFFQPF FGNGSGSNAGGGFTGGAPAAA VVARAVFVPIGIVGVAGAEAGGDVAVVF					
	:					
a255	FRAEFFFQPF FGNGSGSNAGGGFAGGTPAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
m255.pep	AALVGIADX					
a255	AALVGIADX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```

g256.seq
1   atgctcgcgg tacgcaatcg ggggtggcac ggcgcagtcg tccatttcg
51  cagctcgcggc ggcgtagcga acaccgcccc ggtgttctac cacttgggtg
101 ataccgccga aatcgccctt gctttggaca cgctcaccgc gcgttaccgt
151 gaaatatacg ccgtcggcgt atcgctgggc ggcaacgcgc cggcaaaata
201 tttggggcga cagggcaaaa aggcattgcc gcacgcctcg gccgccgtat
251 ccgccccgct tgatgcagag gcggcaggca gccgcttcga cagcggcatc
301 acgcggctgc tctacacgcg ctacttcctc cgcacactga taccctaaagc

```

g256.pcp

```

1  MLAVNRNRGWH  GAVVHFRSCG  GVANTAPVVFY  HLGDTAEIAF  ALDTLTARYR
51  EIYAVGVSLG  GNAPAKYLGE  QGKKALPHAS  AAVSVPVDAA  AAGSRFDSGI
101  TRLLYTRYFL  RTLLPKARSL  QGGQTAFAGA  CKTLGEFDDR  FTAPLHGFD
151  RHDDYRQTSC  KPLLKHVAKP  LLLLNAAANDP  FLPELAPRA  DEASEVTLF
201  QPAGYGHAGF  VSSSTGRLHL  QWLPPQTVLSY  FDSFRNRR*

```

m256.seq

seq	ATGCTTGCGG	TACGCGATCG	GGGTGGCAC	GGCGTAGTCG	TCCATTTCGG
51	CAGCTGCGGC	GGCATTGCCA	ACACCGCTCC	GGTGTCTAC	CA.CTtGGCG
101	ATACCGCCGA	AATCGCCTTT	ACTTTGGACA	CGTTGCGCGC	GCGTTACCGT
151	GAAAtATACG	CCGTGCGCGT	ATCGCTGGGC	GGCAACGCGC	TGGCAAAATA
201	TTTGGGCGAA	CAGGGCAAAA	AGGCATTGCC	GCAAGCCGCT	GCGTCATCT
251	CCGCCCCGCT	CGATGCAGAG	GCGGCAGGCA	GACGCTTCGA	CAGCGGCATC
301	ACGCGGCTGC	TCTACACGCG	CTACTTCTCT	CGCACCTTGA	TACCCAAAGC
351	AAATTCGCTC	CAAGGTTTTT	AGACGCGATT	TGCCGCGAGG	TGCAAAACAC
401	TGGGCGAGTT	TGACGACCGC	TTCACGCGAC	CGCTGCACGG	CTTTGCCGAC
451	CGGCACGACT	ACTACCGCCA	AACTTCTGTC	AAACCGCTGC	TCAAACACGT
501	TGCCAAACCG	CTGCTCCTGC	TCAATGCCGT	CAACGACCCC	TTCTTGCCGC
551	CCGAAGCCCT	GCCCCGCGCA	GACGAAGTAT	CCGAAGCCGT	TACCCTGTTC
601	CAGCCGGCAT	ATGGTGGTCA	TGTCGGCTTT	GTCAGCAGCA	CCGGCGGCAG
651	GCTGCACCTG	CAATGGCTGC	CGCAGACCGT	CCTGTCTAT	TTGCACAGT
701	TCCGCACAAA	CAGGCGTTAA			

m256.pcp

```

1  MLAVRDRGWH  GVVVHFRSCG  GIANTAPVFY  XLGDTAEIAF  TLDTFAARYR
51  EIYAVGVSIG  GNALAKYLGE  QGKKALPQAA  AVISAPVDAE  AAGRRRFDSCI
101 TRLLYTRYFL  RTLLPKAKSL  QGFQOTAAAG  CKTLGEFDNR  FTAPLHGFDN
151 RHDDYRQTSC  KPLLKLVAKP  LLLNNAVNDP  FLPEALPRA  DEVSEAVTLF
201 OPAYGGHVG  VVSSGTGRLL  OWLPQTVLSY  FDSFRNRR*

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 256 shows 92.9% identity over a 239 aa overlap with a predicted ORF (ORF 256.ng) from *N. gonorrhoeae*:

m256/g256

	10	20	30	40	50	60
m256.pep	MLAVDRGRGWHGVVHFRSCGGIANTAPVFYHLGDTAEIAFTLDTFAARYREIYAVGVSLG					
g256	MLAVRNRRGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAFALDTLTARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGKKALPQAAAVISAPVDAAAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
g256	GNAKPYLYLGEQGKKALPHASAAVSAPVDAAAGSRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAGCKTLGFEDDRFTAPLHGFADRHDYYRQTSCKPLLKHVAKPLLLLNVAANDP					
g256	QGFQTAFAGCKTLGFEDDRFTAPLHGFADRHDYYRQTSCKPLLKHVAKPLLLLNAANDP					

589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVG FVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAG FVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

a256.seq	1	ATGCTCGCGG	TACGCGATCG	GGGTTGGAAC	GGCGTAGTCG	TCCATTTCCG
	51	CAGCTGCGGC	GGCGTAGCGA	ACACCGCCCC	GGTGTCTAC	CACTTGGGCG
	101	ATACCGCCGA	AATTGCCTTT	ACTTTGGACA	CGCTCGCCGC	GCGTTACCGT
	151	GAAATATACG	CCGTCGGCGT	ATCGCTGGGC	GGCAACGCGC	TGGCAAAATA
	201	TTTGGGCGAA	CAGGGCGAAA	ACGCGCTGCC	GCAAGCCGCC	GCGTCATCT
	251	CCGCACCCGT	CGATGCAGAG	GCGGCAGGCA	ACCGCTTCGA	CAGCGGCATC
	301	ACACGGCTGC	TCTACACGCG	CTACTTCCTC	CGCACACTGA	TACCCAAAGC
	351	ACGGTCGCTC	CAAGGTTTTT	AGACGGCATT	TGCCGCAGGG	TGCAAAACAC
	401	TGGGCGAGTT	TGACGACCGT	TTCACCGCAC	CGTCGCACGG	CTTTGCCGAT
	451	CGGCACGACT	ACTACCGCCA	AACCTCCTGC	AAACCGCTGC	TCAAACACGT
	501	TGCCAAACCG	CTGCTCCTGC	TCAATGCCGT	CAACGACCCC	TTCCTGCCGC
	551	CCGAAGCGCT	GCCCCGCGCA	GACGAAGTGT	CCGAAGCCGT	TACCCTGTTC
	601	CAGCCGACAC	ACGGTGGTCA	TGTCGGCTTT	GTCGGCAGCA	CCGGCGGCAG
	651	GCTGCACCTG	CAATGGTTGC	CGCAGACCGT	CCTGTCTAT	TTGCACAGCT
	701	TCCGCACAAA	CAGGCGTTAA			

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

a256.pep	1	MLAVRDRGWN	GVVHFRSCG	GVANTAPVY	HLGDTAEIAF	TLDTLAARYR
	51	EIYAVGVSLG	GNALAKYLGE	QGENALPQAA	AVISAPVDAE	AAGNRFDSGI
	101	TRLLYTRYFL	RTLIPKARSL	QGFQTAFAAG	CKTLGEFDDR	FTAPLHGFD
	151	RHDYRQTS	KPLLKHVAKP	LLLLNAVNDP	FLPPEALPRA	DEVSEAVTLF
	201	QPTHGGHVG	VGSTGGRLHL	QWLPQTVLSY	FDSFRTNRR*	

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVRDRGWG VVHFRSCGGIANTAPVYFXLGD TAEIAFTLDTFAARYREIYAVGVSLG					
	: : : : :					
a256	MLAVRDRGWNG VVHFRSCGGVANTAPVYHLGD TAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQ GKALPQAAVISAPVDAE AAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	: : : : :					
a256	GNALAKYLGEQ GENALPQAAVISAPVDAE AAGNRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDR ETAPLHGFA DRHDYRQTSCKP LLLKHVAKP LLLNAVNDP					
	: : : : :					
a256	QGFQTAFAAGCKTLGEFDDR ETAPLHGFA DRHDYRQTSCKP LLLKHVAKP LLLNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVG FVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVG FVSGTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

g256-1.seq	1	ATGATTTTGA	CACCGCCGGA	CACGCCCTTT	TTCTCCGCA	ACGGCAATGC
	51	CGACACGATT	GCCGCCAAT	TCTGCAACA	CCCCGCACCC	GCATACCGCC

590

```

101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CAAAACCCG CTACGACTTT
151 TCAGCAGGCG GCATTTCGCC CGATGCGCGG CTGGTCGTGC TGTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTCGAACGT ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GGCAGAGTCG TCCATTTCGG CAGCTGCGGC
301 GCGGTACGCA ACACCGCCCC GGTGTTCTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACCGC GCATTACCGT GAAATATACG
401 CCCTCGCGCT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGGCAAAA AGGCATTGCC GCACGCCTCG GCCGCCGTAT CCGCCCCCGT
501 TGATGACAGG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTC AGACGGCATT TGCCGCGAGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGGCGAC CGGCACGACT
701 ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCTGCGCG CCGAAGCCCT
801 GCCCGGTGCA GACGAAGCGT CCGAAGCCGT TACCCTGTTC CAACCTGCAC
851 ACGGCGGGCA CGCCGGCTTT GTCAGCAGCA CCGGCGGCAG GCTGCACCTG
901 CAATGGGTGC CGCAGACCGT CCTGTCTAT TTTGACAGCT TCCGCACAAA
951 CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVNRNGWH GAVVHFRSCG
101 GVANTAPVYF HLGDTAEIAF ALDTLTARYR EIYAVGVSLG GNAPAKYLG
151 QGKKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFQTAFAAG CKTLGEFDDR FTAPLHGFA DHDYRQTSC KPLLKHVAKP
251 LLLNNAANDP FLPEALPRA DEASEAVTLF QPAHGHHAGF VSTGGRLHL
301 QWLQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```

1 ATGATTTTAA CACCGCCGGA CACGCCCTTT TTCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCGCGCGCCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAGTTCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCGGA TCGCGCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGACGCC ATTACGCGGT CGAACTGATG CTTGCGGTAC
251 GCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTTCGCGAG CTGCGGCGGC
301 ATTGCCAACA CCGCTCCGGT GTTCTACCA CTTGGGCGATA CCGCCGAAAT
351 CGCCTTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACCGCTGG CAAAATATTT GGGCGAACAG
451 GGCAAAAAGG CATTGCCGCA AGCCGCTGCG GTCATCTCCG CCCCCTCGA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCACG CGGCTGCTCT
551 ACACGCCTTA CTCCTCCGCG ACCCTGATAC CCAAAGCAA ATCGCTCCAA
601 GGTTTTTACA CGGCATTGCG CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCCCTTC ACCGACCGCG TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCTGTCTCA ATGCCGTCAG CGACCCCTTC CTGCCGCCCG AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTTAC CCTGTTCAG CCGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGCTGCCCG AGACCGTCCT GTCCTATTTT GACAGCTTCC GCACAAACAG
951 CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQRPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVRDRGWHG VVHFRSCGG
101 IANTAPVYFH LGDTAEIAFT LDTFAARYRE IYAVGVSLGG NALAKYLGEQ
151 GKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIPKAKSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFA DR HDYRQTSC KPLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PAYGGHVG FV SSTGGRLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

m256-1/g256-1 93.1% identity in 319 aa overlap

```

          10      20      30      40      50      59
m256-1.pep MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
          |||||
g256-1      MILTPPDTPFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP
          10      20      30      40      50      60

          60      70      80      90     100     110     119
m256-1.pep LVVLFHGLEGSSSRSHYAVELMLAVRDRGWHGVVHFRSCGGIANTAPVYFHLGDTAEIAF

```

591

```

|||||
g256-1  LVVLFHGLEGSSRSYHAVELMLAVNRNGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
          70      80      90      100     110     120

          120     130     140     150     160     170     179
m256-1.pep  TLDTFAARYREIYAVGVSLGGNALAKYLGEQKKALPQAAAVISAPVDAEAAGRFRDSCI
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1  ALDTLTARYREIYAVGVSLGGNAPAKYLGEQKKALPHASAAVSAPVDAEAAGSRFDSCI
          130     140     150     160     170     180

          180     190     200     210     220     230     239
m256-1.pep  TRLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDDYRQTSC
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1  TRLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDDYRQTSC
          190     200     210     220     230     240

          240     250     260     270     280     290     299
m256-1.pep  KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHGVFVSTGGRLHL
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1  KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEASEAVTLFQPAHGGHAGFVSTGGRLHL
          250     260     270     280     290     300

          300     310     319
m256-1.pep  QWLPQTVLSYFDSFRTNRRX
          |||||||:|||||
g256-1  QWLPQTVLSYFDSFRTNRRX
          310     320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

```

a256-1.seq
1  ATGATTTTGA CACCGCCGGA CACACCCCTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACG CTCGCCACCT GCATACCGCC
101 GCGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAACCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCCGA TCGCGCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAGGGCGGC AGTGGCAGCC ATTACGCGGT CGAACTGATG CTCGCGGTAC
251 GCGATCGGGG TTGGAACGGC GTAGTCGTCC ATTTCCGCAG CTGCGCGGGC
301 GTAGCGAACA CCGCCCGGT GTTCTACCAC TTGGCGGATA CCGCCGAAAT
351 TGCCTTTACT TTGGACACGC TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGCGCGC AACCGCGCTG CAAATATTT GGGCGAACAG
451 GGGCAAAACG CGCTGCCGCA AGCCGCCGCC GTCATCTCCG CACCCGTCGA
501 TGCAAGGCGC GCAGGCAACC GCTTCGACAG CGGCATCACA CGGCTGCTCT
551 ACACGCGCTA CTTCTCCGC AACTGATAC CAAAGCACG GTCGCTCCAA
601 GGTTTTCAGA CGGCATTTGC CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGTTT ACCGCACCGC TGCACGGCTT TGCCGATCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCTGTCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCGGTGCC
801 CCGCGCAGAC GAAGTGTCGG AAGCCGTTAC CCTGTTCCAG CCGACACACG
851 GTGGTCATGT CGGCTTTGTC GGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGTTGCCGC AGACCGTCTT GTCCTATTTT GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

```

a256-1.pep
1  MILTPPDTPF FLRNGNADTI AAKFLORSAP AYRRELLPDS TGKTKTAYDF
51  SDGISPDAPL VVLFHGLEGG SGSHYAVELM LAVRDRGWNG VVHFRSCGG
101 VANTAPVFYH LGDTAEIAFT LDTLAARYRE IYAVGVSLGG NALAKYLGEQ
151 GENALPQAAA VISAPVDAEA AGNRFDSGIT RLLYTRYFLR TLIPKARSLQ
201 GFQTAFAAGC KTLGEFDDR FTAPLHGFADR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PTHGGHGVFV GSTGGRLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

          10      20      30      40      50      60
a256-1.pep  MILTPPDTPFFFLRNGNADTIAAKFLORSAPAYRRELLPDSTGKTKTAYDFSDGISPDAPL
          |||||||:|||||:|||||:|||||:|||||:|||||
m256-1  MILTPPDTPFFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFSDGISPDAPL
          10      20      30      40      50      60

          70      80      90      100     110     120
a256-1.pep  VVLFHGLEGGSGSHYAVELMLAVRDRGWNGVVHFRSCGGVANTAPVFYHLGDTAEIAFT
          |||||||:|||||:|||||:|||||:|||||:|||||
m256-1  VVLFHGLEGSSRSYHAVELMLAVRDRGWNGVVHFRSCGGIANTAPVFYHLGDTAEIAFT

```

592

	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVSLGGNALAKYLGEQGENALPQAAAVISAPVDAEAAAGNRFDSGIT					
m256-1	LDTFAARYREIYAVGVSLGGNALAKYLGEQKKALPQAAAVISAPVDAEAAAGRRFDSGIT					
	130	140	150	160	170	180
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAGCKTLGEFDDRFTAPLHGFADRHDYRQTSCK					
m256-1	RLLYTRYFLRTLIPKAKSLQGFQTAFAGCKTLGEFDDRFTAPLHGFADRHDYRQTSCK					
	190	200	210	220	230	240
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNAVNDPFLPEALPRADEVSEAVTLFQPTHGGHVGFGVSTGGRLHLQ					
m256-1	PLLKHVAKPLLLNAVNDPFLPEALPRADEVSEAVTLFQPAYGGHVGFGVSTGGRLHLQ					
	250	260	270	280	290	300
a256-1.pep	310	319				
	WLPQTVLSYFDSFRTNRRX					
m256-1	WLPQTVLSYFDSFRTNRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

g257.seq

```

1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgcccgttc
51  tgtggccggt gcggcggttt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaaacg caacatggat aaaaaacgcg atgaaaatgt gtttttctgg
151 aaagggtgctg cgctgggttc cggcgcgagg ctgcgcctgt tcggcggtgga
201 cgacagacag gcggcggatt tggccaataa ggttttggcg gaagtggcgc
251 gtttggaaaa aatgttcagc cttaccgtg aagacagcct gatcagccgt
301 ctgaaccgcg acggttatct gacttcgcct ccggcggatt ttttggaaat
351 gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

g257.pep

```

1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKLVA EVARLEKMF5 LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AAIPT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

m257.seq

```

1  ATGGGCAGGC ATTTCCGGCG .CAGCGTTTT CTGACGGTTG CCGCCGTTGC
51  GCGGGGgAc. GCGGcGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAACGGGAT GAAAAACGCA ATGAAATGT GTTTTTCTGG
151 AAAGGTGTCT CACTGGGTTC CCGTGCGGgA. CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA ATTGTTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTTATCT GACTTCGCCG TCGGCGGATT TTTTGGAACT
351 GkTGAGCCTG GCCGCGATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

m257.pep

```

1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNGD EKRNEVFFW
51  KGVALGSGAX LRLFGVDDRR AADLVNKLVA EVARLEKLFS LYREDSLISR
101 LNRDGYLTSP SADFLELXSL AAIPTX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng) from *N. gonorrhoeae*:

m257/g257

10

20

30

40

50

60

593

```

m257.pep  MGRHFGRRFLTVAAVAAGTAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAD
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g257      MGRHFGRRRFLTAAAVAVAGA AVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVALGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRADLVNKKVLA EVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:
g257      LRLFGVDDRQAADLVNKKVLA EVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTXX
          |||||
g257      AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
1  ATGGGCAGGC ATTTCTGGGCG CAGGCGTTTT TTGACAGTTG CCGCCGTTGC
51 GCGGCGGGGC GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAACG CAATAAAGAT GAAAAACGCA ATGAAAATGT GTTTTTCTGG
151 AAAGGTGTCG CACTGGGTTC CGGTGCGGAG CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
251 GTTTGGA AAAA AATGTTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGT
301 CTGAACCGTG ACGGTTATTT GACTTCGCCG CCGGCGGATT TTTTGGAACT
351 GTTGAGCCTG GCCGTGATAT TCACGCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
1  MGRHFGRRRF LTVAAVAAG AAVSFLPNPF AADDEKRNKD EKRNENVFFW
51  KGVALGSGAE LRLFGVDDRR AADLVNKKVLA EVARLEKMFS LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGXQRF LTVAAVAAGXAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAX
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:
|||
a257      MGRHFGRRRFLTVAAVAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAE
          10      20      30      40      50
60

          70      80      90      100     110
120
m257.pep  LRLFGVDDRRADLVNKKVLA EVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:
||
a257      LRLFGVDDRRADLVNKKVLA EVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110
120

m257.pep  AAIFTXX
          |||||
a257      AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

g258.seq

```

1 atgcgccgct tcctaccgat cgcagccata tgcgccgtcg tcctgtgtga
51 cggattgacg gcggcgaccg gcagaccag ttcgctggcg gattatttct
101 ggtggatagt ctcgttcagc gcaatgctgc tgctggtgtt gtccgccgtt
151 ttggcacggt atgtcatatt gctgttgaaa gacaggcgca acggcggtgtt
201 cggttcgcag attgccaaac gcctttccgg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttcctg ttcggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggccgcagac aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgccca
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatc
551 cgcaccaatt cgaccagccg cttcccagca aagaacattg ggaacagatt
601 cagcagaccg gttcggttcg gagtttgaaa agcataggcg gcgtattgta
651 cgcgcaggga tgggtgtcgg caggtacgca caacggggcg gattacgcgc
701 tgttcttccg ccagccgatt cccgaaaatg tggcacagga tgcggttctg
751 attgaaaagg cgcgggcgaa atatgcccga ttgagttaca gcaaaaagg
801 tttgcagacc ttttttctgg taacctgct gattgcctcg ctgctgtcga
851 tttttcttgc gctgtaatg gactgtatt ttgcccgcg tttcgtcgaa
901 ccattctgt cgcttgccga gggcgcaaag cgggtggcg agggtgattt
951 cagccagacg cgccccgtat tgcgcaacga cgagttcgga cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc ccggcgcgca ggaagccgcc cgtcactacc tcgaagtcgt
1101 gttgatggg ttgactaccg gtgtggtggt ctctacccc ctctctgtt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctcccctct ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

g258.pep

```

1 MRRFLPIAAI CAVLLYGLT AATGSTSSLA DYFWIVSFS AMLLVL SAV
51 LARYVILLK DRRNGVFGSQ IAKRLSGMFT LVAVLPGLFL FGISAQFING
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVPO IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQ LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKGLQT FFLVTLIAS LLSIFLALVM ALYFARRFVE
301 PILSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLDG LTTGVVVSYP LSCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

m258.seq

```

1 ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCG TCCTGTTGTA
51 CGGACTGACG GCGGCAACCG GCAGACCAG TTCGCTGGCG GATTATTCT
101 GGTGGATTGT TCGGTCAGC GCAATGCTGC TGCTGGTGT GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCCG CGTGTTCG TCGGCGTTT CCGCAGATT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTG AGCAAGTCCG CATTGAATT GCGGCGAGAC AACGCCCTCG
401 GCAACGCCGT CCGGTGCAG ATAGACCTCA TCGGCGGCGC TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGCGAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAA AGCATCAACC
551 CGCACAAGCT CGATCAGCCG TTTCAGGTA AGGCGCGTTG GGAAAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCT
701 TGTTTTCCG TCAGCCGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAAGG
801 TTTGAGACC TTTTCTCTGG CAACCTGCT GATTGCTCG CTGCTGTGGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCGCGC TTTCGTGGA
901 CCCGCTCTAT CGCTTGCCGA GGGGGCGAAG CCGGTGGCGC AAGGCGATT
951 CAGCCAGACG CGCCCCGTGT TCGCAACGA CGAGTTCGGA CGCTTGACCA

```

m258.pwp

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m258.pep	MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAMLLLVL SAVLARYVILLK :					
g258	MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVSFSAMLLLVL SAVLARYVILLK :					
	10	20	30	40	50	60
	70	80	90	100	110	120
m258.pep	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLPGVSAQFINGTINSWF GNDTHEALERSLN :					
g258	DRRNGVFGSQIAKRLSGMFTLVAVLPGLFLPGISAQFINGTINSWF GNDTHEALERSLN :					
	70	80	90	100	110	120
	130	140	150	160	170	180
m258.pep	SKSALNLAADNALGNAPVQIDLIGAASLP GDMGRVLEHYAGSGFAQLAL YNAASGKIEK :					
g258	SKSALDLAADNAVSNAPVQIDLIGTASLSGNMGSVLEHYAGSGFAQLAL YNAASGKIEK :					
	130	140	150	160	170	180
	190	200	210	220	230	240
m258.pep	SINPHKL D Q P F PG KAR WEKIQR AG SV RD LES I GG VLYAQ GW LSAG TH N GRDY AL FF RQP V :					
g258	SINPHQFDQPLPDKEHWEQIQQTGSVRSL ES I GG VLYAQ GW LSAG TH N GRDY AL FF RQ P I :					
	190	200	210	220	230	240

596

	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAELSYSKKGLQTFPLATLLIASLLSIFLALVMALYFARRFVE					
g258	PENVAQDAVLIEKARAKYAELSYSKKGLQTFPLVTLIASLLSIFLALVMALYFARRFVE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDPSQTRPVLNRNDEFGRITKLFNHNTEQLSIAKEADERNRRREEAA					
g258	PILSLAEGAKAVAQGDPSQTRPVLNRNDEFGRITKLFNHNTEQLSIAKEADERNRRREEAA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVFDEQGCLKTFNKAQEILGMPLTPLWGSRRHGWHGVSQAQQLL					
g258	RHYLECVDGLTTGVVVSYPSCCRTAVFSTCHSSPLSYFX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1027>:

a258.seq

1	ATGCGCCGTT	TTCTACCGAT	CGCAGCCATA	TGCGCCGTCG	TCCTGTTGTA
51	CGGACTGACG	GCGGCAACCG	GCAGCACCAG	TTGCTGGCG	GATTATTTCT
101	GGTGGATTGT	TGCGTTCAGC	GCAATGCTGC	TGCTGGTGTT	GTCCGCCGTT
151	TTGGCACGTT	ATGTCATATT	GCTGTTGAAA	GACAGGCGCG	ACGGCGTATT
201	CGGTTGCGAG	ATTGCCAAAC	GCCTTTCCGG	GATGTTTACG	CTGGTTGCCG
251	TACTGCCCGG	CGTGTTCCTG	TTGCGGCTTT	CCGCACAGTT	TATCAACGGC
301	ACGATTAATT	CGTGGTTCGG	CAACGATACC	CACGAGGCGC	TTGAACGCAG
351	CCTCAATTG	AGCAAGTCCG	CATTGAATCT	GGCGGCAGAC	AACGCCCTTG
401	GCAACGCCAT	CCCCGTGCAG	ATAGACCTCA	TCCGCGCGGC	TTCCCTGCCC
451	GGGGATATGG	GCAGGGTGCT	GGAAACATTAC	GCCGGCAGCG	GTTTTGCCCA
501	GCTTGCCCTG	TACAATGCCG	CAAGCGGCAA	AATCGAAAAA	AGCATCAACC
551	CGCACAAAGCT	CGATCAGCCG	TTTCCAGGTA	AGGCGCGTTG	GGAAAAATC
601	CAACAGGCGG	GTTGCGTCAG	GGATTGGAA	AGCATAGGCG	GCCTATTGTA
651	CGCGCAGGGC	TGGCTGTCGG	CAGGTACGCA	CAACGGGCGC	GATTACGCCT
701	TGTTTTTCCG	TCAGCCGGTT	CCCAAAGGCG	TGGCAGAGGA	TGCCGCTCTA
751	ATCGAAAAGG	CAAGGGCGAA	ATATGCTGAG	TTGAGTTACA	GCAAAAAAGG
801	TTTGCAGACC	TTTTTCTGG	CAACCCTGCT	GATTGCCTCG	CTGCTGTCGA
851	TTTTTCTTGC	ACTGGTCATG	GCACTGTATT	TCGCCGCGCG	TTTCGTGCAA
901	CCCGTCTTAT	CGCTTGCCGA	GGGGGCGAAG	GCGGTGGCGC	AAGGCGATTT
951	CAGCCAGACG	CGCCCGGTGT	TGCGCAACGA	CGAGTTCGGA	CGCTTGACCA
1001	AGTTGTTCAA	CCACATGACC	GAGCAGCTTT	CCATCGCCAA	AGAAGCAGAC
1051	GAGCGCAACC	GCCGGCGCGA	GGAAGCCGCC	AGACATTATC	TCGAATGCGT
1101	GTTGGAGGGG	CTGACCACGG	GCGTGGTGGT	GTTTGACGAA	CAAGGCTGTC
1151	TGAAAACCTT	CAACAAAGCG	GCGGAACAGA	TTTTGGGGAT	GCCGCTTACC
1201	CCCCTGTGGG	GCAGCAGCCG	GCACGGTTGG	CACGGCGTTT	CGGCGCAGCA
1251	GTCCCTGCTT	GCCGAAGTGT	TTGCCGCCAT	CGGCGCGGCG	GCAGGTACGG
1301	ACAAACCGGT	CCATGTGAAA	TATGCCGCGC	CGGACGATGC	CAAAATCCTG
1351	CTGGGCAAGG	CAACCGTCCT	GCCCGAAGAC	AACGGCAACG	GCGTGGTAAT
1401	GGTGATTGAC	GACATCACCG	TTTTGATACA	CGCGCAAAAA	GAAGCCGCGT
1451	GGGGCGAAGT	GGCAAAACGG	CTGGCACACG	AAATCCGCAA	TCCGCTCAGC
1501	CCCATCCAGC	TTTCTGCCGA	ACGGCTGGCG	TGGAAATTGG	GCGGGAAGCT
1551	GGACGAGCAG	GACGCGCAAA	TCCTGACACG	TTGACCGAC	ACCATCATCA
1601	AACAAGTGGC	GGCATTAAAA	GAAATGGTCG	AGGCATTCCG	CAATTACGCG
1651	CGTTCCCTT	CGCTCAAATT	GGAAATCAG	GATTTGAACG	CCTTAATCGG
1701	CGATGTGTTG	GCATTGTACG	AAGCTGGTCC	GTGCCGGTTT	GCGGCGGAAC
1751	TTGCCGGCGA	ACCGCTGATG	ATGGCGGCGG	ATACGACCGC	CATGCGGCGAG
1801	GTGCTGCACA	ATATTTTCAA	AAATGCCGCC	GAAGCGGCGG	AAGAAGCCGA
1851	TGTGCCCGAA	GTCAGGTAA	AATCGGAAGC	GGGCGAGGAC	GGACGGATTG
1901	TCCTGACAGT	TTGCGACAAC	GGCAAGGGGT	TCGGCAGGGA	AATGCTGCAC
1951	AATGCCTTCG	AGCCGTATGT	AACGGACAAA	CCGGCTGGAA	CGGGATTGGG
2001	ACTGCCCGTG	GTGAAAAAAA	TCATTGAAGA	ACACGGCGGC	CGCATCAGCC
2051	TGAGCAATCA	GGATGCGGGC	GGCGCGTGTG	TCAGAATCAT	CTTGCCAAAA
2101	ACGGTAGAAA	CTTATGCGTA	G		

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```

a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLDEQ DAQILTRSTD TTIKQVAALK EMVEAFRNYA
551 RPSLKLLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601 VLHNIFKNAA EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIEEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*

```

m258/a258 99.0% identity in 584 aa overlap

m258.pep	10	20	30	40	50	60
	MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAML VLLVLSAVLARYVILLK					
a258	MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAML VLLVLSAVLARYVILLK					
	10	20	30	40	50	60
m258.pep	70	80	90	100	110	120
	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL					
a258	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL					
	70	80	90	100	110	120
m258.pep	130	140	150	160	170	180
	SKSALNLAADNALGNAVQIDLIGAASLPDGMGRVLEHYAGSGFAQLALYNAASGKIEK					
a258	SKSALNLAADNALGNAIPVQIDLIGAASLPDGMGRVLEHYAGSGFAQLALYNAASGKIEK					
	130	140	150	160	170	180
m258.pep	190	200	210	220	230	240
	SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV					
a258	SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV					
	190	200	210	220	230	240
m258.pep	250	260	270	280	290	300
	PKGVAEDAVLIEKARAKYAE LSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE					
a258	PKGVAEDAVLIEKARAKYAE LSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE					
	250	260	270	280	290	300
m258.pep	310	320	330	340	350	360
	PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA					
a258	PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA					
	310	320	330	340	350	360
m258.pep	370	380	390	400	410	420
	RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLTPLWGSSRHGW HGVSAQQSLL					
a258	RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLTPLWGSSRHGW HGVSAQQSLL					
	370	380	390	400	410	420
m258.pep	430	440	450	460	470	480
	AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK					
a258	AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK					

598

	430	440	450	460	470	480
	490	500	510	520	530	540
m258.pep	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDEQDAQILTRSTDTIVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDEQDAQILTRSTDTIHKQVAALK					
	490	500	510	520	530	540
	550	560	570	580	589	
m258.pep	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNI FKNAEEAAEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

g259.seq

```

1  atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaactctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgcgcgatt gtccgccgtc
151 gcgctggtgt ggctggcgtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatacacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaatgttc
301 gccctgctgg tcaaaaacca cggcaaaggc atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccc acgacgaaga cgcgcgacg attgcccgcg
401 agttggcaaa aatggatatg ttgcgattgg ggacggacgc ggtcgccctg
451 ggcgaaacct atggcgcggt gttcgccgat attttcgagt tgcggcgccg
501 tttggaagg cgcggttca aaggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgcccgttc gaaacggcgt tggatttggg
601 cgcgctcaat caggcggtta gggaaatctc gaaaacgccg gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

g259.pep

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAELAKMDM PALGTDVAAS
151 GETYGRVFD IFELSAALER RAFKGILKLT AEYKHLRRC LPFGNGVGFG
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

m259.seq (partial)

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGCTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACKGACGC GGTGCGCTCG
451 GGCgAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGMGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGGMGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

m259.pep (partial)

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAELAKMDM PALGTDVAAS

```

599

151 GETYGRVFAD IFELSXALEG RAFKGLMLKT AEYKXHLRRC LPFGNGVGVG
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGMAEQVRFKAE					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSXALEGRAFKGLMLKT					
g259	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALERRAFKGILKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRC LPFGNGVGVGR TQSGVAGDF KNIR					
g259	AEYKXHLRRC LPFGNGVGVG FRAQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

1	ATGATGATGC	ACGCTTCTGT	CCAAAGCCGT	TTCGCACCGA	TACTTTATGT
51	TTTGATTTTC	TTTGCCGGTT	TTTGACCGC	GCAATCTGG	TTCAATCAGA
101	AAGCCTATAC	TGAAGAGCTG	CCTCCGCTTC	TGTCCGCATT	GTCCGCCGTC
151	GCGCTGGTGT	GGCTGGCGTG	GGCGTTCGTG	TCGGCGCGTT	CAAAGGCTAA
201	GGCGGAAAAG	TTCTACCGCG	AAAAAATGAT	ACAGAACGAA	AGCATACACC
251	CCGTCTTGCA	CGCTTCTTTG	CAACACTTGG	AACACAAGCC	GCAATGCTC
301	GCCCTGCTGG	TCAAAAACCA	CGGCAAAGGG	ATGGCGGAAC	AGGT CAGGTT
351	CAAGCGGAA	GTGCTGCCCG	ACGACGAAGA	CGCGCGCACG	ATTGCCGCCG
401	AGTTGGCAA	AATGGATATG	TTTGCATTGG	GGACGGACGC	GGT CGCCTCG
451	GGCGAAACCT	ATGGACGCGT	GTTCCGCCGAT	ATTTTCGAGT	TGTCGGCGGC
501	TTTGGAAGGG	CGCGCGTTCA	AAGGAATGTT	GAAACTGACG	GCGGAATATA
551	AAAA.CATCT	TCGGCGATGC	CTGCCGTTTC	GAAACGGCGT	TGGAGTTGGG
601	CGCGCTCAAT	CAGGCGTTGC	AGGAGATTTC	AAAAACATCG	GAAAAGTCCA
651	A				

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

1	MMMHASVQSR	FAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALSAV
51	ALVWLAWAFV	SARSKAKAEK	FYREKMIQNE	SIHPVLHASL QHLEHKPQML
101	ALLVKNHKGK	MAEQVREKAE	VLPDDEDART	IAAELAKMDM FALGTD AVAS
151	GETYGRVFAD	IFELSAALEG	RAFKGLMLKT	AEYKXHLRRC LPFGNGVGVG
201	RAQSGVAGDF	KNIGKVQ		

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					

600

	10	20	30	40	50	60
m259. pep	70	80	90	100	110	120
a259	70	80	90	100	110	120
m259. pep	130	140	150	160	170	180
a259	130	140	150	160	170	180
m259. pep	190	200	210			
a259	190	200	210			

SARSKAKAEK FYREKMIQNESIHPVXHASLOHLEHKPQILALLVKNHGKGMAEQVRFKAE
 SARSKAKAEK FYREKMIQNESIHPVLHASLOHLEHKPQMLALLVKNHGKGMAEQVRFKAE
 VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFEL SXALEGRAFKGMLKLT
 VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFEL SAALEGRAFKGMLKLT
 AEYKXHLRRCLPFGNGVGVGRTQSGVAGDFKNIR
 AEYKXHLRRCLPFGNGVGVGRAQSGVAGDFKNIGKVQ

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1. seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCGATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGTGCGTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGGCGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1. pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTD AVAS
151 GETYGRVFAD IFELSAALE
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1. seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCGATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGCGCGTT CAAAGGCCAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTCTG AAACGGCGTT GGAGTTGGGC
601 GCACTCAATC AGGCGTTGCA GGAGATTCA AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1. pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTD AVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQAQLEIS KTSEKSKRIF Y*
  
```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF FAGELTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
m259-1	MMMHASVQSRFAPILYVLIF FAGELTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEKFYREKMIQNESIHPVLHASLOHLEHKPQMLALLVKNHKGKMAEQVRFKAE					
m259-1	SARSKAKAEKFYREKMIQNESIHPVLHASLOHLEHKPQILALLVKNHKGKMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFDIFELSAALE					
m259-1	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFDIFELSAALEGRAFGMLKLT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTGCGCGTT TTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCTAA
201 GCGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTCCGCTCG
451 GCGGAACCT ATGGACCGGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTCCG AAACGGCGTT GGAGTTGGGC
601 GCGCTCAATC AGCGGTTGCA GGAGATTTC AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGELTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL OHLEHKPQML
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDVAS
151 GETYGRVFDAD IFELSAALEG RAFRGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQALQEIS KTSEKSKRIF Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF FAGELTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
m259-1	MMMHASVQSRFAPILYVLIF FAGELTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEKFYREKMIQNESIHPVLHASLOHLEHKPQMLALLVKNHKGKMAEQVRFKAE					
m259-1	SARSKAKAEKFYREKMIQNESIHPVLHASLOHLEHKPQILALLVKNHKGKMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFDIFELSAALEGRAFGMLKLT					
m259-1	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFDIFELSAALEGRAFGMLKLT					
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALELGALNQALQEISKTSEKSKRIFYX					
m259-1	AEYKNIFGDACRSETALELGALNQALQEISKTSEKSKRIFYX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

602

```

1  atgggtgctg  gtgtagtatt  cgttgtcttt  cagccgttct  tcagcctgtt
51  tcgagcgttg  ttcgagggcg  gtagtcggtat  agtcgagggg  gcgcacgatg
101 cgcgtgaatg  cgacttcttg  tccgaggaat  ttaccctgat  ccggatcggg
151 gatgttttta  ttgattcggg  aggtcagata  acggcccggg  tctttcaggc
201 ctttggtgta  aacctggtcg  cctttgggtg  acagcagcct  gccttccggg
251 cccgagagca  ggcgcggcgc  ggcagcgggt  tctttgctgg  aaacgatttg
301 cgggtgctgc  ataaagacgc  ggtagaagtt  gacatcgatg  gcgggaatac
351 cgtatccgga  cacttcctta  tccggactga  ttttgacgac  ggggatgccg
401 tctgtctgtt  ccaagccgag  gcgcgggttc  ccgccaacgt  agcgcaacac
451 caatacctgg  cccggataaa  tcaggtcggg  attgtggatt  tgatcccggt
501 tcgcgcccc  caggggggga  ccattgccac  gggctgtaca  ggtatttgcc
551 cgaaatacc  cacaggtgt  cgcctgttt  ga

```

This corresponds to the amino acid sequence <SEQ ID 1042; ORF 260.ng>:

g260.pep

```

1  MGAGVVFVVF QPFSSLFRL FEGGVGIVEG AHDAECDFL SEEFTRIRIG
51  DVFIDSVGQI TARFFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVLHKDAVEV DIDGNTVSG HFLIRTDfDD GDAVCLFQAE ARFAANVAQH
151 QYLARINQVG IVDLIPVRAP QGGTIATGCT GICPKYPTGC RPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1043>:

m260.seq

```

1  ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTCTT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCGGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTFTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CCTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGwCA sGCGCGGyGC GGCAGCGGTT TCTTTGCGGG AAACGATTG
301 CGGATGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTCC CCGTCAACGT GCGCGAACAC
451 CAATACCTGG TCCGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTyCCA CAG

```

This corresponds to the amino acid sequence <SEQ ID 1044; ORF 260>:

m260.pep

```

1  MGAGMVVFVF RPFSSLFRL FEDRVGIVEG AHDAECDFL PEEFTRIRIG
51  DVFIDSVGVV AARLFQAFGV NPGAFGVQQP AFRARXXARX GSGFFAGNDL
101 RMPHKDAVEV DIDGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVIRINQVG IVDLIPVRVP Q

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/g260

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFSSLFRLFEDRVGIVEGAHDAECDFLPEEFTRIRIGDVFIDSVGQV					
g260	MGAGVVFVVFQPFSSLFRLFEGGVGIVEGAHDAECDFLSEEFTRIRIGDVFIDSVGQI					
	10	20	30	40	50	60
m260.pep	AARLFQAFGVNPGAFGVQQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGNTVSG					
g260	TARFFQAFGVNPGAFGVQQPAFRAREQARRGSGFFAGNDLRVLHKDAVEVDIDGNTVSG					
	70	80	90	100	110	120
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVIRINQVGIVDLIPVRVPQ					
g260	HFLIRTDfDDGDAVCLFQAEARFAANVAQHQYLARINQVGIVDLIPVRAPQGGTIATGCT					
	130	140	150	160	170	180

g260

GICPKYPTGCRPV

190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

a260.seq

```

1  ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CCACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CCTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GCGCGCGGCG GGCAGCGGTT TCTTTCGGG AAACGATTTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTCT CCGTCAACGT GCGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC CCATTGCCAC GGGCTGTACA GGTATTGCCC
551 CGAAATGCCC CACAGGTGT CGCCCTGTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

a260.pep

```

1  MGAGMVFFVF RPFSSLFRL FEDRVGIVEG AHDAECDFL PEEFTRIRIG
51  DVFIDSVGVQ AARLFQAFGV NPGAFVQVQP AFRAREQARR GSGFFAGNDL
101 RVPKDAVEV DIDGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*

```

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVFFVFRPFSSLFRLFEDRVGIVEGAHDAECDFLPEEFTRIRIGDVFIDSVGVQV					
a260	MGAGMVFFVFRPFSSLFRLFEDRVGIVEGAHDAECDFLPEEFTRIRIGDVFIDSVGVQV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAFVQVQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGNTVSG					
a260	AARLFQAFGVNPGAFVQVQPAFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGNTVSG					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQINQVGIVDLIPVRVPQ					
a260	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQINQVGIVDLIPVRVPQAAXIATGCT					
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

g261.seq

```

1  atggagcttg ggcataatcgt attccttggtg ctttgcgcg gttcagacgg
51  cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag
101 ctcgggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctgttcgagg atgtagtcca acacgcccatt ttcgtccgcc aacgcccacg
201 tttgcgcctt ggtcaggtac atcagcgggc tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcatg gatttgacga acacgccgcg
301 gcagtcggga tagcccgaaa aatcggtttc gcacacgccc gcgatgatgt
351 gccggatacc ctgcccttgg gcaaaaatgg cggcgtaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgcccgtgt cggcggtttc
451 gatggcgggc gtttcgatgg cggcggtttc gtccatcagg gcgttggtgcg
501 taatctgccg catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tcctgcgcga tccactctgc gcgttccagc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggctt ggacgttttc gcgccgtag gtttgattg

```

651 cctgaatcag gcaggtggtc gaatcctgac cgcccagaaa gatgaccaag
701 gcttttttgg ttga

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep

1 MELGHIVFLV LCARSDGLFT FQTFRQPAFA QDTARAFAAA ADDTLVAGVG
51 LFADVVQHAH FVRQRPRLRL GQVHQRRVDL KIVVHRQIKG NVHGFDEHAA
101 AVGIARKIGF AHARDDVPDT LPFGKNGGVK QEKRVTPVHK GIGNAVVGGF
151 DGGGFDGGG VHQGVVRNLP HQAQIEYGLT DTQILRDPLC AFQLDGMALP
201 VSEGDLDFV APVGLDCLNQ AGGRILTARE DDQGLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq

1 ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG
51 CCTTTTACT TTCCAGATAT TCCGCCAGCC cGcGTTCCG CAGATACAG
101 CTCGGGCATT CGCGgCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCACGCCCAT TTCGTCGCGC AACGCCACG
201 TTTGCGCCTT GGTACAGATAC ATCAGCGGCG TGTGGATTTG AAAATCATAG
251 TCCATCGCCA AATTAAGGT AACGTTTCATC GATTTGACAA ACACGTCGCG
301 GCAGTCGGGA TAGCCGAGA AGTCGGTTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 gCGTTGCGGC CGTCTACAAA GGTATTGCGA ACGCCGTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GgCTcAAGTC GAGTACGGTT TGTGTGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTG TTGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep

1 MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51 LLADIVQHAH FVRQRPRLRL GQIHQRRVDL KIIVHRQIKG NVHRFDKHVA
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRAAVYK GIRNAVFGSF
151 DGGGVVHGGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFPVGL DCLNQAGGRI LTARKDDQGL LV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng) from *N. gonorrhoeae*:

m261/g261

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
	:::					
g261	MELGHIVFLVLCARSDGLFTFQTFRQPAFAQDTARAFAAAADDTLVAGVGLFADVVQHAH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA AVGIAGEVGF AHARDDVPYP					
g261	FVRQRPRLRLGQVHQRRVDLKIVVHRQIKGNVHGFDEHAA AVGIARKIGF AHARDDVPDT					
	70	80	90	100	110	120
	130	140	150	160	170	
m261.pep	LPFGVNRGIEQEKRAAVYKGIRNAVFGSFDGGGV-----VHQGIVRNLPHQAVVEYGLF					
	::: : :					
g261	LPFGKNGGVKQEKRVTPVHKGIGNAVVGGFDGGGFDGGGFVHQGVVRNLPHQAQIEYGLT					
	130	140	150	160	170	180
	180	190	200	210	220	230
m261.pep	DAQILRNPAFTFQLDGMALPVLESNGLDVFPVGLDCLNQAGGRILTARKDDQGLLVX					
	: : : : : : : : : : :					
g261	DTQILRDPLCAFQLDGMALPVSEGDLDFVFPVGLDCLNQAGGRILTAREDDQGLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1  ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCCAAG
201 TTTGCGCCTT GGTCAAGTAC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGGA AGTCGGTTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTTCGGA ACGCGTTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGTT TGTGTGACGC CCAAATCCTG CGCAATCCAG
551 CGGCGACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1  MELGHIVFLM VCACSDGLFT FOIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPSLRL GQIHQRRVDL KIIVHRQIKG NVHGFDKHTV
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFOLD GMALPVLESN
201 GLDVFAFVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

m261.pep	10	20	30	40	50	60
	MELGHIVFLMVCACSDGLFTFOIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
a261	MELGHIVFLMVCACSDGLFTFOIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQRAH					
	10	20	30	40	50	60
m261.pep	70	80	90	100	110	120
	FVRQRPRRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVAAVGIAGEVGFHAARDDVPYP					
a261	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHGFDKHVTAVGIAGEVGFHAARDDVPYP					
	70	80	90	100	110	120
m261.pep	130	140	150	160	170	180
	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAVVEYGLFDAQIL					
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAVVEYGLFDAQIL					
	130	140	150	160	170	180
m261.pep	190	200	210	220	230	
	RNPAGTFOLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
a261	RNPAGTFOLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1  atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgcca
51  accgcgcgta gaggccgtac ccaaaaacaa cggtttatc cccaacctca
101 tcggcgattt ggcaaacgcc cccgaagctt tggcgtttta ccaagaagtc
151 ggcaagctca acgccgcca cagcctgacc gccggcggaag tcgaagtgat
201 ccggtatcat gccgtccgca ccaaccaatg cagcttctgc gtggcagggc
251 acaccaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgccccgc ctttgccggc aggtaaatct gacgatgcca aactcggcgc
351 gcttgccgcc ttcacccaag ccgtaaatgc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```

q263.ppt

```

1 MARLTVHTLE TAPEAAKPRV EAVPKNNGFI PNLIGVLANA PEALAFYQEV
51 GKLNAANSLT AGEVEVIRII AVR TNQCSFC VAGHTKLATL KLLSEQSLN
101 AARALAAGKS DDAKLGALAA FTQAVMAKKG AVSDELNAF LEAGYNRQQA
151 VEVVMGVALA TLCNYANL LA QTEINPKLOA YA*

```

m263.seq (partial)

1	GCAGCAGGCG	AATTTGACGA	TGCCAAACTC	GGCGCGCTCG	CCGCCCTTCAC
51	CCAAGCCGTA	ATGGCGAAAA	AAGGCGCGGT	ATCCGACGAG	GAACTCAAAG
101	CATTTTTCGA	TGCGGGCTAC	AACCAACTAC	AGGCAGTCTGA	AGTCGTGATG
151	GGCGT.AsyC	TGGCAACCCCT	GTGCAACTAC	GTCAACAACC	TCGGACAAAC
201	CGAAATCAAC	CCGCAATTGC	AGGCTTACGC	CTGA	

m263.pep (partial)

1	GCAGCAGGCG	AATTTGACGA	TGCCAAACTC	GGCGCGCTCG	CCGCGCTTCAC
51	CCAAGCCGTA	ATGGCGAAAA	AAGGCGCGGT	ATCCGACGAG	GAACTCAAAG
101	CATTTTTCGA	TGCGGGCTAC	AACCAAGACG	AGGCAGTCGA	AGTCGTGATG
151	GGCGT.AsyC	TGGCAACCTT	GTGCAACTAC	GTCAACAACC	TCGGACAAAC
201	CGAAATCAAC	CCGGAATTGC	AGGCTTACGC	CTGA	

ORF 263 shows 85.7% identity over a 77 aa overlap with a predicted ORF (ORF 263.ng) from *N. gonorrhoeae*:

m263/g263

m263.pep
 AAGEFDDAKLGALAAFTQAVMAKKGAVSDE
 |||: |||||
 g263
 QCSFCVAGHTKLATLKLLEQSLNAARALAAGKSDDAKLGALAAFTQAVMAKKGAVSDD
 80 90 100 110 120 130
 40 50 60 70
 m263.pep
 ELKAFFDAGYNQQQAVEVVMGVXLATLCNYVNNLGQTEINPELQAYAX
 |||: |||||
 g263
 ELNAFLEAGYNRQQAVEVVMGVALATLCNYANNLAQTEINPKLQAYAX
 140 150 160 170 180

a263.seq

1	ATGGCACGTT	TAACCGTACA	CACCCTCGAA	ACCGCCCCG	AAGCCGCCAA
51	AGCGCGCGTC	GAGGCGGTAC	TTCAAACAA	CGGCTTTATC	CCCAACCTTA
101	TCGGCGTATT	ATCAAACGCC	CCCGAGCTT	TGGCGTTTTA	CCAAGAAGTC
151	GGCAAGTCA	ACGCGCCAA	CAGCTGACC	CGCGCGAAG	TCGAAGTAAT
201	CGAGATTATT	CGCGCGCCGA	CCAACCAATG	CGGCTTCTGC	GTGGCAGGGC
251	ACACCAAAC	CGCAACCTG	AAAAAACTCC	TTTCCGAACA	ATCCGTCAAA
301	GCCGCGCGCG	CTTTGGCGGC	AGGCGAATTT	GACGATGCTA	AACTCGGCGC
351	GCTCGCGGCT	TTTACCCAAG	CCGTATATGGC	AAAAAAGGC	GCGGTATCCG
401	ACGAGGAAC	CAAGCAATT	TTTGATGCGG	GCTACAACCA	GCAGCAGGCA
451	GTCGAAGTCG	TGATGGCGT	AGCCTTGGC	ACTTTGTGCA	ACTACGTCAA
501	CAACCTCGGA	CAAACCGAAA	TCAACCCCGA	ATTGAGGCTT	TACGCTCGA

a263. pep

```

1 MARLTVHTLE TAPEAAKARV EAVLQNGGFI PNLIGVLSNA PEALAFYQEV
51 GKLNAAANSLT AGEVEVIQII AARTNQCQFC VAGHTKLATL KLLSEQSVK
101 AARALAAGEF DDAKLGALAA FTQAVMAKKG AVSDEELKAF FDAGYNQQQA
151 VEVVMGVALA TLCNYVNNLG OTEINPELOA YA*

```

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m263/a263 97.4% identity in 77 aa overlap

					10	20	30
m263.pep					AAGEFDDAKLGALAAFTQAVMAKKGAVSDE		
a263	QCGFCVAGHTKLATLKKLLSEQSVKARALAA	GEFDDAKLGALAAFTQAVMAKKGAVSDE					
	80	90	100	110	120	130	

		40	50	60	70
m263.pep	ELKAFFDAGYNQQQAVEVVMGXLLATLCN	YVNNLGQTEINPELOAYAX			
a263	ELKAFFDAGYNQQQAVEVVMGVALATLCN	YVNNLGQTEINPELOAYAX			
	140	150	160	170	180

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

g264.seq

```

1   ttgactttaa cccgaaaaac ccttttcttc ctcaccgccg cgttcggcac
51  acactccctt cagacggcat ccgccgacgc agtgggtcaag ccgaaaaaac
101 tgcacgcctc cgccaaccgc agctacaaag tcgccgaatt cacgcaaacc
151 ggcaacgcct cgtggtagcg cggcaggttt cacggggcgca aaacttccgg
201 cggagaccgc tacgatatga acgcctttac cgccgcccac aaaaccctgc
251 ccattccccag ccatgtgcgc gtaaccaaca ccaaaaacgg caaaagcgctc
301 atcgtccgcg tcaacgaccg cggccccttc cacggcaacc gcatcatcga
351 cgtatccaaa gccgcccgcg aaaaattggg ctttgtcagc caagggacgg
401 cacacgtcaa aatcgaacaa atcgtcccgc gccaatccgc accggttgcc
451 gaaaaacaaag acatctttat cgacttgaaa tctttcggtc cggaacacga
501 agcacaagcc tatctgaacc aagccgccca aaatttcgcc gtttcgctcat
551 caagcccgaa cctctcggtt gaaaaacgcc gttacgaata cgttgtaaaa
601 atggggccgt ttgcctcgca ggaacgcgcc gccgaagccg aagcgcaggg
651 acgcggtatg gttcgggcgg tactgacctc cggttga

```

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

g264.pep

```

1   LTLTRKTLFL LTAAFGTHSL QTASADAVVK PEKLHASANR SYKVAEFTQT
51  GNASWYGGRF HGRKTSGGDR YDMNAFTA AH KTLPIPSHVR VTNTKNGKSV
101 IVRVNDRGPF HGNRIIDVSK AAAQKLG FVS QGTAHV KIEQ IVPQGSAPVA
151 ENKDIFIDLK SFGTEHEAQA YLNQAAQ NFA ASSSSPNLSV EKRRYEYVVK
201 MGPFPASQERA AEAEQAQARGM VRVLTSG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

m264.seq

```

1   TTGACTTTAA CCCGAAAAAC CCTTTTCCTT CTCACCGCCG CATTCCGGCAG
51  ACACCTCCCTT CAGACGGCAT CCGCCGACGC AGTGGTCAAG GCAGAAAAAC
101 TGCACGCCTC CGCCAACCGC AGCTACAAAG TCGCCGGA AA ACGCTACACG
151 CCGAAAAACC AAGTCGCCGA ATTACGCAA ACCGGCAACG CCTCGTGGTA
201 CGGCGGCAGG TTTCACGGGC GCAAACTTC CGCGGAGAA CGATACGATA
251 TGAACGCCTT TACCGCCGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAAA CGGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CCGCGGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAAATT GGGCTTTGTC AACCAAGGGA CGGCACACGT CAAAATCGAA
451 CAAATCGTCC CGGGCCAATC CGCACCGGTT GCCGAAAACA AAGACATCTT
501 TATCGACTTG AAATCTTTTC GTACGGAACA CGAAGCACAA GCCTATCTGA
551 ACCAAGCCGC CCAAACTTC GCCGTTTCGT CATCGGTAC GAACCTCTCG
601 GTTGAAAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTTACCTC
651 GCAGGAACGC GCCGCCGAAG CCGAAGCTCA GGCGCGCGGT ATGGTTCGGG
701 CGGTATTGAC CGCCGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264.pep

```

1   LTLTRKTLFL LTAAFGTHSL QTASADAVVK AEKLHASANR SYKVAGKRYT
51  PKNQVAEFTQ TGNASWYGGR FHGRKTS GGE RYDMNAFTA HKTLPISYV
101 RVTNTKNGKS VIVRVNDRGP FHGNRIIDVS KAAQKLG FV NQTAHV KIE
151 QIVPQGSAPV AENKDIFIDL KSFGEHEAQ AYLNQAAQNF AVSSSGTNLS
201 VEKRRYEYVV KMGPPTSQER AAEEAQAARG MVRVLTAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTS GGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHGRKTS GGDYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLK SFGTEHEAQ					
g264	FHGNRIIDVSKAAQKLG FVSQGT AHVKIEQIVPGQSAPVAENK DIFIDLK SFGTEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGT NLSVEKRRYEYVVKMGPF TSQERAAEAEQA RGMVRAVLTAGX					
g264	AYLNQAAQNFAASSSP NLSVEKRRYEYVVKMGPF ASQERAAEAEQA RGMVRAVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

1	TTGACTTTAA	CCCGAAAAAC	CCTTTTCCTC	CTCACC GCCG	CATTCCGGCAT
51	ACATTCCTTT	CAGACGGCAT	CCGCCGACGC	AGTGGTCAGG	GCAGAAAAAC
101	TGCACGCCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGAAA	ACGCTACACG
151	CCGAAAAACC	AAGTCGCCGA	ATTCACGCAA	ACCGGCAACG	CCTCGTGGTA
201	CGCGCGCAGG	TTTCACGGGC	GCAAACTTC	CGGCGGAGAA	CGATACGATA
251	TGAACGCCTT	TACCGCCGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGCAAAAGC	GTCATCGTCC	CGGTCAACGA
351	CCGCGGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCCG
401	CGCAAAAT	GGGCTTTGTC	AACCAAGGGA	CGGCGCACGT	CAAAATCGAA
451	CAATCGTCC	CGGGCCAATC	CGCACC GGTT	GCCGAAAACA	AAGACATCTT
501	CATCGACTTG	AAATCTTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCGC	CCAAAACCTG	GCTTCATCGG	CATCAAACCC	GAACCTCTCG
601	GTTGAAAAAC	GCCGTTACGA	ATACGTCGTC	AAAATGGGAC	CGTTTGCTC
651	GCAGGAACGC	GCCGCCGAGG	CCGAAGCTCA	GGCGCGCGGT	ATGGTTCGGG
701	CGGTATTAAC	CGCCGGTTGA			

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

1	LTLTRKTLFL	LTAAFGIHSF	QTASADAVVR	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGR	FHGRKTS GGE	RYDMNAFTA	AHKTLPIPSYV
101	RVNTKNGKS	VIVRVNDRGP	FHGNRIIDVS	KAAQKLG FV	NQGT AHVKIE
151	QIVPGQSAPV	AENKDIFIDL	KSFGTEHEAQ	AYLNQAAQNL	ASSASNP NLS
201	VEKRRYEYV	KMGPFASQER	AAEAEQA RQ	MVRAVLTAG*	

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQTAHV KIEQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ					
a264	FHGNRIIDVSKAAQKLG FVNQTAHV KIEQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF T SQERAAEAE AQARGMVR AVL TAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF T SQERAAEAE AQARGMVR AVL TAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```

m265 . seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GGCGCGGCTG ATGATTTTGT CTTGTTTGTG GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGGCGGAA
151 ATGCTCAGCA GTGCGGTGTC GCGCGAGGTC AAGAGAAGGT GTTTGATGTT
201 CATAT.TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251 AGGTATCAAA TAACCGTCAG CCGCGCGTCA ATACCGCCCG AACCATACCG
301 CGCGCCTGAG CTTTCGGCTTC GCGCGCGCGT TCCTGCGAGG TAAACGGTCC
351 CATTTTGACG ACGTATTCGT AA
  
```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```

m265 . pep
1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MLSSAVAAEV KRRCLMFI XFVNRGLENV DINKVSNNRQ PAVNTARTIP
101 RAXASASAAR SCEVNGPILT TYS*
  
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265 . pep	MSVILPPTRANAFA SAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLS AVAAEV					
g265	MSVILPPTRAQAFA SAWARLMILSCLPCWCAACPWSSSPCPSWWASAGAEMPNS AVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFAFVNRGLENV DINKVSNNRQ PAVNTARTIP RAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNG DINKVSNNRQPEVSTARTIP RACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1067>:

a265 . seq

```

1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GGC GCGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCCATCA GTGCGGTTGC GGC GCGGCTC AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... ..GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCCGAAC CATACCGCGC
301 GCCTGAGCTT CGGCCTCGGC GGC GCGTTC TCGAGGCAA ACGGTCCCAT
351 TTTGACGACG TATTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

a265 . pep

```

1  MSVILPPTRA NAAFAWARL MILSCLLCWC ACPWSSSPC PSWWASAGAE
51  MPISAVAAAV KRRRLKFIFA PAKYLX..XC LKDVKAGHQP AVNTARTIPR
101 A*ASASAARS CEANGPILTT YS*

```

m265/a265 79.7% identity in 123 aa overlap

	10	20	30	40	50	60
m265 . pep	MSVILPPTRANAFAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSAVAAEV					
a265	MSVILPPTRANAFAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMPISAVAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFIXFAFVNRGLENDINKVSNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
	: : : : : : : : : : : : : : :					
a265	KRRRLKFI---FAPAKYLXXCLKDKVAGHQPAVNTARTIPRAXASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
a265	TYSX					
	120					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

g266 . seq

```

1  agttcagacg gcatcgccgc cgacaatgcc caaacagaaa gcccatcatg
51  accgcatcca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcttc acgaccagac tggtcggcgt ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgatc gagctggcgg caggtttcgc gctgaccgcc
201 tctcttgccct acatcctcga atcccgtagc ggagcggtac acaatcaggg
251 ttgggagttt tacgccaccg tcgtctgcct gtacctcatt ttcgccttcc
301 cgtgttcgt gcggcggtat ttttggcaca cgcgcaacag ggaataa

```

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

g266 . pep

```

1  MQFRRHRRRO CPNRKPIMTA SMYILLVLAL IFANAPFLT RLFGVAALKR
51  KHFGHHLIEL AAGFALTASL AYILES RAGA VHNQGWEFYA TVVCLYLIFA
101 FPCFVRRYFW HTRNRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

m266 . seq

```

1  ATGCCGTTCC GCAACGCGTt cAGACGCGCAT CGCCGCCGAC AACGCCTAAA
51  CAGAAAGCCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGGCAC
101 TCATCTTTGC CAACGCCCCC TTCCTCACGA CCAGACTGTT CGGCGTGGCC
151 rCACTCAAGC GCAAACATTT CGGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTsGAATCC CGTGCAAGAT
251 CGGTACACGA TCAGGGTTGG GAGTTTATG CCACAGTCGT CTGCCTGTAC
301 CTGATTTTGG CGTTCCATG TTTGTGTGG CCGTATTTT GGCACACGCG
351 CAACAGGGAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

m266.pep

```

1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101 LIAFPFCFVW RYFWHTRNRE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

m266/g266

```

              10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
           |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g266       MQFRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH
              10      20      30      40      50

              70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLYLIFAFPCFVWRYFWHTRNREX
           :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
g266       LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLYLIFAFPCFVRRYFWHTRNREX
              60      70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

a266.seq

```

1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTTG CTGCTTGCCCT
101 TGATTTTTCG CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151 CCGCTCAAGC GCAAACATTT CGGACACCAC CTGATCGAGC TGGCGGCAGG
201 TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTCGAATCC CGTGC GGAG
251 CGGTACACGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
301 CTGATTTTTC CGTTCCCTG TTTCGTGTGG CGGTATTTT GGCACACGCG
351 CAACAGGGAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

a266.pep

```

1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101 LIAFPFCFVW RYFWHTRNRE *

```

m266/a266 91.7% identity in 120 aa overlap

```

              10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
           |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a266       MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTLKLGIVPLKRKHFGHH
              10      20      30      40      50      60

              70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLYLIFAFPCFVWRYFWHTRNRE
           :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
a266       LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLYLIFAFPCFVWRYFWHTRNRE
              70      80      90      100     110     120

```

```

m266.pep  X
           |
a266      X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

g267.seq

g267.pep

m267.seq

m267.pcp

m267/g267

a267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	GGTCGGGCAG	GCTTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TGGTCAGGTC	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTGC	CGTCTTCGGC
151	TTCTTCCGAT	TCGATGTTGA	TGCCCATATG	GGGGCAAACG	GCTTCACACA
201	ATTTACACGC	GATGCAGCGT	TCCTCGCCGT	TTGGATAACG	CGGTTCGCGC
251	TGCAGACCGC	GGAAACGCAC	GGATTTCGGC	GTTTTCTCTT	CGGGAAAATA
301	AATCGTGTCT	TTCGCGGGCA	AAAAGTTTTT	GAGCGTTACG	CCCATACCTT
351	TTACCAATTC	GCCGAAGCAGA	AAGGTTTTTA	CTAA	

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDVV	TLGAARTVFTFFRFDVNRHC			
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFAFFRFDVDRHC			
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPLFAVRIP	PLRVQTAETHGLRRFLFGE	INCVFAGEKVFERYAHTFYQF			
a267	GANGFTQFTRDAAFLAVWIT	ALRVQTAETHGLRRFLFGK	INRVFAGKKVFERYAHTFYQF			
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaattt
101 cctgcggaag cgaagagact aaagagattt tggtaaact ggtccgcgac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaga
201 ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggtcgaac
251 gtttgggcat aaccgtcgat gaagtccgaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccagcga
351 tgttgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401 agaaaacgcc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451 tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaagcaa
501 aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctggtgtc tatggcactg attaaagagc cgttggacaa agcgaaacaa
601 aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgagggg
651 ggcagaagaa gcggcgggcg aggaggcatt gggtcgggag caggaaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaaggatt gcctcaact gtacagaata agctgcaagc
801 ctgcgagaaa acatggaaaa gcggtatgga caagatctgt gccacaatg
851 cgaaagccga aggtgaaacg ccaaacggca taaaagtcag tgagttggcg
901 tgtaaaacgg cagaaaccga agcacgcttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggt ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
1  MKKNLPALAL ASMLILSGCD RLGIGNPFSG KEISCGSEET KEILVKLVDR
51  NVEGETVKTF DDAFKDQAF ADIGISHIRR MVERLGITVD EVRTTEKTD
101 SSKLKCEAL KLDVPDDVD YAVANQSIG NSHKTPDFF EPYYRKEGAY
151 YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201 RNEKLEAAEA TAQEAREAE AAAQEALGRE QEAARVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKLOASQK TWKSGMDKIC ANNAKAEGET PNGIKVSELA
301 CKTAETEAREL ERLHNRKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
1  ..ATGGCACTGA TTAAAGAGCC GTTGGACAAA GTGAAACAAA GGAACGAAGA
```

```
m268.pep (partial)
  1  ..MALIKEPLDK VKQRNEELEA AEEAAQEAAL GREQEAARVS EWEERYKLSR
51  XQFEQFWKGL  POTVQNKLQP  SQKTWKSMD  KICANNAKAE  GKTPNGIKFS
101 ELACKTAKTE  ARLEELHNRK  KALIDEMXRE  ADXKELSKRL  *
```

m268/g268

[illegible]

1	ATGGCACTGA	TTAAAGAGCC	GTTGGACAAA	GCGAAACAAA	GGAACGAAGA
51	ACTTGAAGCG	GCAGAAGAAG	CGGCGGCGCA	GGAGGCATTG	GGTCGGGAGC
101	AGGAAGTCGA	CCGCGTATCC	GAATGGGAAG	AACGCTACAA	GCTGTCGCGC
151	AGCGAGTTCG	AGCAGTTCTG	GAAAGGATTG	CCTCAAACCG	TACAGAATAA
201	GCTGCAAGCC	TCACAGAAAA	CATGGAAAAG	CGGGATGGAT	AAAATCTGTG
251	CCAACAATGC	GAAAGCTGAA	GGTGAACGC	CAAACGGCAT	AAAATTCAGC
301	GAACTGGCAT	GCAAAACGGC	GGAACCGAA	GCACGCTTGG	AAGAGCTGCA
351	CAACCGTAAA	AAAGCCCTTC	TCGACGAAAT	GGCCAGGGAA	GCGACAAGA
401	AAGAACTGCC	AAAGCGGCTC	TGA		

1	MALIKEPLDK	AKQRNEELEA	AEEAAAQEAL	GREQEVDRVS	EWEEERYKLSR
51	SEFEQFWKGL	PQTQVNKLQA	SQKTWKSMD	KICANNAKAE	GETPNGIKFS
101	ELACKTAETE	ARLEELHNRK	KALLDEMARE	ADKKELPKRL	*

```

          10      20      30      40      50      60
m268.pep  MALIKEPLDKVKQRNEELEAAEEAAAEALGREQEAARVSEWEERYKLSRXQFEQFWKGL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a268      MALIKEPLDKAKQRNEELEAAEEAAAEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```

615

	10	20	30	40	50	60
	70	80	90	100	110	120
m268.pep	PQTVQNKLPQSQKTKWSGMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNKR					
	: : : : : : : : : : : :					
a268	PQTVQNKLPQSQKTKWSGMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNKR					
	70	80	90	100	110	120
	130	140				
m268.pep	KALIDEMKREADKKELSKRLX					
	: : : : : : : : : : :					
a268	KALLDEMAREADKKELPKRLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1087>:

m268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGTGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CCGCCCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAAC CGAAGCACGC TTGGAAGAGC
401 TGCACAACCG TAAAAAAGCC CTTATCGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG GCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.pep

```

1  VQSRDGLHK FKHICSAAMA LIKEPLDKVQ ORNEELEAAE EAAAEALGR
51  EQEAARVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLOASQ KTWKSGMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNKRKA LIDEMAREAD
151 KKELSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

		10	20	30	
m268-1.pep		VQSRDGLHKFKHICSAAMALIKEPLDKVKORNE			
		: : : :			
g268	KEGAYVYKTISYSVQPTDDKSKIFAELSOAHDIHPLSELVS--MALIKEPLDKAKORNE				
	150	160	170	180	190 200
	40	50	60	70	80
m268-1.pep	ELEAAE-----EAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
	: : : : : : : : : : : :				
g268	KLEAAEATAQEAREEAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
	210	220	230	240	250 260
	90	100	110	120	130 140
m268-1.pep	KLOASQKTKWSGMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRRKALIDE				
	: : : : : : : : : : :				
g268	KLOASQKTKWSGMDKICANNAKAEGKTPNGIKVSELACKTAKTEARLEELHNRRKALIDE				
	270	280	290	300	310 320
	150	159			
m268-1.pep	MAREADKKELSKRLX				
	:				
g268	MVREEDKKELPKRLX				
	330				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGCGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG TCGACCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAAGC TGAAGGTGAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGGAAAC CGAAGCACGC TTGGAAGAGC

```

401 TGCACAACCG TAAAAAGCC CTTCTCGACG AATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep
1 VQSRDGLHK FKHCSAAMA LIKEPLDKAK QRNEELEAAE EAAAEALGR
51 EQEVDVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLOASQ KTWKSGMDKI
101 CANNKAEGE TPNGIKFSEL ACKTAETEAR LLELHNRKKA LLDEMAREAD
151 KKELPKRL*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHCSAAMALIKEPLDKAKQRNEELEAAEAAAQALGREQEVDRVSEW					
m268-1	VQSRDGLHKFKHCSAAMALIKEPLDKVQRNEELEAAEAAAQALGREQEAARVSEW					
	10	20	30	40	50	60
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGETPNGIKFSEL					
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGKTPNGIKFSEL					
	70	80	90	100	110	120
a268-1.pep	ACKTAETEARLEELHNRKKA LLDEMAREADKKELPKRLX					
m268-1	ACKTAETEARLEELHNRKKA LLDEMAREADKKELSKRLX					
	130	140	150	159		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq
1 atggtttggc gtgtgaattg gcgggcaacg gcggcgctga ttttttcgct
51 cagcccttgg atttgggagg tggtgtgggt gtggtcgagg tcggcttttt
101 cctgcaaacc ttgcgccagc cttgacgcgt ccagtgcgcc ggcgttggcg
151 gtttcgccgt gggactttat ccggaacacg gcttcgcca aggtgtcggc
201 ggctttgatg cacagtttta aaaccagggc tttggggcgg ttttctgcgc
251 cgcccggtgc cattttgctg tccaatcgcg ggggtaaaa accgttgcg
301 ttaagtgcg cgtccgtcca agtcgatacg agcgcgcttc tttgccttc
351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep
1 MVWRVNCAAT AALIFSSSPW IWAUVVWSR SAFSCKPCAS LDASSAPALA
51 VSPWDFIRNT ASPKVSALM HSPKTRALGR FSAPPVAILL SNRGVKKPLS
101 FKSPSVQVDT SALLCLSLRS S*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq
1 ATGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGTCTCGG TCGGCTTTGT
101 CTTGCAAACC TTGCGCCaCG TGCCCGCGTC CAGCGCCTGC GTTGATGGTT
151 TCGCCGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTGCGCGGC
201 TTTGATGCAC AGTTTAAAA CCAGGGCTTT GGGGCGGTTT TCGTCCCGC
251 CTGTCGCCAT TTTGCTGTCC GAGCGCGGGG TAAAAAGCC GTTGTCTGTT
301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGCTTCTCT GCCTTTCGTT
351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep
1 MVWRVNCAAT AVLIFSSSPW IWAUVVWSR SALSCKPCAT CPRPAPALMV
51 SPWDFIONTA SPKVSALMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF
101 KFSSVQVDT ALLCLSLRSS *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng) from *N. gonorrhoeae*:

```

m269 . pep      MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT  59
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g269            MVWRVNCAATAALIFSSSPWIWAVVWVWSRSAPFCKPCASLDASSAPALAVSPWDFIRNT  60

m269 . pep      ASPKVSAAALMHSEKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTALLCLSLRS 119
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g269            ASPKVSAAALMHSEKTRALGRFSAPPVAILLSNRGVKKPLSFKSPSVQVDTALLCLSLRS 120

m269 . pep      SX 121
                ||
g269            SX 122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269 . seq
1  ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGGCGCGG TCTGCTTTGT
101 CTTGGAGGTT TTGCCCAGC GTGCCCGCGT CCAGCGCGCC GGC GTTGACG
151 GTTTCGCCGT GGGACTTTAT CCAGAACACG GCTTCGCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTTA AAACCAGGGC TTTGGGGCGG TTTTCGTCGC
251 CGCCTGTGCG CATTTTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTTGTCG
301 TTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

```

a269 . pep
1  MVWRVNCAAT AVLIFSSSPW IWA AVVWVAR SALSWRFCAS VPASSAPALT
51 VSPWDFIQNT ASPKVSAAAL HSEKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

m269 . pep      10      20      30      40      50      59
                MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a269            10      20      30      40      50      60
                MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSWRFCASVPASSAPALTVPWDFIQNT

m269 . pep      60      70      80      90      100     110     119
                ASPKVSAAALMHSEKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTALLCLSLRS
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a269            60      70      80      90      100     110     120
                ASPKVSAAALMHSEKTRALGRFSSPPVAILLSGRGVKKPLSFKFSSVQVDTALLCLSLWS

m269 . pep      120
                SX
                ||
a269            SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270 . seq
1  atgaataaaa accgcaaatt actgcttgcc gcaactgctgc tgactgcctt
51 tgccgccttc aagctcggtt tgttgcaatg gtggcaggcg cagcagcgcg
101 aagccgtggc ggcgcaatgc gatttgaccg agggttgcac gctgccggac
151 ggaagccgtg tccgcgccgc cgccgtttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgcccg ccggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg ggtttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcacg cgctgcccg tctgtgtcga
351 aggcaggcgc gattttacgg cggacattac aatcggcagc cggacatttc
401 agacggcatt taccgccgaa taa

```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

g270.pep

1 MNKNRKLLLA ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
 101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq

1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
 51 TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG Ca. CAGCCGC
 101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC
 151 GGAAGCCGCG TCCGCGCCGC CGCgGTTTCA ACCAAAAAAC CGTTTGATAT
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
 251 GTATGAAAAA TATGGATATG GGTTTCaACC GCTATATGTT CGAGCGGCAA
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTGCA
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTC
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep

1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
 101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng) from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRKLLLAALLLIAFAAVKLVLLQWWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
g270	MNKNRKLLLAALLLTAFAAFKLVLLQWWQAQQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFEROPSGTWQAVRIRLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFEROPSGTWQAARIRLPVCVEGRR					
	70	80	90	100	110	120
	130 140					
m270.pep	DFTADITIGSRTFQTAFTAE					
g270	DFTADITIGSRTFQTAFTAE					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq

1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
 51 TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG CAGCAGCCGC
 101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC
 151 GGAAGCCGCG TCCGCGCCGC CGCCGTTTCA ACCAAAAAAC CGTTTGATAT
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
 251 GTATGAAAAA TATGGATATG GGTTTCAACC GCTATATGTT CGAGCGGCAA
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTGCA
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTC
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep

1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKLALLAALLLIAFAAVKLVLQWQAXQPQAVAAQCDELTEGCTLPDGSRVRAAAVS					
a270	MNKNRKLALLAALLLIAFAAVKLVLQWQAXQPQAVAAQCDELTEGCTLPDGSRVRAAAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRI RLPICVEGRR					
a270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRI RLPICVEGRR					
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAE					
a270	DFTADITIGSRTFQTAFTAE					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

```

1  atgttcagtt  cgcggatggc  gaggatttgg  gcgacggggg  taacgttgtg
51  tatggtcagt  ccgtgtccgg  cggtgacgac  caagcccaaa  tcgccggcga
101  aatgcgcgcc  gttttggatg  cgctcgaaact  gcctgatttg  ttcggcggtg
151  ctttgtgctg  cggcatatgc  gccggtgtgc  agctcgacaa  cgggcgcgcc
201  gacatcacgg  gcggcttggg  ttgctctgtc  gtcggcatcg  ataaacaagg
251  acacgcgtat  gcccgcgctc  gtcaggattt  tggcgaattc  ggcgattttt
301  tcctgttgct  ccaatacgtc  caaaccgcct  tcggtcgtga  tttcctgcgc
351  tttttcaggc  acgatgcaca  cgtcttccgg  catcacttta  agcgcgtttt
401  cgagcatttc  ttccgtcaac  gccatttcaa  ggttcaggcg  cgtgcggatg
451  gcgtttttga  cggcaataac  atccgcgtct  ttgatgtggc  ggcggtcttc
501  gcgcaggtgc  atggtaatca  ggtctgcacc  gtgcgtttcg  gcaaccagtg
551  ccgcctccac  ggggctggga  taa

```

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

```

1  MFSSRMARIW  ATGVTLCMVS  PCPALTTKPK  SPAKCAPFWM  RSNCLICSAW
51  LCASAYAPVC  SSTTGAPTSR  AAWICLSSAS  INKDRMPAS  VRILANSAIF
101  SCCANTSKPP  SVVISCRFSG  TMHTSSGITL  SAFSSISSVN  AISRFRRVRM
151  AFLTANTSAS  LMWRRSSRRC  MVIRSAPCVS  ATSAASTGLG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

```

1  AwGTTcAGTT  CGCGGATGGC  GAGGATTtGG  GCGATGGGGG  TAACGtTGtG
51  TATGGtCAGT  CCGTGTCCGG  CGTTGACgAC  CAAGCCCAAA  TCGCCGGcGA
101  AATGCGCGCC  GTTTTGGATG  CGCTCGAACT  GCCTGATTtG  TTCGGCGtGG
151  CTGCGCGCGT  CGGCATACGC  GCCTGTGTGC  AGCTCGACAA  CGGGCGCGCC
201  GACATCACGG  GCGGCTTGGa  TTTGCCtGTc  GTCGGcATCG  ATAAACAAAG
251  ACACGCGTAT  GCCTGCGTcG  GTCAGGATTt  TGGTGAACCC  GGCgATTtTT
301  TCCTGTtGCG  CCAATACGTc  CAAACCGCCT  TCGGTcGTGA  TTTCTGACG
351  TTTTtCAGGC  ACGATGCACA  CGTCTTCCGG  CATCACTtTC  AAAGCGTtTT
401  CCAACATTtC  TTCCGTCAAC  GCCATTtCAA  GGTTCAGGCG  CGTGCcGATG
451  GCGTtTTtGA  CGGCAAAcAC  GTCCGCGTCT  TTGATGTGGC  GGCgGTCTTC
501  GCGCAGGTGC  ATGgTAATCA  AATCCGCACC  GTGCgTTtCG  GCAACcAGTG
551  CCGCCTCCAC  GGGGCTGGGA  TAA

```

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

```

1  XFSSRMARIW  AMGVTLCMVS  PCPALTTKPK  SPAKCAPFWM  RSNCLICSAW
51  LRASAYAPVC  SSTTGAPTSR  AAWICLSSAS  INKDRMPAS  VRILVNPAIF
101  SCCANTSKPP  SVVISXRFSG  TMHTSSGITF  KAFSSISSVN  AISRFRRVRM
151  AFLTANTSAS  LMWRRSSRRC  MVIKSAPCVS  ATSAASTGLG *

```

Computer analysis of this amino acid sequence gave the following results:

620

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTL CMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTL CMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNP AI FSCCANTSKPPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANS AI FSCCANTSKPPSVVISCRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANT SASLMWRRSSRRRCMVIR SAPCVS					
g271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANT SASLMWRRSSRRRCMVIR SAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271.seq

```

1  ATGTTCA GTT CGCGGATGGC GAGGATT TGG GCGATGGGGG TAACGTTGTG
51  TATGGTCAGT CCGTGTCCGG CGTTGACGAC CAAGCCCAA TCGCTGGCAA
101 AATGCGCGCC GTTTTGGATG CGCTCGA ACT GCCTGATTG TTCGGCGTGG
151 CTGCGCGCGT CGGCATACGC GCCTGTGTG AGCTCGACA CGGGCGCGCC
201 GACATCACGG GCGGCTTGGA TTTGCCTGT GTCGGCATCG ATAAACAAGG
251 ACACGCGTAT GCCCGCGTCG GTCAGGATT TGGTGAATC GGCAATTTTG
301 TCTTGTTGCG CCAATACGTC CAAGCCGCT TCGGTCGTA TTTCCTGACG
351 TTTTTCGGG ACGATGCACA CGTCTCCGG CATCACTTA AGCGCGTTTT
401 CGAGCATTTT TTCCGTCAAC GCCATTCAA GGTTCAGGCG CGTGCGGATG
451 GCGTTTTTGA CAGCAAACAC GTCCGCGTCT TTGATGTGGC GGCGGTCTTC
501 GCGCAGGTGC ATGGTAATCA GGTCGGCACC GTGCGTTTCG GCAACCAAGT
551 CCGCTCCAC GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271.pep

```

1  MFSSRMARIW AMGVTLCMVSPCPALTTKPK SLAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNSAIL
101 SCCANTSKPP SVVIS*RFSG TMHTSSGITL SAFSSISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRAPCVS ATSAASTGLG *

```

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTL CMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTL CMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNP AI FSCCANTSKPPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAIL SCCANTSKPPSVVISXRFSG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m271. pep	TMHTSSGITFKAFSN	ISSVNAISRFRVRMA	FLTANTSASLMWRR	SSRRRCMVKSAPCVS		
a271	TMHTSSGITLSAFSS	ISSVNAISRFRVRMA	FLTANTSASLMWRR	SSRRRCMVIRSAPCVS		
	130	140	150	160	170	180
	190					
m271. pep	ATSAASTGLGX					
a271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1  atgactgcaa aggaagaact gttcgcatgg ctgcgccata tgaacaaaaa
51  caaagggtcc gacctgtttg tgacgacca tttccgccc gctatgaagc
101 tggacggcaa aatcacccgc atcacggacg aaccgctgac ggcggaaaaa
151 tgtatgaaa tcgcttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcacgcacc aacgagtgcg atttcgccat cagcctgccg gacaccagcc
251 gcttcgcgct caatgcgatg atacagcgcg gtgcgacggc gttggtatcc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgcccgc
351 ggccctgaag gatgttgccg tgaaaaaacg cgggctggtt attttgtcgc
401 gcggcaccgg ctccggcaaa tcgacttcgc tcgcctcgct tatcgactac
451 cgcaatgaaa attcgttcgg acacatcatc accatcgaag atccgatcga
501 gtttgtccac gaacacaaaa actgcatcat taccagcgc gaggtcggcg
551 tggacacgga aaactggatg cgggcgttga aaaatacgtc gcgtcaggcg
601 ccgatgtgta tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc ttgcccgaag cggggcattt gtgtatggcg acgctgcacg
701 ccaacagcac caatcaggcg ctgcacgcga tcatcaactt cttccccgag
751 gagcgcgcg aacaattgct gacggatttg tcgtcaacc ttcaggcggt
801 tatttcgcaa cgcctcgctc cgcgagacgg cggcaaggcg aggggtggcg
851 cagtcgaggt gctgctcaat tcgcccctga tttcggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttgctg
1051 ttggcggtac agttgcgcag ccgcagggca caaagtccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1  MTAKBELFAW LRHMNKNKGS DLFVTTHFPP AMKLDGKTR ITDEPLTAEK
51  CMEIAPSIMS AKQAEFSST NECNFAISLP DTSRFRVNM IORGATALVF
101 RAITSKIPKF ESLNLPALK DVALKKRGLV IFVGGTGS GK STSLASLIDY
151 RNENSPGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYIA FAETGHL CMA TLHANSTNQA LDRIINFPPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHL YQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAwCCAAAA
51  CAAAGGTTCC GACCTGTTCC TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GGCGGAAAAA
151 TGTATGAAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCAATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCGCGCT CAATGCGATG ATACAGCgCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCGGCC
351 AGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 CGGCACCCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTGCGCG

```

```

551 TGGATACGGA AACTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCTGA TTTCGGAGTT GATTACAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAATGCCG ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CaaAGTTyCA GCCCGGATT
1101 GGAAGTCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272.pep

```

1  MTAKEELFAW LRHMxQNKGs DLfVtTHfPP AMKLdGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEfSSST NECNfAISLP DTSRfRVNAM IQRGATALVF
101 RTITSKIPKF ESLNLPpVLK DVALKKRGLV IFVGGTGSgK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLcMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLvPRDGGKG RvAAVEVLlN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQhLYQLYE KGDISLQeAL KNADSAHDlR
351 LAVQLRSRRA QsXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

m272.pep	10	20	30	40	50	60
	MTAKEELFAWLRHMxQNKGsDLfVtTHfPPAMKLdGKITRITDEPLTAEKMEIAFSIMS					
g272	MTAKEELFAWLRHMKNKGsDLfVtTHfPPAMKLdGKITRITDEPLTAEKMEIAFSIMS					
	10	20	30	40	50	60
m272.pep	70	80	90	100	110	120
	AKQAEfSSSTNECNfAISLPDTSRfRVNAMIQRGATALVFRTITSKIPKFESLNLPpVLK					
g272	AKQAEfSSSTNECNfAISLPDTSRfRVNAMIQRGATALVFRAITSKIPKFESLNLPpALK					
	70	80	90	100	110	120
m272.pep	130	140	150	160	170	180
	DVALKKRGLVIFVGGTGSgKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR					
g272	DVALKKRGLVIFVGGTGSgKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR					
	130	140	150	160	170	180
m272.pep	190	200	210	220	230	240
	EVGVDTENWMALKNLTlRQAPDVILIGEIRDRtMDYAIAFAETGHLcMATLHANSTNQA					
g272	EVGVDTENWMALKNLTlRQAPDVILIGEIRDRtMDYAIAFAETGHLcMATLHANSTNQA					
	190	200	210	220	230	240
m272.pep	250	260	270	280	290	300
	LDRIINFFPEERREQLLTDLsLNlQAFISQRLvPRDGGKGvAAVEVLlNSPLISELIHN					
g272	LDRIINFFPEERREQLLTDLsLNlQAFISQRLvPRDGGKGvAAVEVLlNSPLISELIHN					
	250	260	270	280	290	300
m272.pep	310	320	330	340	350	360
	GNIHEIKEVMKKSTTLGMQTfDQhLYQLYEKGDISLQeALKNADSAHDlRLAVQLRSRRA					
g272	GNIHEIKEVMKKSTTLGMQTfDQhLYQLYEKGEISLQdALKNADSAHDlRLAVQLRSRRA					
	310	320	330	340	350	360

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```

          370
m272 . pep  QSXSPDLXLLX
             || :||| |||
g272       QSSDPDLELLX
             370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272 . seq
1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTCC TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACC CGC ATCACGGACG AACCGCTGAC GCGGAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCATTGA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGCAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AAATGGATG GCGGCGTTGA AAAACACGCT CGCTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACCTGTCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCGGAGTT GATTACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCTTGCA GGATGCCTTG AAAAAATGCC ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTTCCG GTCCCGATTT
1101 GGAAGTCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272 . pep
1  MTAKEELFAW LRHMNKNKGS DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAI IQRGATALVF
101 RAITSKIPKF ESLNLPVLK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI FAETGHLMA TLHANSTNQA LDRIINFFPE
251 ERREQLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMO FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDLELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

          10      20      30      40      50      60
m272 . pep  MTAKEELFAWLRHMNKNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
          ||||| :|||||
a272       MTAKEELFAWLRHMNKNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
          10      20      30      40      50      60

          70      80      90      100     110     120
m272 . pep  AKQAEFSSTNECNFAISLPDTSRFRVNAI IQRGATALVFRTITSKIPKFESLNLPVLK
          ||||| :|||||
a272       AKQAEFSSTNECNFAISLPDTSRFRVNAI IQRGATALVFRAITSKIPKFESLNLPVLK
          70      80      90      100     110     120

          130     140     150     160     170     180
m272 . pep  DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR
          ||||| :|||||
a272       DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR
          130     140     150     160     170     180

```

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	190	200	210	220	230	240
m272.pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
	190	200	210	220	230	240
	250	260	270	280	290	300
m272.pep	LDRIINFFPEERREQLLTDSLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRIINFFPEERREQLLTDSLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m272.pep	GNIHEIKEVMKKSTTLGMQTFDQHL Y Q L Y E K G D I S L Q E A L K N A D S A H D L R L A V Q L R S R R A					
a272	GNIHEIKEVMKKSTTLGMQTFDQHL Y Q L Y E K G E I S L Q D A L K N A D S A H D L R L A V Q L R S R Q A					
	310	320	330	340	350	360
	370					
m272.pep	Q S X S P D L X L L X					
a272	Q S S G P D L E L L X					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

```

g273.seq
1  atgagctcttc aggcgggtatt tatatacccc ccaagccgta ccgcacaata
51  caacgaaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccgggaact
151 ccattcaccg ttttcctgcc gtttcttgtc gcttttgaaa taaaggatga
201 tgccggcaag cagcgcgcca gccgcgcccg acattggcat tgtgttcatt
251 gttgttcctt aacggttaaa aaccgcgccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcgggcgc gtgccgtga aatcaaggcg
351 gtttgagaag tgtttccnac gcgccgcccg tatgtgccga aatattatgt
401 gtcgctcacc tgcaaatcgc ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgccctg ctttttggtt ttcaagcagt
501 tttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

```

g273.pep
1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHTDRR QDIGVFEAGT
51  PFTVFLPLV AFEIKDDAGK QRGSRRHWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCGR VPLKSRRFEK CFXRRPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

```

m273.seq
1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCCGG TTTTCCTGCC GCTTCTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT TGTGTTTCATT
251 GTTGTTCTTT AATGCTTAAA AACC CGCCTG TCCGTGCAAC CGTTTAAAGG
301 CGGCAAATTG CAAAATTGTG TTGCGGGCGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTTCCTGAC GCGCCGCCCT GTGTGCCGGA GTTATTGTG
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTACCTGCCT TTTGtKtWTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

```

m273.pep
1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHADRC QDIGVFKAGT
51  PFPVFLPLV AFEIKDDAGK QRGSRRH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCGR VPLKSGRFEG CSRAALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSY A*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/g273

	10	20	30	40	50	60
m273 . pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQSGKQADRCQDIGVFKAGTPFPVFLPLL					
	: : : : :					
g273	MSLQAVFIYPPSRTAQYNENQENGGAHKQSGKHTDRRQDIGVFEAGTPFTVFLPFLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m273 . pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFE					
	: : : : :					
g273	AFEIKDDAGKQGRSRARHWHCVHCCSLTVKNPPGRATVLRRIAKFVCGRVPLKSRFEK					
	70	80	90	100	110	120
	130	140	150	160	170	
m273 . pep	CSRRA-ALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVLPFVXQAVFSYAX					
	: :					
g273	CFXRARPMCRNIICRSPAKSPRTRFAEFPRCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273 . seq

```

1  ATGAGTCTTC AGGCGGTATT TGTATACCCC CCAAGCCGTA CCGCACATA
51 CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCATAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCCGT CAGGATATAG GCGTATTCCA GACCGGAAC
151 CCATTACCG TTTCTCTGCC GCTTTTGTG GCTTTTGAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCG ACATTAGCAT AATGTTTATT
251 GTTGTTCCTT AACGGTTAAA AACCCGCCG TCCGTGCAAC CGTTTTTAA
301 AGGCGGTAAA TCACAAAGTT TGTGGCGGA CGTGCTCTCT TACAATCAG
351 GCGGTTTAA GGCATGATG CACTGCCCG TGTGCCGAT ATTATTTGTC
401 GCTCACCTGC AAAATTGCCA AGAACGCGT TTGCGGGATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTGCCTGCT TTTGTTTTTC AAGCAGTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273 . pep

```

1  MSLQAVFVYP PSRTAQYNEN QENGGAHKQ QSGKHADRR QDIGVFQGT
51 PFTVFLPLFV AFEIKDDAGK QGRSRARH*H NVHCCSLTVK NPPVRATVFK
101 RR*ITKFVGG RALLQSGRFK GHDALPRVD IICRSPAKLP RTRFAGFPHC
151 PLVSYGVCLL FVEQAVFSYA *

```

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273 . pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQSGKQADRCQDIGVFKAGTPFPVFLPLL					
	: : : : :					
a273	MSLQAVFVYPPSRTAQYNENQENGGAHKQSGKHADRRQDIGVFTGTFTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m273 . pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFE					
	: : : : :					
a273	AFEIKDDAGKQGRSRARHNVHCCSLTVKNPPVRATVFKRRXITKFVGGRALLQSGRFK					
	70	80	90	100	110	120
	120	130	140	150	160	170
m273 . pep	GCSRRAALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVLPFVXQAVFSYAX					
	: : :					
a273	GHDALPRV-PDIICRSPAKLPRTFRAGFPHCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

g274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCatCGCC AgcgTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGGATG
101 GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTCCT CATTCTCCCC GATATGAATG CGGCAAAAGT
201 GTTTGTCTGGC ggCgagtTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCCTC
301 GGCAGCGCGC AGAACGGCAG GCGGGAATAT GAGGCGGTgt tcaaAACCCT
351 TCCGCCGGCC AACCACTGGT ATGTGCGCGT GGAggacgCG GCAGGCGTGT
401 GGCAGCGTCGA GAACAAATGG ATTACCAGCC AGGGCAATGC GGTGATTG
451 ACCCCGATGG ACAAACTTTT CAATAATGCA GGAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

g274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFVG GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLPPA NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNA GSK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

m274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAACATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTCTCCCC GATATGAATG CGGCAAAAGT
201 GTTTGTCTGGC GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCCTC
301 GGCAGCGCGC AGAACGGCAG GCGGGAATAT GAGGCGGTGT TCAAAACCCT
351 TTCGCCGACC AACCACTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCAGCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTGATTG
451 ACCCCGATGG ACAAGCTTTT CAATAATACT GAAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

m274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFVG GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
m274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g274.pep	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLPPA					
m274	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
g274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

a274 .seq

```

1   ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCTCC GATATGAATG CCGCAAAAGT
201 GTTTGTCTGGC GGCAGAGTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAACCCCT
351 TTCGCCGACC AACCACTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGC GCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTGATTG
451 ACCCCGATGG ACAAACCTTTT CAATAATACT GAAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

a274 .pep

```

1   MAGPIFVVIA SVAMFFVAQO HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFVG GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQGNVDL
151 TPMDKLFNNT ESK*

```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274 .pep	MAGPIFVVIA SVAMFFVAQO HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
a274	MAGPIFVVIA SVAMFFVAQO HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m274 .pep	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALK PVGSAQNGRAEY EAVFKTLSPT					
a274	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALK PVGSAQNGRAEY EAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
m274 .pep	NHWYVRVEDA AGVWRVENKW ITSQGNVDLT PMDKLFNNTESKX					
a274	NHWYVRVEDA AGVWRVENKW ITSQGNVDLT PMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

g276 .seq

```

1   atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  ggtcaggcgg tggcgacga tgatgccggt gcggttttcc atcaggcggt
101 cgagcgcttg ttggacgagg cgttcggatt cgttgctcaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgcgctc ttcaaatgg cgcgggcat
201 ggcgacgcgt tgccgctgct cgccggataa gttgctgccg ttcgatccga
251 tgggctggtg cagtcgagc ggggatgcgt cgatcaggct ttgcagggtg
301 gcggcttgga gggcgacag gacttcggct tcgccgcgt cgggacggct
351 gtatcggacg ttttcaaaca ggggtgctgc aaacaggaat acgtcttggg
401 agacgagggc gaattgggcg cgcaggcagt cgagtttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccggca gacggttcga caaagcgggg
501 cagaaggttg acgacggttg atttgccgct gccggaacgt ccgaccaggg
551 cgacgcgttc gccttgctct atgtcgaggt tgaagttgtc gagggctttg
601 atgccgtctg aacggtattc gacatcgacg ttgcggaagc tgatgcgccc
651 ttcgacacgc tcggcgcgca gcgtgccttt gtcctgttcg ggcggggtgt
701 cgagaaatgc acatacgccg tcggcgcgca ggaacatcgt ctgcataagg
751 atgctgatgt tggcaaggct tttgatgggg gcgtacattt gcagcatcgc
801 gacgatgaat gccataaatt cgccgatggt ggtgtag

```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276 .pep

```

1  MILPPSMTMM RSADSTVRR WATMPVRF S IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRGRRL TTVDLPLPER PTRATRSPLC MSRLKLSRAL
201 MPSEYSTST LRLMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1129>:

```

m276.seq
1  ATGATTTTGC CGTCGTCCAT CACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTGAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCTAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATAGG CGCGGGCAAT
201 GGCAGACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGGGAGCTGT CAATCAGGCT TTGCAGGTTG
301 GCGGTTTGGG GGGCGAACAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 GTATCGGACG TTTTCAAACA GGGTGTCGTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC GAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGTTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGTTGTC GAGGGCTTTG
601 ATGCCGTCTG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TCGGGTGCGA GCGTGCCCTT GTCCTGTTCT GCGGGGGTGT
701 CGAGAAATGC ACATACACCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTGATGT TGGCAAGGCT TTGATGGGG GCGTACATTT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1130; ORF 276>:

```

m276.pep
1  MILPSSITMM RSAPSMVRR WATMPVRF S IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GELSIRLCRL
101 AVWRANRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRGRRL TTVDLPLPER PTRATRSPLC MSRLKLSRAL
201 MPSEYSTST LRLMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 276 shows 96.8% identity over a 278 aa overlap with a predicted ORF (ORF 276.ng) from *N. gonorrhoeae*:

m276/g276

m276.pep	10	20	30	40	50	60
	MILPSSITMMRSAPSMVRRWATMPVRF S IRRSSACWTRRSDSLSNALVASSNNNIGAS					
g276	MILPSSITMMRSADSTVRRWATMPVRF S IRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
m276.pep	70	80	90	100	110	120
	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
g276	FKMARAMATRCRCPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
m276.pep	130	140	150	160	170	180
	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKRGRRLTTVDLPLPER					
g276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKRGRRLTTVDLPLPER					
	130	140	150	160	170	180
m276.pep	190	200	210	220	230	240
	PTRATRSPLCMSRLKLSRALMPSEYSTSTLRKLRPSTRCGASVPLSCSGGVSRNAHTP					
g276	PTRATRSPLCMSRLKLSRALMPSEYSTSTLRKLRPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240

629

	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

a276.seq

1	ATGATTTTGC	CGTCGTCCAT	TACGATGATG	CGGTCGGCCC	CTTCGATGGT
51	GGTCAGGCGG	TGGGCGACGA	TGATGCCGGT	GCGGTTTTC	ATCAGGCGTT
101	CGAGCGCCTG	TTGGACGAGG	CGTTCGGATT	CGTTGTCCAA	TGCGCTGGTG
151	GCTTCGTCCA	ATAATAATAT	CGGCGCGTCT	TTCAAATGG	CGCGGGCAAT
201	GGCAACGCGT	TGCCGCTGTC	CGCCGGATAA	GTTGCTGCCG	TTGCATCCGA
251	TGGGCTGGTG	CAGTCCGAGC	GGTGATGCGT	CGATCAGGCT	TTGCAGGTTA
301	GCGGCTTGGA	GGGCGGATAG	GACTTCGGCT	TCGCCCCTG	CGGGACGGCT
351	ATATCGGACG	TTTTCAAACA	GGGTGTCGTC	AAACAGGAAT	ACGTCTTGGG
401	AGACGAGGGC	AAATTGGGCG	CGCAGGCAGT	CGAGTTTGAT	GTCGGCGATG
451	TCGATACCGT	CTATGCAGAT	GTTGCCGGCA	GACGGTTCGA	CAAAGCGGGG
501	CAGCAGGTTG	ACGACGGTGG	ATTGCGGCT	GCCGGAACGT	CCGACAGGG
551	CGACGCGTTC	GCCTTGCTG	ATGTCGAGGT	TGAAGCCGTC	GAGGGCTTTG
601	ATGCCGTCCG	AACGGTATTC	GACATCGACG	TTGCGGAAGC	TGATGCGCCC
651	TTGACACGC	TGCGGTGCGA	GCGTGCCTTT	GTCCTGTTG	GGCGGGGTGT
701	CGAGAAATGC	ACATACGCCG	TCGGCGGCGA	GGAACATCGT	CTGCATAGGG
751	ATGCTAATGT	TGGCAAGGCT	TTTGATGGGG	GCGTACATTT	GCAGCATCGC
801	GACGATGAAT	GCCATAAATT	CGCCGATGGT	GGTGTAG	

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

a276.pep

1	MILPSSITMM	RSAPSMVVR	WATMMPVRF	IRRSSACWTR	RSDSLSNALV
51	ASSNNNIGAS	FKMARAMATR	CRCPPDKLLP	FDPMGWCS	PDASIRLCRL
101	AAWRADRTSA	SPASGRLYRT	FSNRVSSNRN	TSWETRANWA	RRQSSILMSAM
151	SIPSMQMLPA	DGSTRKGSRL	TTVDLPLPER	PTRATRSPL	MSRLKPSRAL
201	MPSEYSTST	LRKLRPSTR	CGASVPLSCS	GGVSRNAHTP	SAARNIVCIG
251	MLMLARLLMG	AYICSIATMN	AINSPMVV*		

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMMPVRFIRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVVRWATMMPVRFIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCSGSGELSLRLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPPDKLLPFDPMGWCSGSGELSLRLCRLAARADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIIPSMQMLPADGSTKGRSRLTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIIPSMQMLPADGSTKGRSRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPLMSRLKLSRALMPSEYSTSTLRKLRPSTRCGASVPLSCSGGVSRNAHTP					
a276	PTRATRSPLMSRLKPSRALMPSEYSTSTLRKLRPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

630

250 260 270

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
1  ..atggtacacg tcgccgtagc ttacggtatt gccgtccggc gtttttgccc
51  aaacgaggtc atagacgttt tccacgcctt gcaggtagat cgccaagcgt
101 tcgatgccgt aggtaatctt gccgagtagc gccgtgcaat cgataccgcc
151 gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
201 cttcccagcc caaaccacac gcaccgaggg tggggttttc ccagtcgtct
251 tcgacaaagc ggatgtcgtg gactttggga tcgatgccca attcgcgcag
301 ggagtcgaga tagaggtcct ggatattggc gggggcgggt ttgagggcga
351 cttggaattg gtaatagtgt tgcaggcggg tggggttgtc gccgtagcgg
401 ccgtctttgg ggcggcggct gggttgagc taggcggcaa accaaggctc
451 gggggcggag gcgcgcaggc aggtggcggg atgggatgtg ccggcaccga
501 cttccatgtc gaagggttg atgacggtgc agcctttgtc tgcccagaag
551 gtttgcagtt tgaagatgat ttggtggaag gtaagcatgg cttattgttc
601 gataaaataa aggttttatt ttactgtttc catagccgct tgaatagatt
651 tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
1  ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH RQAFDAVGNF AEYGRAIDTA
51  DLLEIGKLG Y FHAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
101 GVEIEVL D I GGGFEGDLEL VIVLQAVGVV AVAAVFGAAA GLDVGGKPR L
151 GAERAQAGGG MGCAGTDFHV EGLDDGA AFV CPEGLQFEDD LLEGKHGLLF
201 DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGCG AGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAC TGG
101 CGCAGCAGCC AGTCGGCATC GCTGTATTCT AAGTTGTAGG TGGATTGCTC
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTCGA
201 GCGTTTTTGC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT AAAGTGGGTT ACTTCCATGC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTTGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
451 CAATTCGCGC AGAGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGACGGCG GTTGGGGTTG
551 TCGCCGTAGC GGCCGTCTTT GGGGCGGCGG CTGGGTTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGTT GGATGACGGT GCAGCCTTTG
701 TCTGCCCA GA ATGTTGTCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFV VELAQQPVG I AVFEVVGGLL
51  DFLVHVH V GDGVAVERFC PNEVVDV FYT LQVHRQAFDA VGDFAEYGRA
101 VDAADLLEIG KLG Y FHAVEP DFPAQT PRAE GGVFPV VFDK ADVVDFGIDA
151 QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAAVF GAAAGLDVGG
201 KPRLGAECAQ AGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251 GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

g277.pep

10 20 30
MVHVAVAYGI AVRRFCPNEV IDVFHALQVH

632

```

m277.pep  DFPAQT PRAEGGVFPVVDKADVVDFGIDAQFAQRVEIEVL DIGGSGLEGDL ELVIVLQA
          |||||||
a277      DFPAQT PRAEGGVFPVVDKADVVHFGVDAQFAQGV EIEVL DIGGSGLEGDL ELVIVLQA
          130      140      150      160      170      180

          190      200      210      220      230      240
m277.pep  VGVVAVAAVFGAAAGLDVGGK PRLGAECAQAGGGMGCAGTDFHVEGLDDGAA FVCPECLQ
          |||||||
a277      VGVVAVATVFGAAAGLDVGGK PRLGAECAQTGGGMGCAGTDFHVEGLDDGAA FVCPECLQ
          190      200      210      220      230      240

          250
m277.pep  FEDDLLEGKHGLX
          |||||||
a277      FEDDLLEGKHGLX
          250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

```

g278.seq (partial)
1  ttgcgtgcaa tcacgcccgg tgcgattttt tcgacagggg cggtaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgaccaat gcatcgacga
101 cgcgtccgac caattcgcgt ccgaccggca cttctaaaat acggccggta
151 caggtaaccg tgcgccttc ttaatatgt tcgtactcgc ccaacactac
201 ggcaccgacg gagtgcgct ccaggttcat cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcatg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcattc
351 ggcatttaca gacagatttt cgatcttggc ttaatacaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgtca tagtcgtgta
451 caaagcactc agtttgcctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

```

g278.pep (partial)
1  LRAITPGAIF STGAVKVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSFT DRFSILALIR SLISAGLSCM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF....

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

```

m278.seq..
1  TTGCGCGCAA TCACGCCCGG TGCGATTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CCGGTCCGAC CAGTTGCGGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GCGCGCGACG GAGTCGCGCT CCAGGTTTCT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCAATG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGCC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTT GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTGAGC ATTTGCACCA ACTCGCCGAC
601 CTGTTTGTGC GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

```

m278.pep
1  LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPOVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFD FDRDFQLAVET LIQHLHQLAD
201 LFGQIRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng) from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278 . pep	LRAITPGAIFSTGAVKVVLIGPLPSIGRPNASTTRPTNSRPTGTSKIRPVQVTVSPSLIC					
m278	LRAITPGAIFSIGAVKVVLIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC					
	10	20	30	40	50	60
	70	80	90	100	110	120
g278 . pep	SYSPNTTAPTESRSRFIAPKVLPGNSSISPCIASDKPMMRTIPSVTEITVPRVLTSAFT					
m278	SYSPNTTAPTESRSRFIAPKVLPGNSSISPCIASDKPMMRTIPSVTEITVPQVRTSAFT					
	70	80	90	100	110	120
	130	140	150	160	170	
g278 . pep	DRFSILALIRSLISAGLSCKMTLLIRHSRVQSTQFALYRQIQNLITHFNF					
m278	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
	130	140	150	160	170	180
m278	DRDFQLAVETLIQHLHQLADLFVGQRIGTVNDGRFDMVE*					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278 . seq

```

1   TTGCGCGCAA TCACGCCCGG TGCGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GCGGCCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTGAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTGTGCG GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278 . pep

```

1   LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QTVSPSLIC SCSPNTTAPT ESRSRFIAPK KVLPGNSSIS PCIASDKPMM
101 RTIPSVTEIT VPRVRTSAFT DRFSILALIK SLISAGLSCK KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLRQLAD
201 LFVGQRIGTV NDGRFDMVE*

```

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278 . pep	LRAITPGAIFSIGAVKVVLIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC					
a278	LRAITPGAIFSIGAVKVVLIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLIC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m278 . pep	SYSPNTTAPTESRSRFIAPKVLPGNSSISPCIASDKPMMRTIPSVTEITVPQVRTSAFT					
a278	SCSPNTTAPTESRSRFIAPKVLPGNSSISPCIASDKPMMRTIPSVTEITVPRVRTSAFT					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m278.pep	DRFSILALIKSLISAGLSCHKLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
a278	DRFSILALIKSLISAGLSCHKLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
	130	140	150	160	170	180
	190	200	210	220		
m278.pep	DRDFQLAVETLIQHLQLADLFVQGRIGTVNDGRFDMVEX					
a278	DRDFQLAVETLIQHLQLADLFVQGRIGTVNDGRFDMVEX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

g279.seq

```

1  atgacgcgga tttgcggtctg cttgatttca acggttttga gtgtttcggc
51  aagtttgctg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 cgggcagcgg cagggcgcggt ttggtccggt cttctttggc ggcagccatg
151 gtgctgctga cggcgcggtt gttgcttgcg atcacgactt gtccgggcca
201 gttgaagttg acggcttcga ccacttcggt ctgtgcggat tcggcacaaa
251 tctgctcgac ctgttcattc tccaaaccca aaatggcggc cattgcgcct
301 acgccttgct gtacggcgga ctgcatcagt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcgcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279.pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLOWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTSS SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

```

1  ATAACGCGGA TTTGCGGCTG CTTGATTTC ACGGTTTTCA GGGCTTCGGC
51  AAGTTTGTCT GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGGCAGCGG CAGGGCGCGT TTGGCACCGG CTTCTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCTGCTG ATCACGATTT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACTTCGCT TTGGGCGGCT TCGGCACAAA
251 TGCTTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGGGTGT
401 ATTCGCGGAG GCTGTGTCCG GCAACGGCGG CAGGCGTTT GCCGCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLOWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTSS SKPRIAAIAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAA SAVYSPRLCP ATAAGVLPPT
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGLISTVFRASASLSAAGFIRLOWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	:	:	:	:	:	:
g279	MTRICGCLISTVLSVSASLSAAGFIRLOWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m279.pep      ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTFCGTADCISSARRRSLTA
||| ||||| ||||| ||| : ||||| ||| : ||||| ||||| ||||| ||||| |||||
g279          ITTCPGELKLTASTTSPCADSAQICLTSSSKPKMAAIAPTFCGTADCISSARRRSLTA
              70          80          90          100         110         120

              130          140          150
m279.pep      SAKFNAPAATSAVYSPRLCPATAAGVLPASKX
||| ||| ||||| ||||| ||| : |||
g279          SAKSNSAATSAVYSPRLCPATAAGVLPPTSKX
              130          140          150

```

a279.seq

1	ATGACNCNGA	TTTGCGGCTG	CTTGATTTC	ACGGTTTNN	GGGCTTCGGC
51	GAGTTTGTCTG	GCGGCGGGTT	TCATGAGGCT	GCAATTGGGA	GGTACNGACA
101	CNGGCAGCGG	CAGGGCGCGT	TTGGCGCCGG	CTTCTTTGGC	GGCAAGCATA
151	GCGCGCTCGA	CGGCGGCGGC	ATTGCGTCGA	ATCACAGACT	GTCCGGCGGA
201	GTTGAAGTTG	ACGGCTTCAA	CCACTTCATC	CTGTGCGGAT	TCGGCGCAAA
251	TTTGTTTTAC	CTGTTTCATCT	TCCAAGCCGA	GAATCGCCGC	CATTGCGCCC
301	ACGCCTTGCG	GTACGGCGGA	CTGCATCAGT	TCGGCGCGCA	NGCGCACGAG
351	TTTGACCCGC	TCGGCAAAAT	CCAATGCGCC	GGCGGCAACN	AGTGCGGTGT
401	ATTGCGCCAN	GCTGTGTCCG	GCAACGGCGG	CAGGCGTTTT	GCCGCCCGCT
451	TCCGAATAG				

a279.pep

1	<u>MTXICGCLIS</u>	<u>TVXRASASLS</u>	<u>AAGFMRLQWE</u>	<u>GTDTGSGRAR</u>	<u>LAPASLAASI</u>
51	<u>ARSTAAALPA</u>	<u>ITTCGELKL</u>	<u>TASTSSCAD</u>	<u>SAQICFTCSS</u>	<u>SKPRIAATAP</u>
101	<u>TPCGTADCIS</u>	<u>SARXRTSLTA</u>	<u>SAKSNAPEAT</u>	<u>SAVYSPXLCP</u>	<u>ATAAGVLPPA</u>
151	SE*				

	10	20	30	40	50	60
m279. pep	ITRICGCLISTVFRASASLSAAGFIRLOWEGTDTGSGRRARLAPASLAAMARPTAAALPA					
a279	MTXICGCLISTVXRASASLSAAGFMRLQEWGTDTGSGRRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279. pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
a279	ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARXRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279. pep	SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX					
a279	SAKSNAPAATSAVYSPXLCPTAAAGVLPPASEX					
	130	140	150			

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Ouakky et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaaacttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttcagg ttgtaaccag tttcagcatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgcgtag ccgtacaaag cctcgtcgga
151 gccaaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgctcaa cggcttggga cttgaagccg
251 ccgacatcca acgcgccgtc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagaccacg atcatgacca cgaaggacac caccacgacc
401 acggcgaata tgacccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccata acgtcgctga aaccctgata aaggccgac cgaaggcaa
501 agtttattat caacaacgct tgggcaacta ccaaatgcag cttaaaaaac
551 tgcacagcga cgcacaagcc gcatttaatg ccgtccctgc cgccaaacgc
601 aaagtcctga ccgggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgcccgc aaggcgtag cagcgaagcc gagccgtccg
701 ccaacaagat cgccgccatc atccggcaaa tcaaacgcga aggcatacaa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtg accgcatcgc
801 caaagaaacc ggcgtcaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcggca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTLIA ALLATAATAA PLFVVSFSI LGDVAKQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNLGL LEAADIQRAV KQSKVSYAEA
101 TKGIQPLKAE EEGGHHHDH HDHDHDHGH HDHGEYDPH VWNDFVMSD
151 YAQNVAEITLI KADPEGKVYY QORLGNVQMQ LKKLHSDAQA AFNAVPAKR
201 KVLTHGDAFS YMGNRYNISF IAPQVSSEA EPSAKQVAI IRQIKREGIK
251 AVFTENIKDT RMVDRIKET GVNVSGLYS DALGNAPADT YIGMYRHNVE
301 ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAACAC CTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCG TTGTAACCAG CTTAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAACTCG TCCTGCTCAA CCGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGT AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCAG AAGGACACCA CCATGACCAC GGCGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCTA TGCCCAAAAC
451 GTTGCCAAAG CCTTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGT CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CCTTTTCCTA TATGGGCAA CGTTACCATA TCGAATTCAT
651 CGCCCCGCAA GGCGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTTACC
751 GAAAACATCA AGGACACCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACCGCCCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTLIA ALLTASATAA PLFVVSFSI LGDVAKQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNLGL LEAADVQRAV KQSKVSYTEA
101 TKGIQPLKAE EEGGHHHDH HDHGEHHDH GEYDPHVND PVLMSAYAQN
151 VAKALIKADP EGKVYYQRL GNYQMQLKKL HSDAQAAFNA VPAKRKVL

```

637

201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA QVAAIIRQI KREGIKAVFT
 251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNKALTN
 301 AMKQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng) from *N. gonorrhoeae*:

m280/g280

	10	20	30	40	50	60
m280.pep	MKHLKLTIAALLTASATAAPLPVVTFSILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
	::					
g280	MKHLKLTIAALLATAATAAPLPVVTFSILGDVAKQIGGERVAVQSLVGANQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRSAKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAEEEGGHHHDH-					
	::					
g280	TSGDIKKIRSAKLVLLNGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAEEEGGHHHDH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---DHDHEGHHHDHGEYDPHVWNPVLMSAYAQNVAKALIKADPEGKVYYQORLGNYQMQ					
	::					
g280	HDHDHDHEGHHHDHGEYDPHVWNPVLMSDYAQNVAEATLIKADPEGKVYYQORLGNYQMQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQAAAFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSSAEPSAKQVAAI					
	::					
g280	LKKLHSDAQAAAFNAVPAAKRKVLTGHDAFSYMGNRYNISFIAPQGVSSAEPSAKQVAAI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	::					
g280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNVE					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
g280	ALTNAMKQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

```

1  ATGAAACACC CCAAACAC CTTATCGCC GCATTGCTGA CCACTGCCGC
51  AACTGCCGCC CCCCTGCCG TTGTAACCAG CTTACAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAG ATACGCACGC CTATCATATG ACCAGCGCGC ACATTAAAAA
201 AATCCGCAGT GCAAACCTCG TCCTGATTAA CGGCTTAGGA CTTGAAGCTG
251 CCGACATCCA ACGTGCCGTC AAACAGAGCA AAGTATCCTA TGCCGAAGCG
301 ACCAAAGGCA TCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG ACCATGACCA CGAAGGACAC CACCACGACC
401 ACGCGGAATA TGACCCCCAC GTCTGGAACG ACCCGTCCT TATGTCCGCC
451 TATGCCCAAA ACGTCGCCGA AGCCCTGATA AAGGCCGACC CCGAAGGCAA
501 AGTTTATTAT CAACAACGCT TGGGCAACTA CCAATGCAG CTCAAAAAAC
551 TGACAGTGA CGCACAGCC GCATTTAATG CCGTCCCTGC CGCCAAACGC
601 AAAGTCCTGA CCGGGCACGA TGCCTTTTCC TATATGGGCA AACGTTACCA
651 TATCGAATTC ATCGCCCCAC AAGGTGTGAG CAGCGAAGCC GAGCCTTCAG
701 CCAAACAAGT CGCCGCCATC ATCCGACAAA TCAAACGCGA AGGCATCAAA
751 GCCGTATTTA CCGAAAATAT CAAAGACACC CGCATGGTTG ACCGCATCGC

```

638

801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep
 1 MKHPKLTLLIA ALLTTAATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
 51 ANQDTHAYHM TSGDIKKIRS AKLVLLINGLG LEAADIQRAV KQSKVSYAEA
 101 TKGIQPLKAE EEGGHHHDHD HDHDHDHEGH HHDHGEYDPH VWNDFVLMSA
 151 YAQNVAEALI KADPEGKVYY QQRLGNYQMQ LKKLHSDAQA AFNAVPAAKR
 201 KVLTHGDAFS YMGKRYHIEF IAPQGVSSA EPSAKQVAI IRQIKREGIK
 251 AVFTENIKDT RMVDRIKET GVNVSGLYS DALGNAPADT YIGMYRHNK
 301 ALTNAMKQ*

m280/a280 96.4% identity in 308 aa overlap

	10	20	30	40	50	60
m280.pep	MKHLKLTLLIAALLTASATAAPLPVVT	SFSILGDVAKQIGGERVSIQSLVG	ANQDTHAYHM			
a280	MKHPKLTLLIAALLTTAATAAPLPVVT	SFSILGDVAKQIGGERVSIQSLVG	ANQDTHAYHM			
	70	80	90	100	110	120
m280.pep	TSGDIKKIRS	AKLVLLINGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE	EEGGHHHDHD			
a280	TSGDIKKIRS	AKLVLLINGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAE	EEGGHHHDHD			
	130	140	150	160	170	
m280.pep	HDH----	EGHHHDHGEYDPHVWNPVLSA	YAQNVAKALIKADPEGKVYYQQRLGNYQMQ			
a280	HDHDHDHEGHHHDHGEYDPHVWNPVLSA	YAQNVAEALIKADPEGKVYYQQRLGNYQMQ				
	180	190	200	210	220	230
m280.pep	LKKLHSDAQA	AFNAVPAAKRKVLTHGDAFSYMGKRYHIEF	IAPQGVSSA	EPSAKQVAI		
a280	LKKLHSDAQA	AFNAVPAAKRKVLTHGDAFSYMGKRYHIEF	IAPQGVSSA	EPSAKQVAI		
	240	250	260	270	280	290
m280.pep	IRQIKREGIK	AVFTENIKDTRMVDRIKETGVNVSGKLYSDALGNAPADTYIGMYRHNK				
a280	IRQIKREGIK	AVFTENIKDTRMVDRIKETGVNVSGKLYSDALGNAPADTYIGMYRHNK				
	300					
m280.pep	ALTNAMKQX					
a280	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:

g281.seq
 1 atgcactacg ccctcgcatc cgtcttctgc ctgtccctca gcgcgcacc
 51 cgtcggcgta ttctcgtca tgcgcggtat gagcctgata ggcgacgcat
 101 tgagccacgc cgtcctgccc ggtgccgcgc tcggctacat gtttgccggc
 151 ttgagcctgc ccgctatggg tgtgggcggg tttgccgcgc gtatgctgat
 201 ggcgctgctt gccggactcg tcagccgctt taccaccctg aaagaagatg
 251 ccaactttgc cgctttttac ctgagcagcc tcgccatcgg cgtaatcctc
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc
 351 tgtgcttgcc gtcgatattc ccgcactgca actcatcgcc gccgtctccg
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa
 451 agcatagacc cccttttctt caagtccgct aacggcaaa gcgggctttg

639

```

501 gcacgtcatt ttcctcatcc tcgtcgttat gaacctcgta tccggttcc
551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt
601 accgcccggt tatgggcaag aaatatgggg acgctcattc tgttgccgt
651 cctcatcgcc cttttttgcg gtttgatcgg gctgctcatt tcctaccaca
701 tcgaaatccc ttccggcccc gccatcatcc tctgttgag cgctctttat
751 cttttttccg tcatactcgg caaagaaggc ggcattctgc ccaaatggtt
801 caaaaaccac cgccaccaca ccacctga

```

This corresponds to the amino acid sequence <SEQ ID 1158; ORF 281.ng>:

g281.pep

```

1  MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51 LSLPAMGLGG FAAGMLMALL AGLVSRTTTL KEDANFAAFY LSSLAIGVIL
101 ISKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSGLTLITL AVIYRPLVLE
151 SIDPLFLKSV NGKGGWLHVI FLILVVMNLV SGFQALGILM SVGIMMLPAI
201 TARLWARNMG TLILLSVLIA LFCGLIGLLI SYHIEIPSGP AIILCCSVLY
251 LFSVILGKEG GILPKWFKNH RHHTT*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

m281.seq (partial)

```

1  ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51  CGTCGGCGTA TTCCTCGTCA TGCGCCGTAT GAGCCTGATA GCGCAGCAT
101 TGAGCCACGC CGTCTGCCCC GGTGCCGCGC TCGGCTACAT GTTTGCCGGC
151 TTGAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGAG GCATGCTGAT
201 GGCAGTCTT GCCCGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG CGTAGTCCTC
301 GTCAGCAAAA ACGGGAGCAG CGTCGATTG CTCCACCTCC TTTTCGGCTC
351 TGTACTTGCC GTCGATATTC CTGCCCTGCA GCTCATCGCC GCCGTCTCCA
401 GCCTCACGCT CATTACCCTT GCCGTACAT ACCGCCCGCT CGTACTCGAA
451 AGCATCGACC CCTGTCTTCT CAAATCCGTC GCGGCGAAAG GCGGGCTTTG
501 GCACGTCCTC TTTCTCGTCC TGGTCGTCAT GAACTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TCATGATGCT GCCAGCCATT
601 ACCGCCCGCC TGTGGGCGAA GCATATGGGC GCACTCATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTCC TTCGGTCCC GCCATCATCC TCTGTTGCAG CGTCTTTAT
751 CTCATTTCCG TCATACTCG CAAAGAAGGC GGCATTCTGA CC..

```

This corresponds to the amino acid sequence <SEQ ID 1160; ORF 281>:

m281.pep (partial)

```

1  MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51 LSLPAMGLGG VAAGMLMALL AGLVSRTTTL KEDANFAAFY LSSLAIGVIL
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSSLTLITL AVIYRPLVLE
151 SIDPLFLKSV GGKGGWLHVL FLVLVVMNLV SGFQALGILM SVGLMMLPAI
201 TARLWAKHMG ALILSVLTA LLCGLSGLLI SYHIEIPSGP AIILCCSVLY
251 LFSVILGKEG GILT..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng) from *N. gonorrhoeae*:

m281/g281

```

          10      20      30      40      50      60
m281.pep  MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPAAVGYMFAGLSLPAMGLGG
          |:|||||
g281      MHYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPAAVGYMFAGLSLPAMGLGG
          10      20      30      40      50      60

          70      80      90     100     110     120
m281.pep  VAAGMLMALLAGLVSRTTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA
          |||:|||||
g281      FAAGMLMALLAGLVSRTTTLKEDANFAAFYLSSLAIGVILISKNGSSVDLLHLLFGSVLA
          70      80      90     100     110     120

          130     140     150     160     170     180
m281.pep  VDIPALQLIAVSSLTLITLAVIYRPLVLESIDPLFLKSVGGKGGWLHVLFLVLVVMNLV

```

```

g281      |||||:|||||:|||||:|||||:
VDIPALQLIAAVSGLTLITLAVIYRPLVLESIDPLFLKSVNGKGGMLHWHVIFLILVVMNLV
          130          140          150          160          170          180

          190          200          210          220          230          240
m281.pep  SGFQALGTILMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g281      SGFQALGILMSVGIMMLPAITARLWARNMGTLILLSVLIALFCGLIGLLISYHIEIPSGP
          190          200          210          220          230          240

          250          260
m281.pep  AIILCCSVLYLFSVILGKEGGILT
          |||||:|||||:|||||:|||||:
g281      AIILCCSVLYLFSVILGKEGGILPKWFKNHRHHTTX
          250          260          270

```

```
a281.seq
1  ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51  CGTCGGCGTA TTCTTCGTCA TGCGCCGTAT GAGCGTGATA GGCGACGCAT
101 TGAGCCACGC CGTCTCTGCC GGTGCCGCCG TCGGCTACAT GTTTGCCGGC
151 TTAAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGCAG GTATGCTGAT
201 GGCAGTGTCT GCCCGACTCG TCAGCCGCTT CACCACCCGT AAAGAAGATG
251 CCAACTTTGC CGCTTTTATC CTCAGCAGCC TCGCCATCGG TGTAGTCCCT
301 GTCAGCAAAA ACGGCAGCAG CTCGATTGCT CTCACCTCC TTTTCGGCTC
351 CGTACTTGCC GTCGATATTC CTGCCCTGCA ACTCATCGCC GCCGTATCCA
401 CCCTCACACT GCTTACCCTT GCCGTCATCT ACCGCCCGCT CGTACTCGAA
451 AGCATCGACC CCCTGTTTCT CAAATCTGTC GCGGGCAAGT GCGGGCCTTG
501 GCACGTCCTC TTTCTCGTCT TGGTCGTAT GAGCCCTGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TTATGATGCT GCCAGCCATT
601 ACCGCCCGCC TATGGGCGAA GCACATGGGC GCACTCATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTC TTTCCGTTCC GCCATCATCC TCTGTTGCAG CGTCTTTTAT
751 CTCTTTTCCG TCATACTCGG CAAGAAGGC GGCATTCTGA CCAATAGGCT
801 CAAAACCAC CGCCACCACA CCACCTGA
```

a281.pep

1	<u>MRYALASVFC</u>	<u>LSLSAAPVGV</u>	<u>FLVMRRMSLI</u>	<u>GDALSHAVLP</u>	<u>GAAVGYMFGA</u>
51	<u>LSLPAMGLGG</u>	<u>VAAGMLMALL</u>	<u>AGLVSRFTTL</u>	<u>KEDANFAAFY</u>	<u>LSSLAIGVVL</u>
101	<u>VSKNGSSVDL</u>	<u>LHLLFGSVLA</u>	<u>VDIPALQLIA</u>	<u>AVSTLTLLTL</u>	<u>AVIYRPLVLE</u>
151	<u>SIDPLFLKSV</u>	<u>GGKGLLWHVL</u>	<u>FLVLVVMNLV</u>	<u>SGFQALGTLM</u>	<u>SVGLMLLPAI</u>
201	<u>TARLWAKHMG</u>	<u>ALILSVLTA</u>	<u>LCGLSGLLI</u>	<u>SYHIEIPSPG</u>	<u>AIILCCSVLY</u>
251	<u>LFSVILKEG</u>	<u>GILTKWLKNH</u>	<u>RHHTT*</u>		

	10	20	30	40	50	60
m281.pep	MRYALASVFCLSLSAAPVGVLVMMRMSLIGDALSHAVLPGAAGVGYMFAGLSLPAMGLGG					
a281	MRYALASVFCLSLSAAPVGVLVMMRMSLIGDALSHAVLPGAAGVGYMFAGLSLPAMGLGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA					
a281	VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIAAVSSLTTLTAVIYRPLVLESIDPLFLKS VGKGGLWHVLFVLVVMNLV					
a281	VDIPALQLIAAVSTLTLLTAVIYRPLVLESIDPLFLKS VGKGGLWHVLFVLVVMNLV					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1  atgggattgg gtatggaaat cggcaagctg attgtggctc ttttgggtgct
51  gatcaatccg tttagcgcgt tgctcgcttta ccttgacctg accaacggac
101 a cagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 t ttgccgtga ttgcggtatt tgcgctgac ggcggtgcgc tattgaaggt
201 t ttgggcatc agcgtcgggt cgtttcaggt cggcggcggg attttgggtgc
251 t gctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 a atctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 aggggcgatt gccgtcgtgc ccatcgccat accgatcacc atcgggtccgg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatcgcgc tgattatcgc ggccgggtttg gtggtcagtg cgatttggtta
501 t gccatttta atcgttgccg ggaaggtcag ccgcctgctg ggcgcgacgg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggcggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattccgc aactggcagg
651 t tga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1  MGLGMEIGKL IVALVLINP FSALSLYLDL TNGHSTKERR KVARTAATAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMLLAAYS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1  ATGGGATTGG GCATGGAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GGCCTGACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGT CTTTTAGGT CCGCGCGCGG ATTTTGGTGC
251 TGCTGATCGC CATTTGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCCG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CCGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTGTGTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGCGCGACGG
551 GGCTGACGAT TTTAAACCGC ATTATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSLYLDL TNGHSTKERR KVARTAATAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMLLAAYS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng) from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	:					
g282	MGLGMEIGKLIVALLVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m282 . pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	:					
g282	GGALLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282 . pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	:					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282 . pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
g282	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282 . seq

1	ATGGGATTGG	GCATGGAAAT	CGGCAAGCTG	ATTGTGGCTT	TTTTGGTGC
51	GATTAAATCCG	TTTAGCGCGT	TGTCGCTTTA	CCTTGACCTG	ACCAACGGGC
101	ACAGCACGAA	GGAGCGCAGG	AAGGTCGCGC	GGACGGCCGC	CGTTGCCGTG
151	TTTGCCGTGA	TTGCGGTATT	TGCGCTGATC	GGCGGTACGC	TGCTGAAGGT
201	TTTGGGCATC	AGCGTCGGTT	CGTTTCAGGT	CGGCGCGGGA	ATTTTGGTGT
251	TGCTGATTGC	CATTTTCGATG	ATGAACGGCA	ACGACAATCC	CGCCAAGCAG
301	AATCTCGCGG	CGCAGCCGGA	AACGGGGCAG	GTGCGCCCCG	CCCGCAATGC
351	CGGAGCGATT	GCCGTCGTGC	CCATCGCCAT	ACCGATCACC	ATCGGCCCGG
401	GCGGTATTTT	GACCGTGATT	ATTTACGCTT	CGGCGGCTAA	AACATACGGC
451	GACATCGCGT	TGATTATCGC	GGCCGGTTTG	GTGGTCAGTG	CGATTTGTTA
501	TGCCATTTTA	ATCGTTGCCG	GGAAGGTCAG	CCGCTGCTG	GGTGCACGG
551	GGCTGACGAT	TTTAAACCGT	ATCATGGGTA	TGATGCTGGC	GGCGGTATCG
601	GTGGAGATTA	TTGTGTCGGG	ACTGAAAATG	ATATTCCTCG	AACTGGCAGG
651	TTGA				

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282 . pep

1	MGLGMEIGKL	IVAFVLINP	FSALSPLYLDL	TNGHSTKERR	KVARTAAVAV
51	FAVIAVFALI	GGTLLKVLGI	SVGSFQVGGG	ILVLLIAISM	MNGNDNPAKQ
101	NLGAQPETGQ	VRPARNAGAI	AVVPIAIPIT	IGPGGISTVI	IYASAAKTYG
151	DIALIIAAGL	VVSAICYAIL	IVAGKVSRL	GATGLTILNR	IMGMLAAVS
201	VEIIVSGLKM	IFPQLAG*			

m282/a282 99.1% identity in 217 aa overlap

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
a282	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARFARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQVRPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282.pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282.pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFFPQLAGX					
a282	GATGLTILNRIMGMLAAVSVEIIVSGLKMIFFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

g283.seq

1	atgaactttg	ctttatccgt	catcacattt	accctcgcct	ctttcctgcc
51	cgtcccgccct	gccggaaccg	ccgtctttac	ttggaagac	ggcggcgcca
101	acagctattc	ggatgtgccg	aaacagcttc	atcccgacca	gagccaaatc
151	ctcaacctgc	ggacgctcca	aaccaaaccg	gcggtcaagc	ccaaacctgc
201	cgtcgatacg	aatgcggaca	gtgcgaagga	aaacgaaaag	gatatcgccg
251	agaaaaacgg	gcagcttgag	gaagaaaaga	aaaaaattgc	cgaaaccgaa
301	cggcagaaca	aagaagaaaa	ctgccggatt	tcaaaaatga	acctgaaggc
351	ggtgggaaac	tcaaatgcga	aaaacaagga	tgatttgatc	cgtaaataca
401	ataacgccgt	aaacaaatac	tgccgttaa		

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

g283.pep

1	MNFALSVITF	TLASFLPVPP	AGTAVFTWKD	GGGNSYSDVP	KQLHPDQSQI
51	LNLRTLQTKP	AVKPKPAVDT	NADSAKENEK	DIAEKNGQLE	EEKKKIAETE
101	RQNKEENCRI	SKMNLKAVGN	SNAKNKDDLI	RKYNNVAVNKY	CR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

m283.seq

1	ATGAACCTTG	CTTTATCCGT	CATTATGTTG	ACCCTCGCCT	CTTTCCTGCC
51	CGTCCCGCCT	GCCGGAGCCG	CCGTCTTTAC	TTGGAAGGAC	GGCGGCGGCA
101	ACAGCTATTC	GGATGTACCG	AAACAGCTTC	ATCCCGACCA	AAGCCAAATC
151	TTAAACCTGC	GGACGCGCCA	AACCAAACCG	GCGGTCAAAC	CCGCCCAAGC
201	ACAGCAGGG	AAGCGCACAG	ACGGCGCGGC	ACAGGAAAAC	AATCCCGACA
251	CTGCCGAGAA	AAACCGGCAG	CTTGAGGAAG	AAAAGAAAAG	AATTGCCGAA
301	ACCGAACGGC	AGAACAAAGA	AGAAACTGTC	CGGATTTCAA	AAATGAACCT
351	GAAGGCGGTG	GGAAATTCAA	ATGCAAAAAA	CAAGGATGAT	TTGATTCGGA
401	AATACAATAA	CGCCGTAAAC	AAATACTGCC	GTAA	

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

m283.pep

1	MNFALSVIML	TLASFLPVPP	AGAAVFTWKD	GGGNSYSDVP	KQLHPDQSQI
51	LNLRTROTQP	AVKPAQADAG	KRTDGAAQEN	NPDTAEKNRQ	LEEKKRIAE
101	TERQNKEENC	RISKMNLKAV	GNSNAKNKDD	LIRKYNNAVN	KYCR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLQTKP					
g283	MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLQTKP					
	10	20	30	40	50	60

```

              70      80      90      100      110      120
m283.pep    AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV
            |||| | :  :| :|:|: | ||| |||||:|:|:|:|:|:|:|:|:|:|:|:|:|
g283        AVKPKPA-VDTNAD-SAKENEKDIAEKNQGLEEEKKKIAETERQNKEENCRI SKMNLKAV
              70      80      90      100      110

              130      140
m283.pep    GNSNAKNKDDLIRKYNNAVNKYCRX
            |||||:|:|:|:|:|:|:|:|:|:|:|:|:|
g283        GNSNAKNKDDLIRKYNNAVNKYCRX
            120      130      140

```

a283.seq

1	ATGAAC	TTTG	CTTTAT	CCGT	CATTAT	GTTG	ACCCTC	GCCT	CTTTCCT	GCC
51	CGTCCC	GCCT	CGCGG	AGCCG	CCGTCT	TTTAC	TTGGA	AGGAC	GGCGG	CGGA
101	ACAGCT	ATTCC	GGATGT	CCCG	AAACAG	CTTC	ATCCCG	ACCA	AAGCC	AAATC
151	TTAAAC	CTTGC	GGACGC	GCCA	AACCAA	AACCG	GCGGT	CAAAC	CCGCCA	AGC
201	CGACGC	AGGG	AAGCGC	ACAG	ACGGCG	CGGC	ACAGGA	AAAC	AATCCC	GACA
251	CTGCCG	AGAA	AAACCG	GCAG	CTTGAG	GGAAG	AAAAG	AAAAG	AATTGC	CGAA
301	ACCGAAC	CGGC	AGAA	CAAGA	AGAAA	ACTGC	CGGATT	TCAA	AAATGA	ACCT
351	GAAAGC	GGTG	GGAAAT	TCAA	ATGCA	AAAAA	CAAGGAT	GAT	TTGATTC	CGGA
401	AATACA	ATAA	CGCCGT	ATAAC	AAATA	CTGCC	GTTAA			

a283.pap

1	<u>MNFALSVIML</u>	<u>TLASFLPVPP</u>	<u>AGAAVFTWKD</u>	GGGNSYSQVP	KQLHPDQSQI
51	LNLRTQTKP	AVKPAQADAG	KRTDGAQEN	NPDTAEKNRQ	LEEEKKRIAE
101	TERONKEENC	RISKMLKAV	GNSNAKNKDD	LIRKYNNAVN	KYCR*

	10	20	30	40	50	60
m283.pep	MNFALSIVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTRQTKP					
a283	MNFALSIVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTRQTKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERONKEENCRI SKMNLKAV					
a283	AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERONKEENCRI SKMNLKAV					
	70	80	90	100	110	120
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNAVNKYCRX					
a283	GNSNAKNKDDLIRKYNNAVNKYCRX					
	130	140				

g284.seq.

1	atgccgtctg	aaactcgaaa	tcggtttcag	acggcattgg	tttacgcggc
51	aggttggggc	ttagcgggtct	ttgtaacggc	attcgcgttt	gcctgcaaaa
101	agtcgcgcgc	cttttgcgtt	gcctttgaag	ccttcgcgtt	ttttttgaa
151	actgtctttc	ttaaagcctt	ctttcttgaa	accctgcgcg	cgcgttttgc
201	cgccgaagcc	ttctttgcc	ggtttatgat	cgccgcgcgc	gccgccggat
251	ttctatcgc	cccagccgc	ttgccttct	ggcttgccgc	ctgcggattt
301	gcgtttgcgc	gccggctcca	tgccctcgat	ggtcagttcg	ggcagtttgc
351	ggttaatgta	tttttcgatt	ttgtggactt	tgacgcattc	gttcaactcg
401	gcaaagctaa	tctgcaatcc	cgtgcgcct	gcgcgcgcgc	tgccgccgat
451	cgcggtgcagc	tagtcttccg	ctgttttcgc	caggctcgtag	tttatgacgt

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501 gggtaatggt cggtagctca ataccgcgtg cggcaacgtc ggtggcaacc
551 aaaattttgc agcggccttt acgcaaattc gtcagcgtgc ggttgcgcca
601 gccctgcggc atatacgccgt gcaggcagtt ggccgcgaaa cctttttcgt
651 acaattcatc cgcgatgact tcggtcatcg ctttggtgga cgtgaaaatc
701 acacattggt cgatgttggc atcgcgcagg atgtggtcga gcaggcggtt
751 tttgtggcgc atatacgtcgc agtacaacaa ctgctcttcg attttgcctt
801 ggccgtccac gcgttcgact tcgataattt cagagtcttt ggtcagtttg
851 cgcgccagtt tgccgactgc gccgtcccaa gtggcgagaa acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

g284.pep

```

1 MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRVAGFAF AFEAFAGFFE
51 TVFLKAFFLE TFAARFAAEA FFARFMIAAP AAGFPIAPAA FAFRLAACGF
101 AFAGRLHAFD GQFGQFAVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDVNGNG RYVNTACGNV GGNQNFAAAF TQIRQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHREFG RENHTLVDPV IAQDVVEQAV
251 FVAHIVAVQQ LFFDFALAVH AFDFDNFRVF GQFARQFADC AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

m284.seq..

```

1 ATGCCGTCTG AAACGCGGAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51 AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCCTTT GCCTTTGAAG CCTTCGCCGG TTTTTTTGAA
151 ACCGTCTCTC TTAAAGCCTT CTCTCTTGAA ACCTTCGCCG CGCGTTTTCG
201 CGCCGAAGCC TTCTTTGCTC GGTATATGAT CGCCGCGCCA ACCGCGCGAT
251 TTACGATCGC CCCAGCGGCC TTGCTCTTTC GGCTTGCCGC CTGCGGATTT
301 GCGTTTGGCG GTCGGTTCCA TGCTTCGAT GGTCACTTCG GGCAGTTTTC
351 GGTTAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCGGCCCT GCGCGGCCGG TCGCGCCGAT
451 GCGGTGGACG TAGTCTTCCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCT ATACCGCGTG CGGCAACATC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT ACGCAAATCC ATCAGCGTGC GGTGCGGCAA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT TGCGGCGAAA CCTTTTTCGT
651 ACAGTTCATC CGCAATGACT TCGGTATGCG CTTTGGTGGA CGTGAAATC
701 ACGCATTGAT CGATATTGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTTCTTCG ATTTTGCCTT
801 GATCGTCCAC GCGTTCGACT TCGATGATTT CAGGGTCTTT GGTCACTTTC
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCG CTCGGCGTTG CTTCACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAATCAG CACTTCCAAA
1001 CGTTCAAAAT CAACTTTGCC GCTTGCATC AGGTCCATCA GACGGCCGG
1051 CGTGGCGACA ATCAGATCGA CCGGTTTGCT CAGGGCACGG GTTTGGTAGC
1101 CGAAAGACGC GCCGCGGACG ATGCTGACGG TGCGGAACCA ACGCATATTT
1151 TTGCGATACG CCAGCGCGTT TTTCTCGACT TGAGCGGCGA GTTCGCGGGT
1201 CGGGGTCAAC ACCAAAGCAC GCGGGCCTTT GCCCGGTTTT TCGTGCCTT
1251 TGTCAGTTT TTGCAAGTC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

m284.pep

```

1 MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE
51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFAHFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNNGNG RYVDTACGNI GGNQNFAAAF TQIHQRAVAP
201 ALRHIAVQAV CGETFFVQFI RNDFGHGFEG RENHALIDIG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALIVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVARRCFHD GFDVVDKAHI QHTVGFVQNG HFQTFKINFA ALHQVHQTAR
351 RGDNQIDRFA QGTGLVAERR AADDADGAEP THIFGIRQV FLDLSRQFAG
401 RGQHQSTRAF ARFFAAGQF LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

646

	10	20	30	40	50	60
m284 . pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284 . pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAFAGRFHAFDQGQFQFSVNV					
g284	TFAARFAAEAFFARFMIAAPAGFFIAPAAFAFRLAACGFAFAGRLHAFDQGQFQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284 . pep	FFDFVDFDFVHFVFGKRNTRACAAGAPDAVDVVFRLFRQVVVDNVGNRGYVDTACGNI					
g284	FFDFVDFDFVHFVFGKRNTRACAAGAPDAVDVVFRLFRQVVVDNVGNRGYVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284 . pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNFAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHRFGGRENHTLVDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284 . pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLLDFALAVHAFDFDNFRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284 . pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNHQFQTFKINFAALHQVHQTARRGDNQIDRFA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284 . seq
1  ATGCCGCTCTG  AAACTCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101 GAATCGCCGG  CTTTGCGTTT  GCCTTTGAAG  CCTTCGCCGG  TTTTTTTGAA
151 ACCGTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTCG
201 CGCCGAAGCC  TTCTTTGCTC  GGTTTATGAT  CGCCGCGCCA  ACCGCCGGAT
251 TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301 CGGTTTGCGG  GTCGGTTCCA  TGCCTTCGAT  GGTCA GTTCG  GGCAGTTTTC
351 GGTAAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTTCACTTCG
401 GCAAACGTAA  TCGCAATACC  CGTGCGGCCT  GCGCGGCCGG  TGCGCCCGAT
451 GCGGTGGACG  TAGTCTTCCG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501 GGGTAATGGT  CGGTACGTGC  ATACCGCGTG  CGGCAACGTC  GGTGGCAACC
551 AAAATTTTGC  AGCGGCCTTT  GCGCAAATCC  ATCAGCGTGC  GGTGCGCCA
601 GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  GGCGCGGAAA  CCTTTTTCGT
651 ACAATTCATC  CGCGATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAAATC
701 ACGCATTGAT  CGATGTCGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751 TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCCT
801 GGTCTGTCAC  GCGTTCGACT  TCGATGATTT  CAGGGTCTTT  GGTCA GTTTG
851 CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901 CTGACGGTCT  TCCGGCGTGG  CTTTCGACGAT  GGTTTCGATG  TCGTCGATAA
951 AGCCCATATC  CAACATACGG  TCGGCTTCGT  CCAAATCAG  CACTTCCAAG
1001 CGGGCGAAAT  CGACTTTGCC  GCTTTCATC  AAGTCCATCA  GACGGCCCGG
1051 CGTGGCGACA  ATCAGATCGA  CCGGTTTGCT  CAGGGCGCGG  GTTTGGTAGC
1101 CGAACGATGC  ACCACCGACG  ATGCTGACGG  TACGGAACCA  ACGCATATTT
1151 TTGGCATACG  CCAGCGCGTT  TTTCTCGACT  TGAGCCGCCA  ATTCGCGGGT
1201 CGGCGTCAAC  ACCAACGCGC  GCGGGCCTTT  GCCCGGTTTT  TCGCTGCGTT
1251 TGGTCAGTCG  CTGCAAAGTC  GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284 . pep
1  MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE

```

```

51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGREHAFD QQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGFGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALVVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNG HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDLSRQFAG
401 RRQHQRRARAF ARFFAAGFQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

	10	20	30	40	50	60
m284.pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
a284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDQFGQFSVNV					
a284	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDQFGQFSVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVFRQVVVDNVGNRYVDTACGNI					
a284	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVFRQVVVDNVGNRYVDTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGFGGRENHALIDIG					
a284	GGNQNFAAFAQIHQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHGFGGRENHALIDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALVHAFDFFDFRVFGQFARQFADRAVPSGGEQQS					
a284	IAQDMIEQAVFVAHIVAVQQLFFDFALVHAFDFFDFRVFGQFARQFADRAVPSGGEQQS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m284.pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNGHFQTFKINFALHQVHQTARRGDNQIDRFA					
a284	LTVFRRGFDDGFDVVDKAHIQHTVGFVQNGHFQAGEIDFAALHQVHQTARRGDNQIDRFA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m284.pep	QGTGLVAERRAADDADGAEPHTHIFGIRQRVFLDLSRQFAGRGQHQSTRAFARFFAAGQF					
a284	QGAGLVAERCTTDDADGTEPHTHIFGIRQRVFLDLSRQFAGRRQHQRRARAFARFFAAGQS					
	370	380	390	400	410	420
m284.pep	LQSRX					
a284	LQSRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

g285.seq
1 atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat ttggcagta

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151 tgtttcctcg gctggatcgc cggtagcgaa gcaggtttgc gtttcgggct
201 gtaccaaact ccgtcctggt tcggcgtaaa catttcctcc caaaacctca
251 aaggcacact gctcgacggc ttcgacggcg acaactggtc gatagaaacc
301 gagggggcag accttaaaat cagccgcttc cgcttcgctg ggaaccgctc
351 cgaactgatg cgccgcagcc tgcacatcac cgacatctcc gccggcgaca
401 tcgccatcgt aaccaaacgc actccgccta aagaagaacg cccgcctcaa
451 ggccctgccg acagcataga cctgcccgcg gctgtctatc tcgaccgctt
501 cgagacgggc aaaatcagca tgggcaaaac ctttgacaaa caaaccgtct
551 atctcgaaac cctcaacgcg gcataaccgtt acgaccgtaa agggcaccgc
601 ctcgacctga aggcggccga cagccgctgg agcagttcgt cggggtcagc
651 gtgccttcggc ttgaaaaaac cgtttgcctt cgataccgcc atttacacca
701 aaggcggatt cgaaggcgaa accatacaca gtacggcgcg gctgagcggc
751 agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg
801 cctctcggga aaatccgtca tccaccggtt tgcgcaatca ttggataaaa
851 cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc
901 gtgccttccc tgcgcgatgc cgggctgaat ttcgacctga ccgccatccc
951 gtcgttttca gacggcatcg cgctggaagg ctcgctcgat ttgaaaaaca
1001 ccaaagccgg ctttgccgac cgcaacggca tccccgtccg tcaggttttg
1051 ggccgctttg tcctccggca ggacggcagc gtgcataatc gcaatacgtc
1101 cgccgccttg ctcggacggg gcggcatcag gctgtcgggc aaaaatcgaca
1151 ccgaaaaaga catccttgat ttaaatatag gcatcaactc cgtcggcgcg
1201 gaagacgtgc tgcaaacgcg gttcaaaggc aggttgagcg gcagcatcgg
1251 catcggcggc acgaccgcct cgcccaaaat ctcttggaac ctcggcaccg
1301 gcacggcagc cagggacggc agcctcccca tcgcaagcga ccccgcaaac
1351 gaacagcgga aactggtggt cgacaccgtc aacatctccg ccggggaagg
1401 cagcctgacc gcgcaaggct atctcgagct gtttaaagac cgctgctca
1451 agctggacat ccgttccgcg gcattcgacc cttcgcgcac cgatccgcaa
1501 ttcccggcag gcaatatcaa cggttcgatt catcttgccg gtgaactggc
1551 aaaagagaaa tttacgggca aaatgcgttt tttgcccgtt acgttcaacg
1601 gcgtgccgat tgccggcagc gccgacattg tttacgagtc ccgccacctt
1651 ccgcgcggcg ccgtcgattt gcggttgggg cggaacatcg tcaaaacaga
1701 cggcggttcc ggcaaaaaag gcgaccggct taacctcaat atcaccgcac
1751 ccgatttatc ccgtttcggg ttccgactcg cggggctctt aaatgtacgc
1801 ggacaccttt ccggcgattt ggacggcggc atccgaacct ttgaaaccga
1851 cttttccggc acggcgcgca acttacacat cggcaaaagc gcagacatcc
1901 tttcgctcga ttttaccctc aaaggctcac ccggcacaag ccgccgatg
1951 cgcgccgata tcaagggcgg ccgcctttcc ctgtcgggcg gcgcggcggt
2001 tgtcgatacc gccggcctga cgctggaagg tacgggcgcg cagcaccgca
2051 tccgcacaca cgccgccatg acgctggacg gcaaaccgtt caaactcgat
2101 ttggacgctt caggcgcat caacaggga cttaccgat ggaaaggcag
2151 catcggcatc ctcgacatcg gcggcgcat caacctcaag ctgcaaaacc
2201 gtatgacgct cgaagccggt gcggaacacg tggcggaag tgcggcaaat
2251 tggcaggcaa tggcgcgag cctcaacctg caaactttt cttgggacag
2301 gaaaaccggc atatcggcaa aaggcggcgc acggcgctg cacatcgccg
2351 agttgcacaa tttcttcaaa ccgcccttcg aacacaatct ggttttaaac
2401 ggcgactggg atgtcgcta cgggcacaac gcgcgggct acctcaatat
2451 cagccggcaa agcggcgatg ccgtattgcc cggcgggcag gctttgggtt
2501 tgaacgcatt ttccctgaaa acgcgcttcc aaaaacgacc catcggaatc
2551 ctgcttgacg gcggcgcgcg tttcggacgg attaacgccg atttgggcat
2601 cggcaacgcc ttcggcggca atatggcaaa tacaccgctc ggcggcagga
2651 ttacagcctc ccttcccagc ttggcgcat tgaagccctt tctgcccgc
2701 gccgcgcaaa acattaccgg cagcctgaat gcctccgcgc aaatcggcg
2751 acgggtaggc tctccgtccg tcaatgccgc cgtcaacggt agcagcaact
2801 acgggaaaat caacggcaat atcaccgtcg ggcaaggcgc ctcttcgat
2851 accgcacctt tggcgcgag gctcaacctg accgttgccg atgccgaagc
2901 attccgcaac ttcctaccgg tcggacaaac cgtcaaaggc agcctgaatg
2951 ccgcgtaac ctcggcggc agcatcgccg acccgcaatt gggcggcagt
3001 atcaacggcg acaagctcta ttaccgcaac caaacccaag gcatactctt
3051 ggacaacggc tcgctgcgtt cgcataattg aggcaggaaa tgggtaatcg
3101 acagcctgaa attccgcac gaagggaacg cggaactctc cggcagcgctc
3151 agcatggaaa acagcgtgcc cgtatgcgat atcggcgcgg tgttcgacaa
3201 ataccgcac ctgtcccgc ccaaccgccg cctgacgggt tccggcaaca
3251 cccgcctgcg ctattcgccg caaaaaggca tatccgttac cggatgatt
3301 aaaactgatc aggggctgtt cggttcgcaa aaatcctcga tgcctccgt
3351 cggcgacgat gtcgtcgat tggcggaagt caagaaagag gcggcgcat
3401 cgctccccgt caatatgaac ctgactttag acctcaatga cggcatccgc

649

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3451 ttctccggct acggcgcgga cgttaccata ggccggcaaac tgaccctgac
3501 cgcgcaaccg ggccggaatg tgcgtggggt gggcacggtc cgcgtcatca
3551 aaggcggtta caaagcatat gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgct caacgacccc aacctgaaca tccgcgcga
3651 acgcccgtt tccccgtcg gtgcggcggt ggaaatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggcagcgcca gcagcgcgga
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctgggt gatgatttgg gctttaccag caagcgcagc
3901 cgcaacggcg aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accggctgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccgttcg tcggcgcgcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacggcaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

g285.pep

```

1 MTDTTPTDTD PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGNWSIET
101 EGADLKISRF RFAWKPSSELM RRS LHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLPA AVYLDRFETG KISMGKTFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTFW SSSSGSASVG LKKPFALDTA IYTKGGFEGE TIHSTARLSG
251 SLKDVRAELT IDGGNIRLSG KSVIHPPAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFs DGIALEGLSD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGTGARTDGL SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTDGGF GKKGDRLNLN ITAPDLRFRG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLSC TARNLHIGKA ADIRSLDFTL KGSPGTSRPM
651 RADIKGGRLS LSGGAAVVDT AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKGSGI LDIGGAFNLK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSNLN QHFSWDRKTG ISAKGGARGL HIAELHNFFK PPFEHNLVLN
801 GDWDVAYGHN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNTIGSLN ASAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSD
951 TAPLGRLNL TVADAEAFRN FLVPGQTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 SMENSVPDVG IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADVTI GSKLTTLTAQP GGNVRGVGT VIKGRYKAY GQDLITKGT
1201 VSVFGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGRS SGGELTYTIR FDRLFSGDKK DSAGNGK GK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

m285.seq

```

1 ATGACCGATA CCGCACCAGC AGATACCGAT CCGACCGAAA ACGGCACGCG
51 CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCCTGAT TTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGCGGTAAA CATTTCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTC CGCTTCGGCT GGAAACCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTCC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCC ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CACGCCGTG AGCAGTTCGT CGGGGGCGGC
651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

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801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
 851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCCTTC
 901 GTGCCTTCCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC
 951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG TTCGCTCGAT TTGGAAAAACA
 1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCGTCCG TCAGGTTTTA
 1051 GGCGGCTTTG TCATCCGGCA GGACGGCAGC GTGCATATCG GCAATACGTC
 1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA
 1151 CCGAAAAAGA CATCTCGAT TTAATATAG GCATCAACTC CGTCGGCCGG
 1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
 1251 CATCGGTGGC ACGACCGCCT CGCCAAAAT CTCTTGGCAA CTCGGCATCG
 1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC
 1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
 1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
 1451 AGCTGGACAT CCGTTCCCGC GCATTTCGACC CTTCCGCGAT CGATCCGCAA
 1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
 1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
 1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
 1651 CCGCGTGCCG CCGTCGATT TCGGCTGGGG CGGAACATTA TTAACACAGA
 1701 CGGCGGCTTC GGCAAAAAG GCGACCGGCT TAACCTCAAT ATCACCGCAC
 1751 CCGATTATAT CCGTTTCGGT TTCGGACTCG CGGGGTCTTT AAATGTACGC
 1801 GGACACCTTT CCGGTGATT GGACGGCGGC ATCCGAACCT TTGAAACCGA
 1851 CCTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
 1901 GTTCGCTCGA TTTCACGCTC AAAGGTTTCG CCGACACAAG CCGCCCGATA
 1951 CGCGCCGACA TCAAAGGCAG CCGCCTTTCG CTGTCGGGCG GAGCGGCGGT
 2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGCA
 2051 TCCGCACACA CGCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
 2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAGGCGAG
 2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
 2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGGGGCAAT
 2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTTGGGATAA
 2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
 2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
 2401 GGCGACTGGG ATGTCGCCTA CGGGCGCAAC GCGCGCGGCT ACCTCAATAT
 2451 CAGCCGGCAA AGCGCGGATG CCGTATTGCC CGGCGGGCAG GCTTTGGGTT
 2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC
 2551 CTGCTTGACG GCGGCGCGCG TTTCCGGGCG ATTAACGCCG ATTTGGGCAT
 2601 CGCCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA
 2651 TTACCGCCTC CCTTCCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC
 2701 GCCGCGCAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG
 2751 ACGGGTAGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
 2801 ACGGGAATA CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT
 2851 ACCGCGCCTT TGGGCGGCAG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
 2901 ATTCCGCAAC TTCCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
 2951 CCGCCGTAA CCGCGCGGC AGCATCGCCG ATCCGCACTT GGGCGGCAGC
 3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCAAG GCATCATCTT
 3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
 3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CGGAACCTC CGGTACGGTC
 3151 GGTATGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTTCGACAA
 3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGTT TCCGGCAACA
 3251 CCCGCTGCG CTATTGCGCG CAAAAGGCA TATCCGTTAC CGGGATGATT
 3301 AAAACGGATC AGGGGCTGTT CGGTTTCGCA AAATCCTCGA TGCCGTCCGT
 3351 CGGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
 3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCG
 3451 TTCGCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAAAC TGACCCTGAC
 3501 CGCCCAATCG GCGGAAGCG TACGGGGCGT GGGCACGGTC CGCGTCATCA
 3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
 3601 GTCTCCTTTG TCGGCCCGCT CAACGATCCC AACCTCAACA TCCGCGCCGA
 3651 ACGCCGCTT TCCCGCGTCG GTGCGGGCGT GGAATATTG GGCAGCTCA
 3701 ACAGCCCGCG CATTACGCTG ACGGCAAACG AACCGATGAG TGAAGAGAGC
 3751 AAGCTCTCTT GGCTCATCCT CAACCGCGCC GGCAGCGGCA GCAGCGGCGA
 3801 CAATGCGGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAAATCA
 3851 ACGACCGCAT CGGGCTGGTG GATGATTGTT GCTTTACCAG CAAGCGCAGC
 3901 CGCAACGCGC AAACCGCGCA ACTCAACCCC GCCGAACAGG TGCTGACCGT
 3951 CGGCAAAACA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
 4001 CCAGCGCGGA ACAGTCCGTC AAATGATTTT ACCGGCTGAC CCGCGCCATA
 4051 CAGGCGGTTG CCGGTATCGG CAGCCGTTTCG TCGGGCGGCG AGCTGACATA

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
 4151 GAAACGGCAA AGGAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep
 1 MTDAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
 51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
 101 EGADLKISRF RFAWKPSSELM RRLSHITEIS AGDIAIVTKP TPPKEERPPL
 151 SLPDSIDLPA AVYLDREFETG KISMCKAFDK QTVYLERLDA SYRYDRKGHR
 201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
 251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF
 301 VPSLPDAGLN FDLTAIPSF S DGIALEGLD LENTKAGFAD RNGIPVRQVL
 351 GGFVIRQDGT VHIGNTSAAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
 401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
 451 GQRKLVLDTV NIAAGQSSLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
 501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
 551 PRAAVDLRLG RNIKTGSGF GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
 601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
 651 RADIKGSRLS LSGGAADVDT ADMLDGTGV QHRIRTHAAM TLDGKPFKFD
 701 LDASGGINRE LTRWKSIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
 751 WQAMGGSNL OHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENHLVLN
 801 GDWDVAYGRN ARGYLNISQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
 851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRTASLPD LGALKPFLPA
 901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYKINGN ITVGQSRSD
 951 TAPLGRLNL TVADAEVFRN FLVPGQTVKG SLNAAVTLGG SIADPHLGS
 1001 INGDKLYRN QTGGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
 1051 GMENSGPDVD IGAVFDKYRI LSRPNRLTV SGNTRLYSP QKGISVTGMI
 1101 KTDQGLFGSQ KSSMPVSGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR
 1151 FAGYGADVTI GGLTLTAQS GGSVRGVGTV RVIKGRYKAY QDLDITKGT
 1201 VSFVGLNDP NLNIRAERL SPVGAGVEIL GSLNSPRITL TANEPMSKD
 1251 KSLWLILNRA GSGSSGDNA LSAAGALLA QINDRIGLV DDLGFTSKRS
 1301 RNAQTGELNP AEQVLTGKQ LTGKLYIGYE YSISSAEQSV KLIYRLTRAI
 1351 QAVARIGSRS SGGELTYTIR FDRFSGSDDK DSAGNGKKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
	: : : : :					
g285	MTDTTPTDPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m285.pep	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRAWKPSSELM					
	: : : : :					
g285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRAWKPSSELM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m285.pep	RRLSHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAYYLDREFETGKISMCKAFDK					
	: : : : :					
g285	RRLSHITDISAGDIAIVTKPTPPKEERPQLPDSIDLPAAYYLDREFETGKISMCKTFDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
	: : : : :					
g285	QTVYLERLNAARYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGFEGE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					

652

g285
|||:|||||
TIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIHPFAESLDKTL EEVLVKGFNINPSAF
250 260 270 280 290 300

m285.pep
310 320 330 340 350 360
VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT
|||:|||||

g285
VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT
310 320 330 340 350 360

m285.pep
370 380 390 400 410 420
VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTA FKGRLDGSIGIGG
|||:|||||

g285
VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTA FKGRLDGSIGIGG
370 380 390 400 410 420

m285.pep
430 440 450 460 470 480
TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
|||:|||||

g285
TTASPKISWQLGIGTARTDGS LPIASDPANEQRKLVFDTVNISAGEGS LTAQGYLELFKD
430 440 450 460 470 480

m285.pep
490 500 510 520 530 540
RLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRF LPGTFNGVPIAGS
|||:|||||

g285
RLLKLDIRSRAFDPSRIDPQFPAGNINGSIHLAGELAKEKFTGKMRF LPGTFNGVPIAGS
490 500 510 520 530 540

m285.pep
550 560 570 580 590 600
ADIVYESRHLPRAAVDLRLGRNIIKT DGGFGKKGDRLNLNITAPDLSRFGFGLAGSLNVR
|||:|||||

g285
ADIVYESRHLPRAAVDLRLGRNIVKT DGGFGKKGDRLNLNITAPDLSRFGFGLAGSLNVR
550 560 570 580 590 600

m285.pep
610 620 630 640 650 660
GHLSGDL DGGIRTFETDLSGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
|||:|||||

g285
GHLSGDL DGGIRTFETDLSGTARNLHIGKAADIRSLDFTLKGSPGTSRPMRADIKGGRLS
610 620 630 640 650 660

m285.pep
670 680 690 700 710 720
LSGGA AVVDADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSIGI
|||:|||||

g285
LSGGA AVVDAGLTLEGTGAQHRIRTHAAMTLDGKPFKLDLDASGGINRELTRWKSIGI
670 680 690 700 710 720

m285.pep
730 740 750 760 770 780
LDIGGA FNKLQNRMTLEAGAERVAASAANWQAMGGSLNLQHFSWDKKTGISAKGGAHGL
|||:|||||

g285
LDIGGA FNKLQNRMTLEAGAEHVAASAANWQAMGGSLNLQHFSWDRKTGISAKGGARGL
730 740 750 760 770 780

m285.pep
790 800 810 820 830 840
HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
|||:|||||

g285
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790 800 810 820 830 840

m285.pep
850 860 870 880 890 900
TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
|||:|||||

g285
TRFQNDRIGILLDGGARFGRINADLGIGNAFGGNMANTPLGGRITASLPDLGALKPFLPA
850 860 870 880 890 900

m285.pep
910 920 930 940 950 960
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a285.seq

1	ATGACCGATA	CCGCACCGAC	AGATAACCGAT	CCGACCGAAA	ACGGCACGCG
51	CAAAATGCCG	TCTGAACACC	GCCCTTACCC	GCCGGCAAAA	AAACGCCGCC
101	CGCTGCTGAA	GCTGTCGGCG	GCACCTGCTGT	CTGTCTCTGAT	TTTGGCAGTA
151	TGTTTCTCTG	GCTGGCTCGC	CGGCACGGAA	CGGGGTTTGC	GCTTCGGGCT
201	GTACCAAATC	CCGTCTTGTT	TCGGCGTAAA	CATTTCTCTC	CAAAACCTCA
251	AAGGCACGCT	GCTCGACGGC	TTCGACGGCG	ACAACCTGGT	GATAGAAACC
301	GAGGGGGCAG	ACCTTAAAA	CAGCCGCTTC	CGCTTCGCGT	GGAAACCGTC
351	CGAAGTATG	CGCCGACGCC	TGCACATTAC	CGAAATTTCC	GCCGGCGACA
401	TCGCCATCGT	TACCAAACCG	ACTCGCCTA	AAGAAGAACG	CCCGCCGCTC
451	AGCCTTCCGG	ACAGCATAGA	CCTGCCTGCC	GCCGTCTATC	TCGACCGCTT
501	CGAGACGGGC	AAATCAGAC	TGGGCAAAGC	CTTTGACAAA	CAAACCGTCT
551	ATCTCGAACG	GCTGGATGCT	TCATACCGTT	ACGACCGCAA	AGGACACCGC
601	CTCGACCTGA	AGGCTGCCGA	CACGCGGTGG	AGCAGTTCTG	CGGGGTCAGC

651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
 701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
 751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG
 801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGATAAAAA
 851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GTCCGCCCTTC
 901 GTGCCCTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC
 951 GTCGTTTCA GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGAAAAACA
 1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCCG TCAGGTTTTA
 1051 GGCAGCTTTG TCATCCGGCA GGACGGCAGG GTGCATATCG GCAATACGTC
 1101 CGTCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA
 1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGCTGCGCGG
 1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
 1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGCAA CTCGGCATCG
 1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAACGGA CCCCGCAAAC
 1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
 1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCTGCTCA
 1451 AGCTGGACAT CCGTTCCCGC GCATTGACC CTTGCGCAT CGATCCGCAA
 1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
 1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACCTTCAACG
 1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
 1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAAAAACAG
 1701 GCGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCAGC
 1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CCGGGTCTTT AAATGTACGC
 1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA
 1851 CCTTTCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
 1901 GTTCGCTCGA TTTCACGCTC AAAGTTTCGC CCGACACAAG CCGCCCGATA
 1951 CCGCCCGACA TCAAAGGCAG CCGCCTTTCG CTGTCGGGCG GAGCGGAGGT
 2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGCA
 2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
 2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAAGGCAG
 2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAAAC
 2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TCGGCAAAAT
 2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTTGGGATAA
 2301 AAAAACCAGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
 2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
 2401 GCGGACTGGG ATGTGCGCTA CCGGCGAAAC GCGGCGGGCT ACCTCAATAT
 2451 CAGCCGCAA AGCGGCGATG CCGTATTGCC CCGGCGGCG GCTTTGGGTT
 2501 TGAACGCATT TTCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC
 2551 CTGCTTGACG GCGGCGCGCG TTTCCGGGCG ATTAACGCGG ATTTGGACAT
 2601 CGGCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA
 2651 TTACCGCTC CTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC
 2701 GCCGCGCAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG
 2751 ACGGGTCGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
 2801 ACGGGAAAAT CAACGGCAAC ATCACCCTCG GGCAAGCCG CTCTTTCGAT
 2851 ACCGCGCCTT TGGGCGGCAG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
 2901 ATTCCGCAAC TTCTTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
 2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGGCAGC
 3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT
 3051 GGACAACGGC TCCTGCGTTC CGCATATCGC GGGCAGGAAA TGGGTAATCG
 3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CGGAACCTC CGGTACGGTC
 3151 GGTATGGAAC ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTGACAA
 3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGTT TCCGGCAACA
 3251 CCCGCTGCG CTATTCGCGC CAAAAAGGCA TATCCGTTAC CGGGATGATT
 3301 AAAACGGATC AGGGGCTGTT CGGTTTCGCA AAATCCTCGA TGCCGTCGGT
 3351 CCGCGACGAT GTCGTGCTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
 3401 CGTCCCGCT CAATATGAAC CTGACTTAG ACCTCAATGA CGGCATCCGC
 3451 TCGCCGGCT ACGGCGCGGA CGTTACCATA GCGGCGAAAC TGACCCTGAC
 3501 CGCCCAATCG GCGGAAGCG TGCGGGCGT GGGCACGGTC CGCGTCATCA
 3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
 3601 GTCTCCTTTG TCGGCCCGCT CAACGACCCC AACCTCAACA TCCGCGCCGA
 3651 ACGCGCCTT TCCCCGTCG GTGCGGGCGT GGAAATATTG GGCAGCCTCA
 3701 ACAGTCCGCG CATTACGCTG ACGGCAAACG AACCGATGAG TGA AAAAGAC
 3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAAGTGCA GCAGCGGCGA
 3801 CAATGCCGCG CTGTCCGCG CCGCCGCGCG GCTGCTTGCC GGGCAAATCA
 3851 ACGACCGCAT CCGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
 3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT

655

3951 CGGCAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
 4001 CCAGCGCGGA ACAGTCCGTC AAAGTGATT ACCGGCTGAC CCGCGCCATA
 4051 CAGGCGGTTG CCCGTATCGG CAGCCGTTG TCGGGCGGCG AGCTGACATA
 4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
 4151 GAAACAGCAA AGGAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

a285.pep
 1 MTDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
 51 CFLGWLAGE AGLRFGlyQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
 101 EGADLKISRF RFAWKPELM RRS LHTEIS AGDIAIVTKP TPPKEERPPL
 151 SLPDSIDLPA AVYLD RFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
 201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
 251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEV LV KGFNINPSAF
 301 VPSLPDAGLN FDLTAIPSF DGIALEGS LD LENTKAGFAD RRGIPVRQVL
 351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
 401 EDVLQTAFCG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
 451 GQRKVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
 501 LPAGNINGSI NLAGE LAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
 551 PRAAVDLRLG RNIKT DGGF GKKGDRLNLN ITAPDLSRFG FGLAGSLNVR
 601 GHLSGDL DGG IRTFETDL SG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
 651 RADIKGSR LS LSGGAEVVD T ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
 701 LDASGGINRE LTRWKGSGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
 751 WQAMGGS LNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENHLVLN
 801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
 851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFPLPA
 901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSPD
 951 TAPLGGRLNL TVADA EVFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGGS
 1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAEISGTV
 1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
 1101 KTDQGLFSGQ KSSMPSVGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR
 1151 FAGYGADVTI GGLTLTAQS GGSVRGVGT VIKGRYKAY GQDLDTKGT
 1201 VSFVGPLNDP NLNIRAERL SPVGAGVEIL GSINSPRITL TANEPMSEKD
 1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
 1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
 1351 QAVARIGSRS SGGELTYTIR FDRFSGSDDK DSAGNSKKG*

m285/a285 99.4% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
a285	MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m285.pep	AGLRFGlyQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRF RFAWKPELM					
a285	AGLRFGlyQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRF RFAWKPELM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m285.pep	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLD RFETGKISMKGAFDK					
a285	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLD RFETGKISMKGAFDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
a285	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVRAELIDGGNIRLSGKSVIHPFAESLDKTLEEV LVKGFNINPAAF					

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a285	TIHSTARLSGSLKDVRAELAI	DGGNIRLSGKSVIH	PF	AE	SLDKTLEEVLVKG	FNINPSAF
	250	260	270	280	290	300
	310	320	330	340	350	360
m285.pep	VPSLPDAGLNFDLTAIP	SFSDGIALEGS	LDLENTKAGFADR	NGIPVRQVLGGF	VIRQDGT	
a285	VPSLPDAGLNFDLTAIP	SFSDGIALEGS	LDLENTKAGFADR	NGIPVRQVLGSF	VIRQDGT	
	310	320	330	340	350	360
	370	380	390	400	410	420
m285.pep	VHIGNTSAALLGRGGIR	LSGKIDTEKDILD	LNIGINSVGAEDV	LQTAFKGR	LDGSIGIGG	
a285	VHIGNTSAALLGRGGIR	LSGKIDTEKDILD	LNIGINSVGAEDV	LQTAFKGR	LDGSIGIGG	
	370	380	390	400	410	420
	430	440	450	460	470	480
m285.pep	TTASPKISWQLGIGTAR	TGSLAIASDPANG	QRKLVLDTVNIAAG	QGS	SLTAQGYLE	LFKD
a285	TTASPKISWQLGIGTAR	TGSLAIASDPANG	QRKLVLDTVNIAAG	QGS	SLTAQGYLE	LFKD
	430	440	450	460	470	480
	490	500	510	520	530	540
m285.pep	RLKLDIRSRAFDPSRID	PQLPAGNINGSIN	LAGELAKEFTGKM	RFLPGTFNGV	PIAGS	
a285	RLKLDIRSRAFDPSRID	PQLPAGNINGSIN	LAGELAKEFTGKM	RFLPGTFNGV	PIAGS	
	490	500	510	520	530	540
	550	560	570	580	590	600
m285.pep	ADIVYESRHLFRAAVDL	RRLGRNIIKTDGG	FGGKGDRLNLNIT	APDLSRFG	FGLAGSLNVR	
a285	ADIVYESRHLFRAAVDL	RRLGRNIIKTDGG	FGGKGDRLNLNIT	APDLSRFG	FGLAGSLNVR	
	550	560	570	580	590	600
	610	620	630	640	650	660
m285.pep	GHLSGDLGGIRT	FETDLSGAARNLHIG	KAADIRSLDFTL	KGSPDTSRPI	RADIKGSRLS	
a285	GHLSGDLGGIRT	FETDLSGAARNLHIG	KAADIRSLDFTL	KGSPDTSRPI	RADIKGSRLS	
	610	620	630	640	650	660
	670	680	690	700	710	720
m285.pep	LSGGAHVVD	TADLMLDGTGVQHR	IRTHAAMTLDGK	PFKFDLDASGG	INRELTRWK	SGSIGI
a285	LSGGAHVVD	TADLMLDGTGVQHR	IRTHAAMTLDGK	PFKFDLDASGG	INRELTRWK	SGSIGI
	670	680	690	700	710	720
	730	740	750	760	770	780
m285.pep	LDIGGAFNLKLQNRMT	LEAGAERVAASAAN	WQAMGGS	LNQHF	SWDKKTGISAK	GGAHGL
a285	LDIGGAFNLKLQNRMT	LEAGAERVAASAAN	WQAMGGS	LNQHF	SWDKKTGISAK	GGAHGL
	730	740	750	760	770	780
	790	800	810	820	830	840
m285.pep	HIAELHNFFKPPFEHN	LVNGDWDVAYGRN	ARGYLNISRQSG	DAVLPGGQAL	GLNAFSLK	
a285	HIAELHNFFKPPFEHN	LVNGDWDVAYGRN	ARGYLNISRQSG	DAVLPGGQAL	GLNAFSLK	
	790	800	810	820	830	840
	850	860	870	880	890	900
m285.pep	TRFQNDRIGILLDGGAR	FGRINADLGIANAF	GGNMANAPLGG	RITASLPDLG	ALKPFLPA	
a285	TRFQNDRIGILLDGGAR	FGRINADLGIANAF	GGNMANAPLGG	RITASLPDLG	ALKPFLPA	
	850	860	870	880	890	900
	910	920	930	940	950	960
m285.pep	AAQNITGSLNAAQIG	GRVGS	PSVNAAVNGSS	NYKINGNITV	QSRSFDTAP	LGGRLNL
	910	920	930	940	950	960

657

a285	AAQNITGSLNAAQIGGRVGS	PSVNA	AVNGSSNY	KINGNIT	VGQSR	SFDTAP	LGGRLNL
	910	920	930	940	950	960	
m285.pep	TVADA	EVFRN	FLPVG	QTVKGS	LNA	AVTLGGS	ADPHL
	970	980	990	1000	1010	1020	
a285	TVADA	EVFRN	FLPVG	QTVKGS	LNA	AVTLGGS	ADPHL
	970	980	990	1000	1010	1020	
m285.pep	SLRSH	IAGRK	WVIDSL	KFRHEG	TAELSG	TVGMEN	SGPDVD
	1030	1040	1050	1060	1070	1080	
a285	SLRSH	IAGRK	WVIDSL	KFRHEG	TAELSG	TVGMEN	SGPDVD
	1030	1040	1050	1060	1070	1080	
m285.pep	SGNTR	LRYS	PQKG	ISVTG	MIKTD	QGLFG	SQKSS
	1090	1100	1110	1120	1130	1140	
a285	SGNTR	LRYS	PQKG	ISVTG	MIKTD	QGLFG	SQKSS
	1090	1100	1110	1120	1130	1140	
m285.pep	LTLDL	NDGIR	FAGY	GADVT	IGGKLT	LTAAQ	SGG
	1150	1160	1170	1180	1190	1200	
a285	LTLDL	NDGIR	FAGY	GADVT	IGGKLT	LTAAQ	SGG
	1150	1160	1170	1180	1190	1200	
m285.pep	VSVFG	PLNDP	NLNIRA	ERRLSP	VGAG	VEILGS	LSNSPR
	1210	1220	1230	1240	1250	1260	
a285	VSVFG	PLNDP	NLNIRA	ERRLSP	VGAG	VEILGS	LSNSPR
	1210	1220	1230	1240	1250	1260	
m285.pep	GSGSS	GDNAAL	SAAAG	ALLAGQ	INDRIG	LVDL	LGFTSK
	1270	1280	1290	1300	1310	1320	
a285	GSGSS	GDNAAL	SAAAG	ALLAGQ	INDRIG	LVDL	LGFTSK
	1270	1280	1290	1300	1310	1320	
m285.pep	LTGKLY	IGYEYS	ISSAEQ	SVKLIY	RLTRAI	QAVAR	IGSRSS
	1330	1340	1350	1360	1370	1380	
a285	LTGKLY	IGYEYS	ISSAEQ	SVKLIY	RLTRAI	QAVAR	IGSRSS
	1330	1340	1350	1360	1370	1380	
m285.pep	DSAGN	GK	GKX				
	1390						
a285	DSAGN	GK	GKX				
	1390						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

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1   CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCCTG CTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACACTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATCACCAGCA TCTCCGCCGG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAGGCCT
351 GCCCGACAGC ATAGACCTGC CCGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAAACAAAC CGTCTATCTC
451 GAACGCCCTA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG

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551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTGGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CCGCGCCGAAC TGACGATCGA CCGCGGCAAT ATCCGCCTCT
701 CCGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTTGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCTGCCCC GATGCCGGGC TGAATTTGCA CTGACCGGCC ATCCCGTCGT
851 TTTACAGACG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTGGGCGG
951 CTTTGTGATC CCGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCCTGTCTCG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TTGATTTAAA TATAGGCATC AACTCCGTG GCGCGGAAGA
1101 CGTGCTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCTCGCCCC AAAATCTCTT GGCAACTCGG CACCGGCAGC
1201 GCACGCACGG ACGCCAGCCT cgcCATGCA AGCGAcCCCC CAAACGAACA
1251 GCGGAAACTG GTGTTGACAC CCGTCAACAT CTCCGCCGGG GAAGGCAGCC
1301 TGACCGGCGA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCCTCG CGCATCGATC CGCAATTTCC
1401 GGCAGGCGat atCAACGGTT CGATTCTCTT TGCCGGTGAA CTGGCAAAAG
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTGC CCGGTACGTT CAACGGCGTG
1501 CCGATTGCCG GCAGCGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 CGCCGCCGCT GATTGCGGT TGGGGCGGAA CATCGTCAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACCGGACA
1701 CCTTCCGGC GATTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCGGTCG
1801 CTCGATTTTA CCCTCAAAGG CTCACCCGGC ACAAGCCGCC CGATCGCGC
1851 CGATATCAAG GCGGCGCGCC TTTCCCTGTC GGGCGGCGCG GCGGTTGTG
1901 ATACCGCCGG CTTGACGCTG GAAGGTACGG GCGCGCAGCA CCGCATCCG
1951 ACACACGGCC CCATGACGCT GGACGGCAA CCGTTCAAC TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGTTCGAAG CCGGTGCGGA ACACGTGGCG GCAAGTGCGG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTTCTTGG GACAGGAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACGCG GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GACGGATTAA CGCCGATTG GGCATCGGCA
2501 ACGCCTTCGG CCGCAATATG GCAATACAC CGCTCGGCGG CAGGATTACA
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTCTGCG CCGCCGCCCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCTC CGCGCAAATC GCGGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGTAGCAG CAACTACGGG
2701 AAAATCAACG GCAATATCAC CGTCGGGCAA AGCCGCTCCT TCGATACCGC
2751 ACCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGCATTC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG GCGGCAGCAT CGCCGACCCG CACTTGGGCG GCAGTATCAA
2901 CGGCACAAG CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT GCGTTCGCAT ATTGCAGGCA GGAAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGCA CGGTACGAT
3051 GGAAAACAGC GTGCCCGATG TCGATATCGG CCGGTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCAAC CGCCGCTGA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGTA TGATTAAAC
3201 TGATCAGGGG CTGTTGCGTT CGCAAAAATC CTCGATCGCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTGGGC GAAGTCAAGA AAGAGGCGGC GGCATCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCTC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCGC
3401 AACCGGGCGG AAATGTGCGT GGGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTACAAAG CATAACGGCA GGATTAGAC ATTACCAAAG GCACAGTCTC
3501 CTTTGTGCGC CCGCTCAACG ACCCAACCT GAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGGC GCGGTGAAA TATTGGGCG CCTCAACAGC
3601 CCGCGCATTA CGTACGCGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCTTGCTC ATCTCAACC GTGCCGCGC GGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC CGCAGCGGCA GCGCGCTGCG TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 GCGGCAAAAC GCGGAACTCA ACCCGCCGA ACAGGTGCTG ACCGTCGGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAAC TATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCGGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTCTTTC GGTTCGGACA AAAAGACTC CGCAGGAAAC
4051 GGCAAGGGA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:
g285-1.pap

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1  LKLSAALLSV LILAVCFLGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAYLD RFETGKISMV KTFDKQTVYL
151 ERLNAAYRYD RKGHRLDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETINST ARLSGSLKDV RAEITIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRDLGS IGIGGTTASP KISWQLGTGT
401 ARTDGSALAIA SDPANEQRKL VFDTVNISAG EGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAGL LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLSG DLDGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKGSFG TSRPMRADIK GGRLSLSGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAEHVA ASAAWQAMG GSNLQHFWS DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISRQSGDAV LPGGOALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIGNAFGGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSNLASAQI GGRVGSFSPVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRNLTVADA EAFRNFLPVG QTVKGSNLAA
951 VTLGGSIAIDP HLGGSINGDK LYRNTQOGI ILDNGLSLRH IAGRWVIDS
1001 LKFRHEGTAE LSGTSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDVVVLG EVKKEAAASL
1101 PVMNLTLDL NDGIRFSGYG ADVTIGKLT LTAQPPGNVR GVGTVRVIK
1151 RYKAYGQDL DITKGTVSFVG PLNDPNLNIR AERRLSFVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGRSSSGGEL TYTIRFDRLF GSDKKDSAGN
1351 GKGR*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGCTCTGC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGTTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGGTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAC CCGTCCGAAC
251 TGATGCGCGC CAGCCTGCAC ATTACCGAAA TTTCCGCCGG CGACATCGCC
301 ATCTGTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCCTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTGCGGG GCGGCCCTCG
551 TCGGCTTGAA AAAACCGTTT GCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGAATCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGCAAT ATCCGCTCT
701 CGGGAAATC CGTCATCCAC CCGTTTCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGCCCG CCTTCGTGCC
801 TTCCCTGCCG GATGCCGAC TGAATTTGCA CCTGACGCC ATCCCGTCGT
851 TTTGAGACGG CATCGCGCTG GAAGGTTGCG TCGATTTGGA AAACACAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTAGGCGG
951 CTTTGTCATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCTGTGCTCG ACGGGCGGCG ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAG CGCCTCGCCC AAAATCTCTT GGCAACTCG CATCGGCACG
1201 CGCGCAGCGG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAACTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGCGGAA CTGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCCG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCGCGCGTC GATTTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGCGGAC CGGCTTAACC TCAATATCAC CGCACCAGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTCCGGT GATTTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCCGTTCC
1801 CTCGATTTCG CGCTCAAAGG TTCGCCCCGAC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCGGCC TTTGCTGTC GGGCGGAGCG GCGGTTGTCG
1901 ATACCGCGCA CCTGATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCCG
1951 ACACACGCGC CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGCG GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATTCCTCGA CATCGCGGCG GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA

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2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GCAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCGG CGATGCCGTA TGGCCGCGCG GGCAGGCTTT GGGTTTGAAC
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2451 TGACGGCGGC GCGCGTTTCG GCGGATTAA CGCCGATTG GGCATCGCCA
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2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCCGCCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAATC GCGGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGG GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CGGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTCGCAT ATCGCGGCGA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTGGTAT
3051 GGAAAACAGC GGACCCGATG TCGATATCGG CGCGGTGTTC GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCTGA CGGTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAAA
3201 GGATCAGGGG CTGTTCCGTT CGCAAAAATC CTCGATGCCG TCCGTGGCG
3251 ACCATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCG
3351 CCGCTACGGC GCGGACGTTA CCATAGCGCG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTACGG GCGGTGGGCA CGGTCCCGCT CATCAAAGG
3451 CGTTATAAGG CATACGGGCA GGATTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTCCGG CGGCTCAACG ATCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGAAA TATTGGGCG CCTCAACAGC
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCTTGGGTC ATCCTCAACC GCGCCGGCAG CGGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC TGCAGCCGCA GGTGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAAG GCAGCCGCAA
3801 CGCGCAAACC GCGCAACTCA ACCCGCCCGA ACAGGTGCTG ACCGTCCGCA
3851 AACACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTGGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCCA CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 GGCAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.pap

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1 LKLSAALLSV LILAVCF LGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51 TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG AASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAEALIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVRGFNI NPAAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGTTASP KISWQLGIGT
401 ARTDGLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLG DLDGGIRTFE TDLGGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA AVVDATDML DGTGVQHRIR
651 THAAMTLDGK PFKEOLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASAANWQAMG GSLNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGM ANAPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSNAAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGO SRSEDTAPLG GRLNLTVADA EVFRNFPVG QTVKGS LNAA
951 VTLGGSIADP HLGGSSINGDK LYRNTQOGI ILDNGLSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DRYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVMNMLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSKDKDSAGN
1351 GRGK*

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g285-1/m285-1 96.5% identity in 1354 aa overlap

10

20

30

40

50

60

g285-1.pep	LKLSAALLSVLILAVCFLGWIAGTEAGLRFGLYQIPSWFGVNISSQNKGTLDDGFDGDN
m285-1	LKLSAALLSVLILAVCFLGWLAGEAGLRFGLYQIPSWFGVNISSQNKGTLDDGFDGDN
	10 20 30 40 50 60
g285-1.pep	70 80 90 100 110 120
	WSIETEGADLKISRFRFAWKPSSELMRRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDS
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPFSLPDS
	70 80 90 100 110 120
g285-1.pep	130 140 150 160 170 180
	IDLPAAYVLDRFETGKISMGKTFDKQTVYLERLNAAYRYDRKGHRDLKAADTPWSSSSG
m285-1	IDLPAAYVLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG
	130 140 150 160 170 180
g285-1.pep	190 200 210 220 230 240
	SASVGLKKPFALDTAIYTKGGFEGETIHSTARLSGSLKDVRAELTIDGGINRLSGKSVIH
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELTIDGGINRLSGKSVIH
	190 200 210 220 230 240
g285-1.pep	250 260 270 280 290 300
	PFAESLDKTLEEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK
m285-1	PFAESLDKTLEEVLVKGFNINPAAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK
	250 260 270 280 290 300
g285-1.pep	310 320 330 340 350 360
	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGI
m285-1	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGI
	310 320 330 340 350 360
g285-1.pep	370 380 390 400 410 420
	NSVGAEDVLQTAFAKGRLDGSIGIGTTASPKISWQLGTGTARTDGLAIASDPANEQRKL
m285-1	NSVGAEDVLQTAFAKGRLDGSIGIGTTASPKISWQLGIGTARTDGLAIASDPANGQRKL
	370 380 390 400 410 420
g285-1.pep	430 440 450 460 470 480
	VFDTVNISAGEGSLTAQGYLELFKDRLLKLDIRSRAFDPSRIDPQFPAGDINGSIHLAGE
m285-1	VLDTVNIAAGQGSLSAAGYLELFKDRLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGE
	430 440 450 460 470 480
g285-1.pep	490 500 510 520 530 540
	LAKKEFTGKMRFPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIVKTDGGFGKKGD
m285-1	LAKKEFTGKMRFPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD
	490 500 510 520 530 540
g285-1.pep	550 560 570 580 590 600
	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTFTDLSGTARNLHIGKAADIRS
m285-1	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTFTDLSGAARNLHIGKAADIRS
	550 560 570 580 590 600
g285-1.pep	610 620 630 640 650 660
	LDFTLKGSPGTSRPMRADIKGRSLSGGAAVVDTAGLTLEGTGAQHRIRTHAAMTLDGK
m285-1	LDFTLKGSPDTSRPIRADIKGRSLSGGAAVVDADMLDGTGVQHRIRTHAAMTLDGK
	610 620 630 640 650 660
g285-1.pep	670 680 690 700 710 720
	PFKLDLASGGINRELTRWKGSGIGLDIGGAFNLKLNRMTELEGAHVAAASAAWQAMG
m285-1	PFKFDLASGGINRELTRWKGSGIGLDIGGAFNLKLNRMTELEGAERVAASAAWQAMG
	670 680 690 700 710 720
g285-1.pep	730 740 750 760 770 780
	GSLNLQHFSWDRKTGISAKGGARGHLHIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYL
m285-1	GSLNLQHFSWDRKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL

662

	730	740	750	760	770	780
	790	800	810	820	830	840
g285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIGNAFGGNM					
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
	850	860	870	880	890	900
g285-1.pep	ANTPLGGRITASLPDLGALKPFLPAAQONITGSLNAAQIGGRVGSFVNAAVNGSSNYG					
m285-1	ANAPLGGRITASLPDLGALKPFLPAAQONITGSLNAAQIGGRVGSFVNAAVNGSSNYG					
	850	860	870	880	890	900
	910	920	930	940	950	960
g285-1.pep	KINGNITVGQSRSFDTAPLGGRNLNTVADAEAFRNFLPVGQTVKGSLNAAVTLGGSADP					
m285-1	KINGNITVGQSRSFDTAPLGGRNLNTVADAEVFRNFLPVGQTVKGSLNAAVTLGGSADP					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
g285-1.pep	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVMENS					
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVIDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVIDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAASLPVNMNLTLDLNDGIRFSGYGADVTIGGKLTTLTAQPGGNVR					
m285-1	SVGDDVVVLGEVKKEAASLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLIRAERRLSPVGAGVEILGSLNS					
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLIRAERRLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANEPMSKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSKDKLSWLILNRAGSGSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRFLFGSDKKDSAGNGK GK					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGK GKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTT CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGCA CGGAAGCGGG TTTGCCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGAAA CCGTCCGAAC
251 TGATCGCGCG CAGCCTGCAC ATTACCGAAA TTTCCGCGCG CGACATCGCC
301 ATCGTTACCA AACCAGCTCC GCCTAAAGAA GAACGCGCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCGGT CTATCTCGAG CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGA CTGGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CCGCGCGAAC TGGCGATCGA CCGCGGCAAT ATCCGCCTCT
701 CGGGAATATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCGG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTCTG CCTGACCGCC ATCCCGTCGT
851 TTTGAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCAG
951 CTTTGTATC CCGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAAGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAACCGGACA
1251 CGGGAATCTG GTGCTCGACA CCGTCAACAT CGCCGCGGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATTC CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GCGAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CCGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGCTC GATTTGCGGC TGGGGCGGAA CATTATTAAG ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGGC GATTTGGACG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGCGCGCGG GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCCGTTCC
1801 CTCGATTTCG CGCTCAAAGG TTCGCCGAC ACAAGCCCGC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTGCTGTC GGGCGGAGCG GAGGTGTGCG
1901 ATACCGCCGA CTGATGCTG GACGGCACGG CGGTGCGACA CCGCATCCGC
1951 ACACACGGCG CCATGACGCT GGATGGCAA CCGTTCAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAG GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAATTTGGCA
2151 GCGAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GGGCAGCAGG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAAACCGCC CTTGGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAGCGCG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAACACGCG CTTTCAAAAC GACCGTATCG GAATCTGTCT
2451 TGACGGCGCG GCGCGTTTCG GCGGATTAA CGCCGATTG GACATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAATGCAC CGCTCGGCGG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CACATTGAAG CCCTTCTGCG CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAATC GCGGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCCGCCGTC ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTT ACCGGTCGGA CAAACCGTCA AAGGCAGCTG GAATGCCGCC
2851 GTAACCTTCG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGGCAGAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACAA
2951 ACGGCTCGCT GCGTTGCGAT ATCGCGGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCG GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTGCGTAT
3051 GGAACACAGC GGACCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCAAC CGCCGCTGCA CCGTTTCGGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAACAA
3201 GGATCAGGGG CTGTTGCGTT CGCAAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGCGGCG GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGTTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGGCG GCGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTGAGC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGC CGCTCAACG ACCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAA TATTGGGCGG CCTCAACAGT
3601 CCGCGCATTG CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCTGGCTTC ATCCTCAACC GCGCCGCGAG TGGCAGCAGC GGCACAAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGCG TTGCGGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GCGCAACTCA ACCCCGCGCA ACAGGTGCTG ACCGTCGGCA
3851 AACCACTGAC CGGCAAACTC TACATCGGCT ACRAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCGGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAGAGCTC CGCCGAAAC
4051 AGCAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

a285-1.pep

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1  LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLIDGFDGDN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPKPE ERPLSLPDS IDLPAAVYLD RFETGKISMV KAFDKQTVYL
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLGRRG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGSIAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPOLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGGFKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLGGAARNL HIGKAADIRS
601 LDFTLKGSPP TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASAAWQAMG GSNLQHFWSV DKKTGISAKG GAHGLHIAEL
751 HNFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL DIGNAFGGNM ANAPLGGRIT
851 ASLPDLGLTK PFLPAAQNI TGSLNAAQI GGRVGSPPSVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRNLTLVADA EVFRNFLPVG QTVKGSNLAA
951 VTLGGSIAEP HLGGSINGDK LYRNQTOGI ILDNGLSRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVMNMLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIK
1151 RYKAYQQLD ITKGTVSFVG PLNDPNLNIR AERRLSFVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGRSSSGGEL YTIREFDRFS GSDKKDSAGN
1351 SKGK*

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a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
	70	80	90	100	110	120
	130	140	150	160	170	180
a285-1.pep	IDLPAAVYLDREFETGKISMVKAQDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG					
m285-1	IDLPAAVYLDREFETGKISMVKAQDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a285-1.pep	SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
	190	200	210	220	230	240
	250	260	270	280	290	300
a285-1.pep	PFAESLDKLTLEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK					
m285-1	PFAESLDKLTLEVLVKGFNINPAAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a285-1.pep	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRRGIRLSGKIDTEKDILDLNIGI					
m285-1	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRRGIRLSGKIDTEKDILDLNIGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
a285-1.pep	NSVGAEDVLQTAFAKGRLDGSIGIGGTTASPKISWQLGIGTARTDGSIAIASDPANGQRKL					
m285-1	NSVGAEDVLQTAFAKGRLDGSIGIGGTTASPKISWQLGIGTARTDGSIAIASDPANGQRKL					
	370	380	390	400	410	420
	430	440	450	460	470	480

665

a285-1.pep VLDTVNIAAGQGSLSAQGYLELFKDRLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGE
m285-1 VLDTVNIAAGQGSLSAQGYLELFKDRLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGE
430 440 450 460 470 480

a285-1.pep 490 500 510 520 530 540
LAKEKFTGKMREFPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD
m285-1 LAKEKFTGKMREFPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD
490 500 510 520 530 540

a285-1.pep 550 560 570 580 590 600
RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTFTDLSGAARNLHIGKAADIRS
m285-1 RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTFTDLSGAARNLHIGKAADIRS
550 560 570 580 590 600

a285-1.pep 610 620 630 640 650 660
LDFTLKGPSPTSRPIRADIKGSRLSLSGGAEVVDADLMDGTGVQHRIRTHAAMTLDGK
m285-1 LDFTLKGPSPTSRPIRADIKGSRLSLSGGAEVVDADLMDGTGVQHRIRTHAAMTLDGK
610 620 630 640 650 660

a285-1.pep 670 680 690 700 710 720
PFKFDLDASGGINRELTRWKSGSIGILDIGGAFNLKLNRMTEAGAERVAASAANWQAMG
m285-1 PFKFDLDASGGINRELTRWKSGSIGILDIGGAFNLKLNRMTEAGAERVAASAANWQAMG
670 680 690 700 710 720

a285-1.pep 730 740 750 760 770 780
GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL
m285-1 GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL
730 740 750 760 770 780

a285-1.pep 790 800 810 820 830 840
NISRSQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM
m285-1 NISRSQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM
790 800 810 820 830 840

a285-1.pep 850 860 870 880 890 900
ANAPLGGRITASLPDLGTLKPFPLPAAQONITGSLNAAQIGGRVGSFVNAAVNGSSNYG
m285-1 ANAPLGGRITASLPDLGTLKPFPLPAAQONITGSLNAAQIGGRVGSFVNAAVNGSSNYG
850 860 870 880 890 900

a285-1.pep 910 920 930 940 950 960
KINGNITVGQSRSFDTAPLGGRNLTVADAIEVFRNFLPVGQTVKGSLNAAVTLGGSIAADP
m285-1 KINGNITVGQSRSFDTAPLGGRNLTVADAIEVFRNFLPVGQTVKGSLNAAVTLGGSIAADP
910 920 930 940 950 960

a285-1.pep 970 980 990 1000 1010 1020
HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS
m285-1 HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS
970 980 990 1000 1010 1020

a285-1.pep 1030 1040 1050 1060 1070 1080
GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP
m285-1 GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP
1030 1040 1050 1060 1070 1080

a285-1.pep 1090 1100 1110 1120 1130 1140
SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSSVR
m285-1 SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSSVR
1090 1100 1110 1120 1130 1140

a285-1.pep 1150 1160 1170 1180 1190 1200
GVGTVRVIKGRYKAYQQLDITKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS
m285-1 GVGTVRVIKGRYKAYQQLDITKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS

666

	1150	1160	1170	1180	1190	1200
a285-1.pep	1210	1220	1230	1240	1250	1260
	PRITLTANEPMSKDKLSWLIINRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
m285-1	1210	1220	1230	1240	1250	1260
	PRITLTANEPMSKDKLSWLIINRAGSGSGDNAALSAAGALLAGQINDRIGLVDDLGF					
a285-1.pep	1270	1280	1290	1300	1310	1320
	TSKRSRNAQTGELNPAEQVLTGKQLTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVAR					
m285-1	1270	1280	1290	1300	1310	1320
	TSKRSRNAQTGELNPAEQVLTGKQLTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVAR					
a285-1.pep	1330	1340	1350			
	IGSRSSGGELTYTIRDFRSGSDKKDSAGNSKGKX					
m285-1	1330	1340	1350			
	IGSRSSGGELTYTIRDFRSGSDKKDSAGNSKGKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

g286.seq

```

1  atgcagaaca ccggtaccat gatgatcaaa ccgaccgccc tgctcctgcc
51  ggctttatatt ttctttccgc acgcatacgc gcctgccgcc gacctttccg
101  aaaacaaggc ggcgggtttc gcattgttca aaagcaaaag ccccgacacc
151  gaatcagtc aattaaaacc caaattcccc gtccgcacgc acacgcagga
201  cagtgaatc aaagatatgg tcgaagaaca cctgccgctc atcacgcagc
251  agcaggaaga ggttttgat aaggaacaga cgggattcct tgccgaagaa
301  gcaccggaca acgttaaaac aatgctccgc agcaaaggct atttcagcag
351  caaggtcagc ctgacggaaa aagacggagc ttatacggtg cacatcacac
401  cgggcccgcg caccaaaatc gccaacgtcg gcgtcgccat cctcggcgac
451  atcctttcag acggcaacct cgccgaatac taccgcaacg cgctggaaaa
501  ctggcagcag ccggtaggca gcgatttcga tcaggacagt tgggaaaaaca
551  gcaaaacttc cgtcctcggc gcggtaacgc gcaaaggcta cccgcttgcc
601  aagctcggca acaccgggc ggccgtcaac cccgataccg ccaccgcga
651  tttgaacgtc gtcgtggaca gcggccgccc cattgccttc ggcgactttg
701  aaatcacccg cacacagcgt taccgccgaac aaaccgtctc cggcctggcg
751  cgcttccaac cgggcacgcc ctacgacctc gacctgctgc tcgacttcca
801  acaggcgctc gaacaaaacg ggcattatcc cggcgcgctc gtacaagccg
851  acttcgaccg cctcccaagg ggaccgcgtc cccgtcaaag tcagcgtaac
901  cgaggtcaaa cgccacaaac tcgaaaccgg catccgcctc gattcgggat
951  acggtttggg cggcaaaatc gcctacgact attacaacct cttcaacaaa
1001 ggctatatcg gctcggtcgt ctgggatatg gacaataacg aaaccacgct
1051 tgccgccggc atcagccagc gcgcgaacta tcggggcaac tactggacaa
1101 gcaacgtttc ctacaaccgt tcgaccaccc aaaacctcga aaaacgcgcc
1151 ttctccggcg gcatctggta tgtgcgcgac cgcgcgggca tcgatgccag
1201 gctggggggc gaatttctcg cagaaggccg gaaaatcccc ggctcggatg
1251 tcgatttggg caacagccac gccacgatgc tgaccgcctc ttggaaaacg
1301 cagctgctca acaacgtgct gcaccccgaa aacggccatt acctcgacgg
1351 caaaatcggg acgactttgg gcacattcct gtcctccacc gcgctaattc
1401 gcacctctgc ccgcgcagg tatttcttca cgcccgaata caaaaaactc
1451 ggcacgttca tcatacgcg acaagcgggt tacaccgttg cagcgacaaa
1501 tgccgatgct ccctcggggc tgatgttccg cagcgcgggc gcgtcttccg
1551 tgccgggtta cgaacttga

```

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

g286.pep

```

1  MONTGTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKSKSPDT
51  ESVKLKPFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101  APDNVKTMLR SKGYFSSKVS LTEKDGAITY HITPGPRTKI ANVGVAIIGD
151  ILSGDNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKGYPLA
201  KLGNTRAAVN PDTATADLNV VVDSGRPIAF GDFEITGTOR YPEQTVSGLA
251  RFQPGTPYDL DLLLDFQQAL EQNGHYSAS VQADFRLPR GPRPRQSQRN
301  RGQTPQTRNR HPPRFGIRFG RQNRLLRLQP LQRLYRLGR LGYGQIRNHA
351  CRRHQPAQAL SGQLLDKQRF LQPFDPKPR KTRLLRRHLV CARPRGHRCQ
401  AGGGISRRRP ENPRLGCRFG QQPRHDADRL LETPAAQORA APRKRPLPRR

```

451 QNRDDFGHIP VLHRANPHLC PRRFLHARK QKTRHVHHR TSGLHRCTRO
501 CRCPLGADV PRRRVFRARL RT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq

```

1 ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC
51 GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GCGGGGTTTC GCATTGTTCA AAAACAAAAG CCCCACACAC
151 GAATCAGTCA AATTAAAACC CAAATTCCCC GTCCTCATCG ACACGCAGGA
201 CAGTGAAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCACCAGC
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301 GCGCCGGACA ACGTTAAAC GATGCTCCGC AGCAAAGGCT ATTTACAGCAG
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCCGCG CACCAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTTCTAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA
501 CTGGCAGCAG CCGGTAGGCA GCGATTTCTGA TCAGGACAGT TGGGAAAAACA
551 GCAAAACTTC CGTCTCGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC
601 AAGCTCGGCA ATACGCAGGC GGCCGTCAAC CCCGATACCG CCACCGCCGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCCC CATCGCCTTC GGCAGCTTTG
701 AAATCACCAG CACACAGCGT TACCCGAAC AAATCGTCTC CGGCCTTGCG
751 CGTTTCCAGC CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA
801 ACAGGCGCTC GAACAAAACG GGCATTATTC CGGCGCTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGGC GACCGCTCC CCGTCAAAGT CAGCGTAACC
901 GAGGTCAAAC GCCACAACT CGAAACCGGC ATCCGCCTCG ATTCGGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAAATACGA AACCACGCTT
1051 GCCGCCGGCA TCAGCCAGCC GCGCAACTAT CGGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCACCA AAACCTCGAA AAACGCGCTT
1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGCGAT CGATGCCAGG
1201 CTGGGGGCGG AATTCTCGC AGAAGGCGCG AAAATCCCGG GCTCGCTGT
1251 CGATTTGGGC AACAGCCACG CCACGATGCT GACCGCCTCT TGGAAACGCC
1301 AGCTGCTCAA CAACGTGCTG CATCCCGAAA ACGGCCATTA CCTCGACGGC
1351 AAAATCGGTA CGACTTTGGG CACATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGTGCAGGTT ATTTCTTAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTCTAT CACACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCGACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGACT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCGA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCGG CGCGGTGTT CACGATATGG GCGATGCCG
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTCCGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTTGGC CCGTTTTCCT TCGACATCGC CTACGGGCAC
1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep

```

1 MHDTRTMMIK PTALLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLKPKFP VLIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFIAEE
101 APDNVKTMLR SKGYFSSKVS LTKDGAYTV HITPGPRTKI ANVGVAILED
151 ILSDGNLAEY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTQAAVN PDTATADLVN VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGMPYDL DLLLDFQAL EQNGHYS GAS VQADFRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAIDYNYL FNKGYIGSVV WMDKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTQNL KRAFGGVVY VRDRAGIDAR
401 LGAEFLAEGR KIPGSAVDLG NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLGTFL SSTALIRTS RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTLGSAVF HDMGDAAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

	10	20	30	40	50	60	
m286.pep	MHDTRTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKNKSPD	TESVKLKPKFP				
g286	MQNTGTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKNSKSPD	TESVKLKPKFP				
	10	20	30	40	50	60	
	70	80	90	100	110	120	
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAE	APDNVKTMLRSKGYFSSKVS					
g286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAE	APDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120	
	130	140	150	160	170	180	
m286.pep	LTEKDGAYTVHITPGPRTKIANVGVAILGDILSDGNLAEYYRNALENWQQPVGSDFDQDS						
g286	LTEKDGAYTVHITPGPRTKIANVGVAILGDILSDGNLAEYYRNALENWQQPVGSDFDQDS						
	130	140	150	160	170	180	
	190	200	210	220	230	240	
m286.pep	WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPD	TATADLN	VVDVSGRPIAFGDFEITGTQR				
g286	WENSKTSVLGAVTRKGYPLAKLGNTAAVNPD	TATADLN	VVDVSGRPIAFGDFEITGTQR				
	190	200	210	220	230	240	
	250	260	270	280	290	299	
m286.pep	YPEQIVSGLARFQPGMPYDLDLLLDFQQA	LEQNGHYSGASVQADFDRL-QGDRVPVKVSV					
g286	YPEQTVSGLARFQPGTPYDLDLLLDFQQA	LEQNGHYSGASVQADFDRLPRGPRPRQSQRN					
	250	260	270	280	290	300	
	300	310	320	330	340	350	359
m286.pep	TEVKRHKLETGIRLDSEYGLGGKIAYDYNNLFNKG	YIGSVVWMDKYETTLAAGISQPRN					
g286	RGQTPQTRNRNHPPRFGIRFGRQNRLLQLQRLYRLG	YQIRNHACRRHQPAQQL					
	310	320	330	340	350	360	

a286.seq

seq	1	ATGCACGACA	CCCGTACCAT	GATGATTAA	CCGACCGCCC	TGCTCCTGCC
51	GGCTTTATTT	TTCTTTCCGC	ACGCATACGC	GCCTGCCGCC	GACCTTTCCG	
101	AAAACAAGGC	GGCGGGTTTC	GCATTGTTCA	AAAACAAAAG	CCCCGACACC	
151	GAATCAGTTA	AATTA AAAC	CAAATTCCCC	GTCCGCATCG	ACACGACAGG	
201	TAGTGAATC	AAGATATTGG	TCAAGAACA	CCTGCGCTC	ATACGCGAGC	
251	AGCAGGAAGA	AGTATTGGAC	AAGGAACAGA	CGGGCTTCCT	CGCCGAAGAA	
301	GCACCGGACA	ACGTTAAAC	AATGCTCCGC	AGCAAAGGCT	ATTTCAGCAG	
351	CAAAGTCAGC	CTGACGGAAA	AAGACGGAGC	TTATACGGTA	CACATCACAC	
401	CGGGCCCGCG	CACCAAAATC	GCCAACGTCG	CGCTGCCCAT	CCTCGGCGAC	
451	ATCCTTTACG	ACGGCAACCT	CGCCGAATAC	TACCGCAACG	CGCTGGAAAA	
501	CTGGCAGCAG	CCGTAGGCA	GTGATTTCGA	TCAGGACAGT	TGGGAAAACA	
551	GCAAAACTTC	CGTCCTCGGC	GCGGTAACGC	GCAAAGCCTA	CCCGCTTGCC	
601	AAGCTCGGCA	ACACCCGGGC	GGCCGTCAAC	CCCGATACCG	CCACCGCCGA	
651	TTTGAACGTC	GTCTGGACA	GCGGCCGCCC	CATCGCTTTC	GGCGACTTTG	
701	AAATTACCGG	CACGCAGCGT	TACCCGGAAC	AAATCGTCTC	CGGCTTGGCG	
751	CGCTTCCAAC	CGGGCAGCCG	CTACGACCTC	GACCTGCTGC	TGCACTTCCA	
801	ACAGGCGGTC	GAACAAAACG	GGCATTATTTC	CGGCGCGTCC	GTACAAGCCG	
851	ACTTCGACCG	CCTCCAAGGC	GACCGCGTCC	CGGTCAAAGT	CAGCGTAACC	
901	GAGGTCAAAC	GCCACAAGCT	CGAAACCGGC	ATCCGCTCTC	ATTCCGAATA	
951	CGGTTTGGCG	GGCAAAATCG	CCTACGACTA	TTACAACCTC	TTCAACAAG	
1001	GCTATATCGG	TTCTGTCGTC	TGGGATATTG	ACAAATACGA	AACCACGCTT	
1051	GCCGCCGGCA	TCAGCCAGCC	GCGCAACTAT	CGGGGCAACT	ACTGGACAAG	
1101	CAACGTTTCC	TACAACCGTT	CGACCACCCA	AAACCTCGAA	AAACGCGCCT	
1151	TCFCCGGCGG	CATCTGGTAT	GTGCGCGCAC	GCGCGGGCAT	CGATGCCAGG	
1201	CTGGGGGGCGG	AGTTTCTCGC	AGAAGGCCGG	AAAATCCCCG	GCTCGGATAT	
1251	CGATTTGCTG	AACAGCCACG	CCACGATGCT	GACGCGCTCT	TGGAAAACGC	
1301	AGCTTGCTCAA	CAACGTGCTG	CATCCCGAAA	ACGGCCATTA	CCTCGACGGC	

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1351 AAAATCGGTA CGACTTTGGG CGCATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTAT CATACGCCGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGCGC CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCG ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCGGG CGCGGTGTTT CACGATATGG GCGACGCCGC
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTCTGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTTCCT TCGACATCGC CTACGGGCGC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

a286.pep

```

1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGYATV HITPGPRTKI ANVGVAAILGD
151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENKTSVLG AVTRKAYPLA
201 KLGNTAAVN PDTATADLNV VVDSGRPIAF GDFEITGTOR YPEQIVSGLA
251 RFQPGTPYDL DILLDFQQAQ EQNGHYS GASVQADFRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKGYIGSVV WMDKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTQNLK KRAFSGGIWY VRDRAGIDAR
401 LGAEFLAAGR KIPGSDIDL NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLGAFL SSTALIRTS RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTLSGAVF HDMGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

```

m286/a286 98.7% identity in 615 aa overlap

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPFP					
a286	MHDTRTMMIKPTALLLPALFFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPFP					
	10	20	30	40	50	60
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
a286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
m286.pep	LTKDGYATVHITPGPRTKIANVGVAAILGDILSDGNLAEYRNALENWQQPVGSDFDQDS					
a286	LTKDGYATVHITPGPRTKIANVGVAAILGDILSDGNLAEYRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
m286.pep	WENKTSVLGAVTRKAYPLAKLGNTQAANVPDPTATADLNVVDSGRPIAFGDFEITGTOR					
a286	WENKTSVLGAVTRKAYPLAKLGNTQAANVPDPTATADLNVVDSGRPIAFGDFEITGTOR					
	190	200	210	220	230	240
m286.pep	YPEQIVSGLARFQPGMPYDL DILLDFQQAQEQNGHYS GASVQADFRLQGDVPVKVSVT					
a286	YPEQIVSGLARFQPGMPYDL DILLDFQQAQEQNGHYS GASVQADFRLQGDVPVKVSVT					
	250	260	270	280	290	300
m286.pep	EVKRHKLETGIRLDSEYGLGKGIAYDYNNL FNKGYIGSVVWMDKYETTLAAGISQPRNY					
a286	EVKRHKLETGIRLDSEYGLGKGIAYDYNNL FNKGYIGSVVWMDKYETTLAAGISQPRNY					
	310	320	330	340	350	360
m286.pep	EVKRHKLETGIRLDSEYGLGKGIAYDYNNL FNKGYIGSVVWMDKYETTLAAGISQPRNY					
a286	EVKRHKLETGIRLDSEYGLGKGIAYDYNNL FNKGYIGSVVWMDKYETTLAAGISQPRNY					
	370	380	390	400	410	420

670

m286.pep	RGNYWTSNVSYNRSTTQNLKRAFSGGVWYVRDRAGIDARLGAEF LAEGRKIPGSAVDLG
a286	RGNYWTSNVSYNRSTTQNLKRAFSGGIWYVRDRAGIDARLGAEF LAEGRKIPGSDIDLG
	370 380 390 400 410 420
m286.pep	NSHATMLTASWKRQLLNVLHPENGHYLDGKIGTTLGTFLSSTALIRTSARAGYFFTPEN
a286	NSHATMLTASWKRQLLNVLHPENGHYLDGKIGTTLGAFLSSTALIRTSARAGYFFTPEN
	430 440 450 460 470 480
m286.pep	KKLGTFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
a286	KKLGTFIIRGQAGYTVARDNANVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
	490 500 510 520 530 540
m286.pep	LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKCLKHSGSLGVRWFSPLAPFSFDIAYGH
a286	LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKCLKHSGSLGVRWFSPLAPFSFDIAYGH
	550 560 570 580 590 600
m286.pep	SDKKIRWHISLGTRFX
a286	SDKKIRWHISLGTRFX
	610

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

```

g287.seq
1  atgtttaaac gcagtgatgat tgcaatggct tgtatttttc ccctttcagc
51  ctgtgggggc ggcggtggcg gatcgcccga tgtcaagtcg gcggaacacgc
101 cgtcaaaaacc ggccgcccccc gttgttgctg aaaaatgccg ggaaggggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgccgcaagc
201 cgatacgag gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 ttcggcgaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaaa atgccgccga
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 cccccgcgtc aaaccctgcc cctgcgaatg gcggtagcga ttttggaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaatataac
501 ttgacccac tgtaaaggcg attcttgtaa tggatgataa ttattggatg
551 aagaagcacc gtcaaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaaagcat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaaacc acctactcgt tctgcacggt cgaggaggtc gcttccggcc
751 gagattccgc tgattcccgt caatcaggcc gatacgtga ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgcccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cgcgggatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttggtgg
951 cacggccgtg tacaacggcg aagtgtctga tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccg caaaagtcga tttcggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgccca tcgatggaaa cggttttaag gggacttgga
1151 cggaaaatgg cggcggggat gtttccggaa ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattccgc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

```

g287.pep
1  MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV
51  LPKEKKDEEA AGGAPOADTQ DATAGEGSQD MAAVSAENTG NGGAATTDNP
101 KNEDAGAOND MPQNAAESAN QTGNNQPAGS SDSAPASNPA PANGGSDFGR

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151 TNVGNVSVVID GPSQNTLTH CKGDSCNGDN LLDEEAPSKS EFEKLSDEEK
201 IKRYKKDEQR ENFVGLVADR VKKDGTNKYI IFYTDKPPTR SARRRSLPA
251 EIPVIPVNOA DTLIVDGEAV SLTGHSGNIF APEGNYRYLT YGAEKLPGGG
301 YALRVQGEPA KGEMLVGTAV YNGEVLHFHM ENGRPYPSGG RFAAKVDFGS
351 KSDGIIDSG DDLHMGTOKF KAAIDGNGFK GTWTENGGGD VSGRFYGPAG
401 EEVAGKYSYR PDAEKGGFV VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
1 ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTGT CCCTTTCAGC
51 CTGCGGGGGC GCGGTTGGCG GATCGCCCGA TGTCAGTCG GCGGACACGC
101 GTCAAAACC TGCCGCCCCCT GTTGTTCCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCCG CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CCGTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAAC AGCGGATAAT CCCAAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CCGTACAGAT AGTTCGACAC CGAATCACAC
351 CCGGATCCG AATATGCTTG CCGGAAATAT GGAAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCGCA GCGGGGCAAA ATGCGCGCAA
501 TACGGGTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCCGGTT
551 CTTGAGATCC CATCCCGCGC TCAAACCTG CACCTGCGAA TGGCGGTAGC
601 AATTTTGAA GGGTTGATTT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGA TGAAGAAGTA CAGCTAAAAT CAGAATTGTA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCGGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGCGGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGCGCAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCCGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCCG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GGCGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATTT CCATACGGAA AACGCGCGTC CGTACCGGAC CAGGGGCAGG
1201 TTTGCCGCAA AAGTCGATTT CCGCAGCAA TCTGTGGACG GCATTATCGA
1251 CAGCGCGGAT GATTTGCATA TGGGTACGCA AAAATTCAAA GCCGCCATCG
1301 ATGGAACCGG CTTAAGGGG ACTTGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCC ACAGATCGCG AAAAGGGCGG ATTCGGCGTG TTTGCCGGCA
1451 AAAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
1 MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAK
51 EDAPQAGSQ QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMANAA
151 DGMQGDPSA GGQNAAGNTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFRGVDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRS
301 ARSRRSLPAE MPLIPVNOAD TLIVDGEAVS LTGHSGNIFA PEGNYRYLTY
351 GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMGTOKF KAAIDGNGFK GTWTENGGGD
451 SGKFYGPAGE EVAGKYSYR PDAEKGGFV VFAGKKDRD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

m287.pep      10      20      30      40      49
               MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSKPAAPVVSE-----KETE
               |||||
g287          10      20      30      40      50      60
               MFKRSVIAMACIFPLSACGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPEKKDEEA

```

[illegible]

```
a287.seq
1 ATGTTTAAAC GCAGTGTGAT TGCAATGGCT TGTATTGTTG CCCTTT CAGC
51 CTGTGGGGGC GCGGTGGCG GATCGCCCGA TGTTAAGTCG GCGGACACGC
101 TGTCAAACCC TGCCGCCCTT GTTGTACTG AAGATGTTCG GGAAGAGGTG
151 CTGCGAAAGC AAAAGAAAGA TGAGGAGGCG GTGAGTGGTG CGCCGCAAGC
201 CGATACGCAG GACGCAACCG CCGGAAAAGG CGGTCAAGAT ATGGCGGCAG
251 TTTCGGCAGA AAATACAGGC AATGGCGGTG CGGCAACAAC GGATAATCCC
301 GAAAATAAAG ACGAGGGACC GCAAATGAT ATGCCGCAA ATGCCGCCGA
351 TACAGATAGT TCGACACCGA ATCACACCCC TGCACCGAAT ATGCCAACCA
401 GAGATATGGG AAACCAACGA CCGGATGCCG GGAATCGGC ACAACGGCA
451 AACCAACGGG ATATGGCAAA TTGCGCGGAC GGAATGCAGG GGCAGCATCC
501 GTCGGCAGGG GAAAATGCCG GCAATACGGC AGATCAAGCT GCAAATCAAG
551 CTGAAAACAA TCAAGTCGGC GGCTCTCAAA ATCCTGCCTC TTCAACCAAT
601 CCTAACGCCA CGAATGGCGG CAGCGATTTT GGAAGGATAA ATGTAGCTAA
651 TGGCATCAAG CTTGACAGCG GTTCGGAAAA TGTAACGTTG ACACATTGTA
701 AAGACAAAGT ATTCGATAGA GATTTCCTAG ATGAAGAACG ACACCAAAAA
751 TCAGAATTTG AAAAATTAAG TGATGAAGAA AAAATTAATA AATATAAAAA
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801 AGACGAGCAA CGAGAGAATT TTGTCGGTTT GGTGCTGAC AGGGTAGAAA
851 AGAATGGAAC TAACAAATAT GTCATCATTT ATAAAGACAA GTCCGCTTCA
901 TCTTCATCTG CGCGATTGAG GCGTTCTGCA CGGTCGAGGC GGTCGCTTCC
951 GGCCGAGATG CCGCTGATTC CCGTCAATCA GGCGGATACG CTGATTGTCG
1001 ATGGGGAAGC GGTCAGCCTG ACGGGGCATT CCGGCAATAT CTTCGCGCCC
1051 GAAGGGAATT ACCGGTATCT GACTTACGGG GCGGAAAAAT TGTCGCGCGG
1101 ATCGTATGCC CTCAGTGTGC AAGGCGAACC GGCAAAAGGC GAAATGCTTG
1151 CGGGCACGGC CGTGACAAAC GGCAGAGTGC TGCATTCCA TATGGAACAA
1201 GGCCGTCCGT CCCCGTCCGG AGGCAGGTTT GCCGCAAAAG TCGATTTCGG
1251 CAGCAATCT GTGGACGGCA TTATCGACAG CGGCGATGAT TTGCATATGG
1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGGCTT TAAGGGGACT
1351 TGGACGAAA ATGGCGGCGG GGATGTTTCC GGAAGGTTT ACGGCCCGGC
1401 CGGCGAAGAA GTGGCGGGA AATACAGCTA TCGCCCGACA GATGCGGAAA
1451 AGGGCGGATT CGGCGTGTTC GCCGCAAAA AAGAGCAGGA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1204; ORF 287.a>:

a287.pep

```

1 MFKRSVIAMA CIVALSAACGG GGGGSPDVKS ADTLSKPAAP VVTEDVGEEV
51 LPKEKKDEEA VSGAPOADTQ DATAGKGGQD MAAVSAENTG NGGAATTDNP
101 ENKDEGPOND MPQNAADTDS STPNHTPAPN MPTRDMGNOA PDAGESAQPA
151 NQPDMAAAD GMQDDPSAG ENAGNTADQA ANQAENNOVG GSONPASSTN
201 PNATNGGSDF GRINVANGIK LDSGSENVTL THCKDKVCDR DFLDEEAPPK
251 SEFEKLSDEE KINKYKKDEQ RENFVGLVAD RVEKNGTNKY VVIYKDKSAS
301 TSSARFRRSA RSRRSLPAEM FLIPVQADT LIVDGEAVSL TGHSGNIFAP
351 EGNRYLYTYG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMEN
401 GRPSPSGGRF AAKVDFGSKS VDGIDSGDD LHMGTQKFKA VIDGNGFKGT
451 WTENGGGDVS GRFYGPAGEE VAGKYSYRPT DAEGGFGVF AGKKEQD*

```

m287/a287 77.2% identity in 501 aa overlap

```

          10      20      30      40      49
m287.pep MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETE
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287      MFKRSVIAMACIVALSAACGGGGGGSPDVKSADTLSKPAAPVVTEDVGEEVLPKEKKDEEA
          10      20      30      40      50      60

          50      60      70      80      90      100     109
m287.pep KEDAPQAGSQGQGPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT
          ||||| :| | :||| ||||| ||||| ||||| ||||| ||||| |||||
a287      VSGAPOADTQ--DATAGKGGQDMAAVSAENTGNGGAATTDNPNKDEGPONDMPQNAADT
          70      80      90      100     110

          110     120     130     140     150     160     169
m287.pep DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMAAADGMQDDPSAGGONAGNTA
          ||||| ||| : :| ||| ||||| ||||| ||||| ||||| ||||| |||||
a287      DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMAAADGMQDDPSAG-ENAGNTA
          120     130     140     150     160     170

          170     180     190     200     210     220     229
m287.pep AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNTLTHCKGDS
          |:||| |||:|||:| :|| :|||:|||:|||:| :| :|:|||
a287      DQANQAENNOVGGSQNPASSTNPNATNGGSDFGRINVANGIKLDSGSENVTLTHCKDKV
          180     190     200     210     220     230

          230     240     250     260     270     280     289
m287.pep CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP
          |: :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287      CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVKNGTNKYVVIYKD
          240     250     260     270     280     290

          290     300     310     320     330     340
m287.pep KP--TSFARFRRSARSRRSLPAEMPLIPVQADTLIVDGEAVSLTGHSGNIFAPEGNRY
          | :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287      KSASSSARFRRSARSRRSLPAEMPLIPVQADTLIVDGEAVSLTGHSGNIFAPEGNRY
          300     310     320     330     340     350

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	350	360	370	380	390	400
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287.pep	GSKSVDDGIIDSGDDLHMGTOQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS					
a287	GSKSVDDGIIDSGDDLHMGTOQFKAVIDGNGFKGTWTENGSGDVSGRFGPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287.pep	YRPTDAEKGFGVFAGKKEQDX					
a287	YRPTDAEKGFGVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288.seq
1  atgcacaccg gacaggcggg aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgctcaag caacctaccc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggctt tgctccgaat ggggtttggc
151 ctgccgcata ttgttaccaa atgcgcgggtg cgcccttacc gcaccttttc
201 acccttgccct gtgctgccaa agcagccatc ggcggttttg ctttctgttc
251 cactttccgt cgcgttaccg cgcccgcccg ttaaccggca ttctaccctg
301 cggagcccg gactttccct ccgtatgcct tacgcgatac gcggcgactg
351 tctgcccgtc ccgtgtgcgg cgcggattat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacaggtt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgtc caagtgcgg tccaatacgg
501 ctttgtggtt gccgacttcg tagcctgtac gcaagtcttt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCGGTTTTC CTTTCTGTTC
251 CACTTTCCTG CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC AAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
g288	PCAAARIITRNTKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADFVACTQVF					
	130	140	150	160	170	180
m288.pep	DTX					
	:					
g288	DAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

a288.seq

1	ATGCACACCG	GACAGGCGGT	AAGCCGGGTT	CTGTCTCGGA	CAGTCATTCC
51	TCTAGGCATA	CGTTGCCCG	TATGCTCAAG	CAACCTACCC	GAACGCTCGG
101	CGGGCAGCGT	CATTGCGTTC	TGTTTGGTCT	TGCTCCGAAT	GGGGTTTGGC
151	CTGCCGCATA	TTGTTACCAA	ATGCGCGGTG	CGCCCTTACC	GCACCTTTTC
201	ACCCTTGCCT	GTGCTGCCAA	AGCAGCCATC	GGCGGTTTTC	CTTCTGTTC
251	CACTTTCCGT	CGGTTACCG	CGCCGGCCG	TTAACCGGCA	TTCTACCCTG
301	CGGAGCCCG	ACTTTCCTCC	CCGTATGCCT	TACGCGATAC	GCGGCGACTG
351	TCTGCCCGTC	CCGTGTGCGG	CGCGGATTAT	AACACGAAAC	GCAAAAATGC
401	CGTCTGAAAC	GGTACAGGTT	TCAGACGGCA	TACAGCCTAA	ACTACACGCC
451	CTGTTTCAGG	CTGGCTTCGA	TAAAGCCGTC	CAAGTCGCCG	TCCAATACGG
501	CTTTGGTGTT	GCCGACTTCG	TAGCCTGTGC	GCAAGTCTTT	AATGCGTGA

This corresponds to the amino acid sequence <SEQ ID 1210; ORF 288.a>:

a288.pep

1	MHTGQAVSRV	LSRTVIPLGI	PLPVCSSNLP	ERSAGSVIAF	CLVLLRMGFG
51	LPHIVTKCAV	RPYRTFSPLP	VLPKQPSAVL	LSVPLSVALP	REAVNRHSTL
101	RSPDFPPRMP	YAIRGDCLPV	PCAAARIITRN	AKMPSETVQV	SDGIQPKLHA
151	LFQAGFDKAV	QVAVQYGFV	ADFVACAQVF	NA*	

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					

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a288 PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADFVACAQVF
 130 140 150 160 170 180

m288.pep DTX
 ::
 a288 NAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

g290.seq
 1 atggcaaaaa tgatgaaatg ggcggtctgtt gcggcggtcg cggcggcagc
 51 ggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata
 101 ttacggaagc ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg
 151 ggcgagattt cgccgtccaa cctgggtatcg gtcggcgcg caggcttcggg
 201 gcagattaaa aagctttatg tcaaaactcg gcaacaggtc aaaaaggcg
 251 atttgattgc ggaaatcaat tcgaccacgc agaccaacac gatcgatatg
 301 gaaaaatcca aattggaaac gtatcaggcg aagctggtgt ccgcacagat
 351 tgcattgggc agcgcgga aaatataa gcgtcaggcg gcgttttgga
 401 aggatgatgc gacctctaaa gaagatttgg aaagcgcgca ggatgcgctt
 451 gccgcgcgca aagccaatgt tgccgagttg aaggctttaa tcagacagag
 501 caaaatttcc atcaataccg ccgagtcgga tttgggtac acgcgcatta
 551 ccgcgacgat ggacggcacg gtggtggcga ttcccgtgga agagggcgag
 601 actgtgaacg cggcgcgatc tacgcccagc attgtccaat tggcgaaatc
 651 ggatatgatg ttgaacaaaa tcgagattgc cgagggcgat attaccaagg
 701 tgaaggcggg gcaggatatt tcgtttacga tttgtccga accggtatcg
 751 ccgatttaag cgaagctcga cagcgtcgac cccgggtgta ccacgatgac
 801 gtcggggcgc tacaacagca gtacggatac ggcttccaat gcggtctatt
 851 attatgcccg ttcgtttgtg ccgaatccgg acggcaaaact cgccacgggg
 901 atgacgacgc agaatacggg tgaatcgac ggtgtgaaaa atgtgttgc
 951 tattccgtcg ctgaccgtga aaaatcgcg cggcaaggcg ttcgtacgcg
 1001 tgttgggtgc ggacggcaag gcagtggaa cgcgaatccg gaccgggatg
 1051 aaagacagta tgaataccga agtgaaaagc ggggtgaaag agggggacaa
 1101 agtggtcac tccgaaataa ccgcccgcga gcagcaggaa agcggcgaac
 1151 gcgccttagg cggcccgccg cgccgataa

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

g290.pep
 1 MAKMMKWA AVAVAAAVWG GWSYLKPEPQ AAYITEAVRR GDISRTVSAT
 51 GEISPSNLVS VQAQASGQIK KLYVKLGQQV KKGDLIAEIN STQTNTIDM
 101 ESKKLETYQA KLVSAQIALG SAEKKYKQRA ALWKDDATSK EDLESAQDAL
 151 AAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEGQ
 201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT
 251 PIKAKLDSVD PGLTMSGG YNSSTDASN AVYYYARFV PNPDKLATG
 301 MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM
 351 KDSMNTVEKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

m290.seq (partial)
 1 ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA
 51 ACTCGGCAAA CAGGTTAAAA AGGGCGATTT GATTGCGGAA ATCAATTCTGA
 101 CCTCGCAGAC CAATACGCTC AATACGGAAA AATCCAAGTT GGAAACGTAT
 151 CAGGCGAAGC TGGTGTCCGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA
 201 ATATAAGCGT CAGGCGGCGT TATGGAAGGA AAACGCGACT TCCAAAGAGG
 251 ATTTGGAAAG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC
 301 GAGCTGAAGG CTTAATCAG ACAGAGCAAA ATTTCCATCA ATACCGCCGA
 351 GTCGGAATTG GGCTACACGC GCATTACCGC AACGATGGAC GGCACGGTGG
 401 TGCGGATTCT CGTGGAAGAG GGCAGACTG TGAACGCGC GCAGTCTACG
 451 CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAATGCA
 501 GATTGCCGAG GGCATATTA CCAAGTGAA GGCGGGGCAG GATATTTCTG
 551 TTACGATTTT GTCCGAACCG GATACGCGA TTAAGGCGAA GCTCGACAGC
 601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GCGGTTTACA ACAGCAGTAC
 651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCGTTTCG TTTGTGCCGA

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701 ATCCGGACGG CAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGAATAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TCGCGGTGTT GGGTGGCGAC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

m290.pep (partial)

```

1  ..VSVGAQASGQ IKILYVKLGQ QVKKGDIAE INSTSQNTL NTEKSKLETY
51  QAKLVSAQIA LGSAAEKKYR QALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTTMSS GGYSSTDSTA SNAVYYARS FVPNPDGKLA TGMTTQNTVE
251 IDGVKNVLI PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTEV
301 KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

m290.pep          10          20          30
                  VSVGAQASGQIKILYVKLGQVKKGDIAE
g290              30          40          50          60          70          80
POAAYITEAVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQVKKGDIAE

m290.pep          40          50          60          70          80          90
INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKKYRQALWKENATSKEDLESAQD
g290              90          100         110         120         130         140
INSTTQNTIDMEKSKLETYQAKLVSAQIALGSAEKKYRQALWKDDATSKEDLESAQD

m290.pep          100         110         120         130         140         150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
g290              150         160         170         180         190         200
ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAIPEEGQTVNAAQST

m290.pep          160         170         180         190         200         210
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
g290              210         220         230         240         250         260
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS

m290.pep          220         230         240         250         260         270
GGYSSTDSTASNAVYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
g290              270         280         290         300         310         320
GGYSSTDSTASNAVYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG

m290.pep          280         290         300         310         320         330
KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
g290              330         340         350         360         370         380
KAFVRVLGADGKAVEREIRTGMKDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG

m290.pep          PPRRX
                  ||||
g290              PPRRX
                  390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1  ATGGCAAAAA TGATGAAATG GCGCGCTGTT GCGGCGGTCG CCGCGGCAGC
51  GGTTTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAAC GGTCAGGCGC GCGGACATCA GCCGGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AACTTTATG TCAAACCTCG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCCTAAA GAAGATTGG AAAGCGCACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAATTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATT
551 CCGCAACGAT GGACGGCAGC GTGGTGGCGA TTCTCGTGA AGAGGGGCAG
601 ACTGTGAACG CCGCGCAGTC TACGCCGACG ATTGTCCAAT TGGCGAATCT
651 GGATATGATG TTGAACAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTTGTCCGA ACCGGATACG
751 CCGATTAAGG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TTCGTTGTG CCGAATCCGG ACGGCAAACT CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAAATCGAC GGTGTGAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCGG CCGCAGGGCG TTTGTGCGCG
1001 TGTGGGTGTC AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CCGCCGCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1  MAKMMKWAAV AAVAAAAVWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDLIAEIN STSQTNTLNT
101 ESKKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATAK EDLESAQDAL
151 AAANKANVAEL KALIROSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYYARFV PNPDKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTGM
351 RDSMNTEVKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*
```

m290/a290 98.2% identity in 334 aa overlap

					10	20	30
m290.pep					VSVGAQASGQIK	LYVKLGQOV	KKGDLIAE
a290	PQAAYITETVRR	GDISRTVSAT	GEISPSNLVS	VQAQASGQIK	KLYVKLGQOV	KKGDLIAE	
	30	40	50	60	70	80	
		40	50	60	70	80	90
m290.pep	INSTSQTNTLN	TEKSKLETYQ	AKLVSAQIAL	GSAEKKYKRQ	AALWKENATS	KEDLESAQD	
a290	INSTSQTNTLN	TEKSKLETYQ	AKLVSAQIAL	GSAEKKYKRQ	AALWKDDATA	KEDLESAQD	
	90	100	110	120	130	140	
	100	110	120	130	140	150	
m290.pep	AFAAAKANVAE	LKALIROSKIS	INTAESELGY	TRITATMDGT	VVAILVEEGQ	TVNAAQST	
a290	ALAAAKANVAE	LKALIROSKIS	INTAESELGY	TRITATMDGT	VVAILVEEGQ	TVNAAQST	
	150	160	170	180	190	200	
	160	170	180	190	200	210	
m290.pep	PTIVQLANLDM	MLNKMQIAEG	DITKVKAGQD	ISFTILSEPDT	PIKAKLDSVD	PGLTTMSS	
a290	PTIVQLANLDM	MLNKMQIAEG	DITKVKAGQD	ISFTILSEPDT	PIKAKLDSVD	PGLTTMSS	
	210	220	230	240	250	260	
	220	230	240	250	260	270	

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```

m290.pép      GGYNSSTDTASNAVYYYARSFVNPDPGKLATGTTQNTVEIDGVKNVLIIPSLTVKNRGG
                |||||||||||||||||||||||||||||||||||||||||||||||||||
a290          GGYNSSTDTASNAVYYYARSFVNPDPGKLATGTTQNTVEIDGVKNVLIIPSLTVKNRGG
                270      280      290      300      310      320

                280      290      300      310      320      330
m290.pép      KAFVRVLGADGKAAEREIRTGMRDSMNTVEVKSGLKEGDKVVI SEITAAEQQESGERALGG
                :|||||||||||||||||||||||||||||||||||||||||||||||||
a290          RAFVRVLGADGKAAEREIRTGMRDSMNTVEVKSGLKEGDKVVI SEITAAEQQESGERALGG
                330      340      350      360      370      380

m290.pép      PPRRX
                |||||
a290          PPRRX
                390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcctgccgct
51  gctggcttgc gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttggacaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaattct atggtgtcag cccgaccgtg ccaaagcgtg gacggattgg
601 atcgtaaaag gcaaattccc ggtcggcggc agcatctgcg acaatcccg
651 cgcggaacc acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tcccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaacc cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pép
1   MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSAVASLKR
51  LEKTYSAQDL KVLVSETPV KGIYEVVVG RQIIYTDAG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPD
251 PTGGNHPQKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTTG AAAGTGTGTA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAA GAAGTGGCGG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTC
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATG CCGGCCTGCA CCCCATGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTGCA CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATCGGTAAAG GCAAATCCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCAACGGG GCGAGCCAAA GCGGCTACAG CCCGATGCC

```

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751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

This corresponds to the amino acid sequence <SEQ ID 1220; ORF 292>:

```

m292.pep
  1 MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAAASLKAR
 51 LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSMP
251 QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238 aa overlap

	10	20	30	40	50	60
m292.pep	MKTKLIKILTPFTVLPLLACGQTPVSNANAEP AVKAESAGKSVAAASLKARLEKTYSAQDL					
g292	MKTKLIKILTPFTVLPLLACGQTPVSNANAESA VKAESAGKSVAAASLKARLEKTYSAQDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m292.pep	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFV GELINIDTRKNLTEERAADLNKIDF					
g292	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFV GELINIDTRKNLTEERAADLNKIDF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m292.pep	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA					
g292	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m292.pep	ARKAQILWCQPDRAKAWTDWMRKGFVPVGGSIDCNPVAETTSLGEQFGFNGTPTLVFPNG					
g292	ARKAQILWCQPDRAKAWTDWMRKGFVPVGGSIDCNPVAETTSLGEQFGFNGTPTLRLPQR					
	190	200	210	220	230	240
	250	260				
m292.pep	RSQSGYSMPQLEEIIRKNQX					
g292	AHPKRLQPDAPTGGNHPQKPAVNPOX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
  1 ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51 GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GAAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGC GCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTT CCGGCCGTGA CCCCAGTCCG GCGCGCAAGG
551 CGCAAATCTT ATGGTGTCTG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATTTCC GGTCCGCCGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCC
751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

```


This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292. pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSPAASLKAR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFGVGLIN
101  IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151  CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSMP
251  QLEEIIRKNQ *

m292/a292 100.0% identity in 260 aa overlap

      10      20      30      40      50      60
m292. pep MKTKLIKILTPFTVLPLLACGQTPVSNANAEPVKAESAGKSPAASLKARLEKTYSAQDL
a292      MKTKLIKILTPFTVLPLLACGQTPVSNANAEPVKAESAGKSPAASLKARLEKTYSAQDL
      10      20      30      40      50      60

      70      80      90     100     110     120
m292. pep KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFGVGLINIDTRKNLTEERAADLNKIDF
a292      KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFGVGLINIDTRKNLTEERAADLNKIDF
      70      80      90     100     110     120

      130     140     150     160     170     180
m292. pep ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
a292      ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
      130     140     150     160     170     180

      190     200     210     220     230     240
m292. pep ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLGEQFGFNGTPTLVFPNG
a292      ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLGEQFGFNGTPTLVFPNG
      190     200     210     220     230     240

      250     260
m292. pep RSQSGYSMPQLEEIIRKNQX
a292      RSQSGYSMPQLEEIIRKNQX
      250     260
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
  1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtctggtc
 51  ggttcgggct gtcagaacat catcgaaccg ctttcctgcg gcgttacgac
101  gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151  tggcatcggg tgccggcggt caagtcgaat cggcggacgc gtggcgtgaa
201  gccgttgaaa aaaccttatc tggcgagggg ggcggaatgc agatgcaggc
251  gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301  ccgagggcgt gcgggaagcg gtatgcggac atcgggggcg atagtatac
351  aatccgtatc cgagttttcc ggttgagca tcgtatgagt atttatgccg
401  tcgcgcacat catccacctg tattgcgcca ccgcctttgt cggcggcggt
451  ttttttgaag tgctggtttt gtccgtcctg catacgggac ggggtgcgcg
501  cgaggcgcgg gcggaagtgg aaaaggcaat gtcttaccgc gccgtcaggg
551  tgatgccgtt tgcggtcgga ctgctgttcg ccaggggaac tctagagtcg
601  actgcagcag catgccctc...
  
```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
  1  MRITCAPMSL LSAAVSVRA VRTSSNRFFA ALRRYSAFRP TIFPKPAGTP
 51  WHRVRRFKSN RRTRGVKPLK KPYLARGAEC RCRRRAWTALS HNIAERARES
101  PRCCKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151  FFEVLVLSVL HTGRVSREAR REVEKAMSyr AVRMPFAVG LLFARGTLES
201  TAAACP....
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

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m294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTTCGGGT GTGAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCGGAC
 101 GATTATCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
 151 TGGCATCGGG TCGCGCGGT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
 201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC
 251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGGCG ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG
 451 TTTTGTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCCGG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT
 701 TCGCCATCGC CGTCGTCAAA ATGGCGCGTT CCACACTGAC GGTGCGTTGG
 751 TCGAAATACA TACAGCCGT CGTCTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep
 1 MRITCAPMSL LSAAVWSIRV VRTSSNRFFA AFRRYSAFQP TIFPKPADTP
 51 WHRVRREFKS RMRGGKPLK KPYRPRGGG RCRRRAWTALS HNAIERARES
 101 PRRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMPEFVVG LLFASGIVMA
 201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVMW
 251 SKYIHAVVET HMLLIVFLAK AMFYISW*

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSAAVWSVRAVRTSSNRFFAALRRYS	AFRPTIFPKPAGTPWHRVRREFKS				
m294	MRITCAPMSLLSAAVWSIRVVRTSSNRFFA	AFRRYSAFQPTIFPKPADTPWHRVRREFKS				
	10	20	30	40	50	60
g294.pep	RRTRGVKPLKKPYLARGAECRCRRRAWTALSHNIAERARES	PRRCGKRYADIGGDSDTIRI				
m294	RMRGGKPLKKPYRPRGGGRCRRRAWTALSHNIAERARES	PRRCGKRYADIGGDSDTIRI				
	70	80	90	100	110	120
g294.pep	RVFRLEHRMSIYAVAHIIHLYCATAFVGGVFFEV	LVLVLSVLTHTGRVSREARREVEKAMSYR				
m294	RVFRLEHRMSIYAVAHIVHLYCAIAFVGGVFFEV	LVLVLSVLTHTGRVSREARREVEKAMSYR				
	130	140	150	160	170	180
g294.pep	AVRVMPEFVGLLFARGTLESTAAACP					
m294	AVRVMPEFVGLLFASGIVMAANRYLSILGE	PFATSFGTMLTLKILLAFSVLAHFAIAVVK				
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTTCGGGT GTGAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCGGAC
 101 GATTATCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGCACGCCT
 151 TGGCATCGGG TCGCGCGGT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA
 201 GCCGTTGAAA AAACCTTATC GTCCGAGGAG GCGGGAATGC AGATGCAGGC
 251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GGTGAGTA CCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCTTTGT CGGCGGCGTG
 451 TTTTGTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCCGG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

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701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
 751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
 801 TTTGCAAAA GCGATGTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294 . pep
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFFA AFRRYSAFRP TIFPKPAGTP
 51 WHRVRFRKSN RRTRGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES
 101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMPEVVG LLFASGIVMA
 201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
 251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

m294/a294 94.9% identity in 277 aa overlap

	10	20	30	40	50	60
m294 . pep	MRITCAPMSLLSAAVWSIRVVRTSSNRFFA	AFRRYSAFQPTTIFPKPADTPWHRVRFRKSN				
a294	MRITCAPMSLLSAAVWSIRAVRTSSNRFFA	AFRRYSAFRPTIFPKPAGTPWHRVRFRKSN				
	10	20	30	40	50	60
	70	80	90	100	110	120
m294 . pep	RRMRGGKPLKKPYRPRGGGCRRAWTALSHNIAERARES	PRRCGKRYADIGDDSDTIRI				
a294	RRTRGGKPLKKTYPRAECRCRRARTALSHNIAERARES	PRRYGKRYADIGDDSDTIRI				
	70	80	90	100	110	120
	130	140	150	160	170	180
m294 . pep	RVFRLEHRMSIYAVAHIVHLYCAIAFVGGV	FFEVLSVLHTGRVSREARREVEKAMSYR				
a294	RVFRLEYRMSIYAVAHIVHLYCAIAFVGGV	FFEVLSVLHTGRVSCEARREVEKAMSYR				
	130	140	150	160	170	180
	190	200	210	220	230	240
m294 . pep	AVRVMPEVVGLLFASGIVMAANRYLSILGE	PFATSFGTMLTLKILLAFSVLAHFAIAVVK				
a294	AVRVMPEVVGLLFASGIVMAANRYLSILGE	PFATSFGTMLTLKILLAFSVLAHFAIAVVK				
	190	200	210	220	230	240
	250	260	270			
m294 . pep	MARSTLTVGWSKYIHAVVFTHMLLIVFLAKAMFYISWX					
a294	MARSTLTVGWSKYIHTVVFTHMLLIVFLAKAMFYISWX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295 . seq
 1 atgctcggga tggcgcggca cgacggccag cagggcatcg ccgcgatatt
 51 gttgccacgc cgccagcagt ttttccgcct cgtcttcgcc ccgataaacg
 101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gtttttcaaa
 151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
 201 tattgccgca cacctgcacg gatgccgcgc ccaatttcgc caaccgcgcc
 251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg
 301 acggatcagg cggcggactt tcagataacc gttcagcgat ttttccgaca
 351 gccgcgcatt cgccaaaaac agcggcacac ccgctcgcgc gcatctcttc
 401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcggggc
 451 gtgttcgcgc aaaaactgcc gtacccacgt tttttgtca tacggaagat
 501 agcggcattg cgcacgcgga aacagaactt gcgcggttc ccgtcccgtc
 551 ggggtcatct cgtcatcag cagcggcgca tcgggaaaac gccgcgcgaa
 601 ctgcgcgtatc aagggtcggg cggcacgcgt ttctccgacc gaaacggcgt
 651 gtatccaaac cgcgcgggta acgggattcg gatcgggctt gccgaaacgc
 701 tcgtccctat gcgcccggta tgccggggca cttccggagc gtttgtccaa
 751 ataacgccgt atccatatcg gcgcaagcag ccacaataca tcataaagcc
 801 attggaacat ctttctattt cctgcaaaac aaatgccgtc cgaacgggtc
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

g295.pep
 1 MLGMARHDDQ QGIAAILLPR RQOFFRLVFA PINARAAAHG NRPASDAFFK
 51 LPRQRHFHVR RHQVVFQIAA HLHGCRAQFR QPRRIRLRLR QTARQSGCG
 101 TDQAADFQIT VQRFFRQPRI RQQRHTRSP AFLHQIGPDF GFHQNAEHRA
 151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PSRRGHLRHQ QRRIGKTPPQ
 201 LAYQGLGGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSGAFVQ
 251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV RTVRTAFRQR NQIS*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq
 1 ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCGATATT
 51 GTTGGCCAGC CGCCAGCAGT TTTCCGCTT CGTCTTCACC CCGATAAACG
 101 CGCGTCTGCG CGCACACGGC AACCGGCCCG CCTCCGATGC GTTTTCAAA
 151 CTGCCCGGCC AGCGTTTTCA TCTGTTCGA CGGTATGATG TCGTATTGG
 201 TATTGCGCGA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
 251 GCATCCGCCT CTGTCTGCGC CAGACACCCC GTCAGCGAAG CGGCGGCAGG
 301 ACGGATCAGG CGCGGACTT TCAGATAACC GTTCAACGAT TTTCCGACA
 351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGCGCGCCG GCATTCCCTC
 401 ATCAGGTTGG GCCAGATTTC GGTTTCCATC AAAATGCCGA ACATCGGCGC
 451 GTGTTCCGCG AAAAAGTCC GTACCCACGT TTTTGTGCA TACGGAAGAT
 501 AGCGGCATTG CGCATCGGGA AACAGAACTT GCGCGGTTT CCGCCCCGTC
 551 GGGGTCTATC GCGTCATCAG CAGCGCGGCA TCGGGAAGC GCCGCCGCA
 601 CTGCGGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGGCGT
 651 GTATCCAAC CGCGCCGTA ACGGGATTCT GATACGGCTT GCCGAAACGC
 701 TCGTCCCGAT CGGCCCGATA TGCCGGGGCA CTTCCGGAGC GTTGTCCAA
 751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAGCC
 801 ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC TGAACGGTTC
 851 AGACGGCATT TCGGCAACGG AATCAATAT CGTAG

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295.pep
 1 MLGMARHDDQ QRIAAILLPR RQOFFRLVFT PINARAAAHG NRPASDAFFK
 51 LPRQRHFHVR RYDVVFQIAA HLHGCRAQFR QPRRIRLRLR QTARQSGGR
 101 TDQAADFQIT VQRFFRQPRI RQQRHTRAP AFPHQVGPDF GFHQNAEHRA
 151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PPRRHLRHQ QRRIGKTPPQ
 201 LAYQGLGGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSGAFVQ
 251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV XTVQTAFRQR NQIS*

m295/g295 93.9% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMARHDDQ	QRIAAILLPR	RQOFFRLVFT	PINARAAAHG	NRPASDAFFK	LPRQRHFHVR
g295	MLGMARHDDQ	QGIAAILLPR	RQOFFRLVFA	PINARAAAHG	NRPASDAFFK	LPRQRHFHVR
	70	80	90	100	110	120
m295.pep	RYDVVFQIAA	HLHGCRAQFR	QPRRIRLRLR	QTARQSGGR	TDQAADFQIT	VQRFFRQPRI
g295	RHQVVFQIAA	HLHGCRAQFR	QPRRIRLRLR	QTARQSGCGT	TDQAADFQIT	VQRFFRQPRI
	130	140	150	160	170	180
m295.pep	RQQRHTRAP	AFPHQVGPDF	GFHQNAEHRA	VFAQKLPYPR	FFVIRKIAAL	RIGKQNLRGF
g295	RQQRHTRSP	AFPHQVGPDF	GFHQNAEHRA	VFAQKLPYPR	FFVIRKIAAL	RIGKQNLRGF
	190	200	210	220	230	240
m295.pep	PPRRGHLRHQ	QRRIGKTPPQ	LAYQGLGGTR	FSDRNGVYPN	RAGNGIRIRL	AETLVPMRPI
g295	PSRRGHLRHQ	QRRIGKTPPQ	LAYQGLGGTR	FSDRNGVYPN	RAGNGIRMRL	AETLVPMRPV
	250	260	270	280	290	
m295.pep	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	XTVQTAFRQR	NQISX
g295	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	RTVRTAFRQR	NQIS

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGCATCAGG TCGTATTGCG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCCGCGC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CCGCGGCAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGTCCGCGC GCATTCCTTC
401 ATCAGATTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTCCGCG AAAAAGTCC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCCGTC
551 GGGGTCACTC GCGTCATCAG CAGCGGCGCA TCGGAAAAC GCTGCCGCAA
601 CTCGCGTATC AAAGGTTGGG CGGCACGCGT TTCCCGACC GAAACGCGT
651 GTATCCAAAC CGCGCCGTA ACGGGATTCG GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCGATA TGCAGGGGCA CTCCCGAGC GTTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CCGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1  MLGMARHDDQ OGIAAILLPR RQOFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRFHLER RHQVVFGLIAA HLHCRAQFR QPRRIRLRLC QTARQSSGGR
101 TDQAADFQIT V*RRFRQPRI RQQRHTRAP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLPO
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

m295.pep	10	20	30	40	50	60
	MLGMARHDDQORIAAILLPRRQOFFRLVFTPINARAAAHGNRPASDAFFKLPQRQFHLER					
a295	MLGMARHDDQOGIAAILLPRRQOFFRLVFTPINARAAAHGNLPVSDAFFKLPQRQFHLER					
	10	20	30	40	50	60
m295.pep	70	80	90	100	110	120
	RYDVVFGLIAAHLHCRAQFRQPRRIRLRLCLRQTFRQRSGGRTDQAADFQITVQRFFRQPRI					
a295	RHQVVFGLIAAHLHCRAQFRQPRRIRLRLCQTARQSSGRTDQAADFQITVXRFFRQPRI					
	70	80	90	100	110	120
m295.pep	130	140	150	160	170	180
	RQQRHTRAPAFPHQVGPDEFGFHQNAEHRVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
a295	RQQRHTRAPAFHLHQIGPDFGFHQNAEHRVFAQKLPYPRFFVIRKIAALCIRKQNLRGF					
	130	140	150	160	170	180
m295.pep	190	200	210	220	230	240
	PPRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDNRGVYPN RAGNGIRIRLAETLVPMRPI					
a295	PSRRGHLRHQRRIGKTLPLAYQRLGGTRFSDNRGVYPN RAGNGIRIRLAETLAPMRPI					
	190	200	210	220	230	240
m295.pep	250	260	270	280	290	
	CRGTSGAFVQITPYPRRKQPQYIIPLEHLSISCKTNAVXTVQTAFRQRNQISX					
a295	CRGTSGAFVQITPYPRRKQPQYIIPLEHLSISCKTNAVRTVRTAFRQRNQISX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
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51  GCTTGCCGTT TCGATTATTC TGGTGTcgcG GGCATACATT Gcttcgacag
101 aggggaccga ggcgcgtcaga ccgcAGCGCG Tggaacaaa ACTGCCGCCG
151 CTGTCTtTGGg ggcgcaacgg CGTtcagacy gcaTATTGGG TGCAGGAGGC
201 GGTGcagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGGacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301 TTGCGgcatt tGCGTGCCGA CCAGTCCGGT CATGTTTGG TCGCGCGCGA
351 CGGCGAGTGC CGCGAAGTGC AGTTTtttaC CGACGAAGAC GGCAGCGCA
401 aTc tGGTTCG TTTGGAAAA AAAGGCGGCA TATGGCGCGC GTCGGCTTCT
451 GATGCGGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAAGCGATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAAGGTGGC GCGGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGGCGGCA
701 CAACCCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGCG
751 GGC AATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCgaG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTA TGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCA
1051 CAAGGCAATG TCGCGGGCGG CGAGGTCATC GGTTTTGTG GTTCGACAGG
1101 GCGTTTCGACC GGGCCGCACC TGCATTACGA GGC CGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCGGAATT GACGCGAGCG
1201 GAC AAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

```

g297.pep
1  MAVFPLSAKH RYALRALAV SIILVSAAYI ASTEGTERVR PORVEQKLPP
51  LSWGGNGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDQSA REVQFFTDDE GERNLVALEK KGGIWRRSAS
151 DADMKVLPTL RSVVVKTSAR GSLARAEPV EIRELSGIF AGRFSLDGLK
201 EGDVRLLYD SLYFHGQOVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251 GNY YDEDRV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGTfVRA SADGVITFKG RKGyYGNAMV IRHANGVETL YAHLSAFSQA
351 QGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
401 DKAAPFAAQK KADALLARLR GIPVTVSQSD *

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

```

m297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGTGC
51  GCTTCCCGTT TCGATTATTT TGGTGTcgcG GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAAACAAA TCTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCG GCGGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCGA ATCAGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TGCGTGCCGA CCAGTCCGGT CATGTTTGG TCGCGCGCGA
351 CGGCGGCGCG CGCGAAGTGC AGTTTtttaC CGACGAAGAC GGCAGCGCA
401 ATCTGGTTCG TTTGGAAAAG AAAGGCGGCA TATGGCGCGC GTCGGCTTCT
451 GAGGGCGATA TGAAGGTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGCG
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCG
1051 GAAGGCAATG TCGCGGGCGG CGAGGTCATC GGTTTTGTG GTTCGACCGG
1101 GCGTTTCGACC GGGCCGCACC TGCATTACGA GGC CGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCGGAATT GACGCGAGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

```

m297.pep
1  MAVFPLSAKH RYALRALAV SIILVSAAYI ASTERTERVV PORVEQNLPP
51  LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDQGA REVQFFTDDE GERNLVALEK KGGIWRRSAS
151 EADMKVLPTL RSVVVKTSAR GSLARAEPV EIRELSGIF AGRFSLDGLK

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201 EGDVRLMYD SLYFHGQQA AGDILAAEVV KGSTRHQAFY YRSDKEGGGG
 251 GNYDEDEGKV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
 301 AAPQGTTPVRA SADGVITFKG RKGgyGNAVM IRHANGVETL YAHLSAFSQA
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPFVS ALPTPELTQA
 401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERVRPQVEQNLPPLSWGSGVQT					
g297	MAVFPLSAKHKYALRALAVSIILVSAAYIASTEGTERVRPQVEQKLPLSWGNGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA					
g297	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTDEDEGERNLVALEKKGGIWRRSASEADMKVLPTLRSVVVKTSARGSLARAEVPV					
g297	REVQFFTDEDEGERNLVALEKKGGIWRRSASDADMKVLPTLRSVVVKTSARGSLARAEVPV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQQAAGDILAAEVVKGSTRHQAFY					
g297	EIRESLSGIFAGRFSLDGLKEGDAVRLLYDSLYFHGQQAAGDILAAEVVKGSTTHQAFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGGNYDEDEGKVLQEKGGFNIEPLVYTRISSPFGyRMHPILHTWRLHTGIDY					
g297	YRSDKEGGGGGNYDEDEGKVLQEKGGFNIEPLVYTRISSPFGyRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGTTPVRASADGVITFKGRKGGYGNAMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
g297	AAPQGTTPVRASADGVITFKGRKGGYGNAMIRHANGVETLYAHLSAFSQAQGNVRGGEVI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVGSTGRSTGPHLHYEARINGQPVNPFVSVALPTPELTQADKAFAAQKQKADALLARLR					
g297	GFVGSTGRSTGPHLHYEARINGQPVNPFVSVALPTPELTQADKAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1 ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
 51 GCTTGCCGTT TCGATTATTT TGGTGTGCGC GGCATACATT GCTTCGACAG
 101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAACAAAA ACTGCCGCCG
 151 CTGTCTTGGG GCGGCAGCGG TGTTTCAGACG GCATATTGGG TGCAGGAGGC
 201 GGTGCAGCCA GCGGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
 251 CGCGGGACGA AATTGCCCGA ATAACGGAAA AATATGGCGG CGAAGCCGAT
 301 TTGCGGCATT TGGTGCCCGA CCAGTCGGTT CATGTTTTGG TCGCGCGCGA
 351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTTAC CGACGAAGAC GCGGAGCGCA
 401 ATCTGGTGC TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
 451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
 501 GTCGGCGCGC GGTTCGCTGG CGCGGCGCGA AGTGCCCGTC GAAATTCGCG

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551 AATCCTTAAG CGGGATTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGC GCCT GATTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGGTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACTTGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TCGCGGCGG CGAGGTCATC GGTTTTGTCT GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACC TGCATTACGA GCGCGCATC AATGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCCGAATT GACGAGGGC
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

a297.pep

```

1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV RQORVEQKLPP
51 LSWGGSGVQT AYWVQEAQVP GDSDLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGGG REVQFFTED GERNLVALEK KGGIWRSSAS
151 EADMKVLP LRSVVVKT SAR GSLARAEV PV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHQQVA AGDILAEV V KGGTRHQAFY YRSDKEGGGG
251 GNYDEDGRV LQEKGGFNIE PLVYTRISSP FG YRMHPILH TWRLHTGIDY
301 AAPQGT PVRASADGVIT FKG RKG GYGNAV M IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVSGTGRST GPHLHYEARI NGQPVNPSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

m297/a297 99.3% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV RQORVEQKLPP LSWGGSGVQT					
a297	MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV RQORVEQKLPP LSWGGSGVQT					
	10	20	30	40	50	60
m297.pep	AYWVQEAQVP GDSDLADVLAR SGMARDEIAR ITEKYGGEAD LRHLRADQSV HVLVGGDGGG					
a297	AYWVQEAQVP GDSDLADVLAR SGMARDEIAR ITEKYGGEAD LRHLRADQSV HVLVGGDGGG					
	70	80	90	100	110	120
m297.pep	REVQFFTED GERNLVALEK KGGIWRSSASE ADMKVLP LRSVVVKT SARGSLARAEV PV					
a297	REVQFFTED GERNLVALEK KGGIWRSSASE ADMKVLP LRSVVVKT SARGSLARAEV PV					
	130	140	150	160	170	180
m297.pep	EIRESLSGIF AGRFSLDGLKEGDAVRLMYDSLYFHQQVA AGDILAEV V KGGTRHQAFY					
a297	EIRESLSGIF AGRFSLDGLKEGDAVRLMYDSLYFHQQVA AGDILAEV V KGGTRHQAFY					
	190	200	210	220	230	240
m297.pep	YRSDKEGGGGNYYDEDGKVLQEKGGFNIE PLVYTRISSP FG YRMHPILH TWRLHTGIDY					
a297	YRSDKEGGGGNYYDEDGKVLQEKGGFNIE PLVYTRISSP FG YRMHPILH TWRLHTGIDY					
	250	260	270	280	290	300
m297.pep	AAPQGT PVRASADGVIT FKG RKG GYGNAV M IRHANGVETL YAHLSAFSQA EGNVRGGEVI					
a297	AAPQGT PVRASADGVIT FKG RKG GYGNAV M IRHANGVETL YAHLSAFSQA EGNVRGGEVI					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m297 . pep	GFVVGSTGRSTGPHLHYEARINGQVPNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQVPNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297 . pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298 . seq

```

1 ATGAAAACT TTCTTTCCT TTTCCCTCC ATACTGATGT CTGCCCTGAT
51 TGCCGTGTGG TTCAGCCAAA ACCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AACCTTCTCG TCCGGCGAAA cgcggcgac ggCTCAAGAC GGCCTTCGG
251 CAGATATGCC GCCTGAAGCC GCCGCATCCG AAGCGCGCCC GCCGCGCGC
301 GGAACAGAAT GGAACAAGG CACCGAAGCC GCCGCGTCC GCAGCGCGCA
351 CAAAGTCTTT TTCCCGGAG ATTCGCTGAT GCAGGGCGTT GCGCTTTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTTCGACT GGCGGAAAAC
501 GATTGAAGAA ACCCTGAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCG GAACGACCCG TGGGATTTC CCGTCGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCGGCACACA CGCACCGCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAATGCTTT CGGAACACTT GAAAGGCAAA ATCATCTGA TTTCCACCGC
801 GCACACCTG AGCGGCGGGA AAGGCGGCTA CACCGATTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGTAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAATAATA ATGGAATAA TCGTTTTGA
951 ACCGAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298 . pep

```

1 MKNFLSLPAS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51 SGAAALQENAY ALSDGIKTFL SGETPPTAQD GGSADMPPEA AASEAAPAG
101 GTEWKQGTEA AAVRSGDKVF FAGDSLMOGV APFVQKSLKQ QYGIESANLS
151 KQSTGLSYPS FFDWPKTIEB TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201 KFASDEWAQE YLKRVDRIE AANTHRVQVW NLGIPYMKKV KLDGQMRYLD
251 KLLSEHLKGG IILPTAQT LSGGKGRYTD VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAEKI MEKIVFEPST QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298 . seq

```

1 ATGAAAACT TTCTTTCCT TTTCTCTCC ATACTGATGT CTGCCCTGAT
51 TGCCGTGTGG TTCAGCCAAA ACCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCTCG TCCGGCGAAA CGCGCGGAC GGCTCAAGAC GGCCTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCGTCCC TCAAACCGGT
301 GAAACAGAAT GGAACAAGA CACCGAAGCC GCCGCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTTGTCCGCG ACTCGCTGAT GCAGGGCGTT GCCCTTTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCGGAAAAC
501 GATTGAAGAA ACCCTGAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCCTTGAA GCGGCACACA CGCACCGCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAATGCTTT CGGAACATT GAAAGGCAAA ATCATCTGA TTTCCACCAC
801 GCACACCTG AGCGGCGGGA AAGACGCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGCAAG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAATAATA ATGGAATAA TCGTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

m298.pep

```

1  MKNFLSLFSS ILMSALIAVW FSONPINAYW QQTYHRNSPL EPLAAYGWNR
51  SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AASEAVPQTG
101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVOKSLKQ QYGIESVNLS
151 KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNDP WDFPVGKLYL
201 KFASDEWAQE YLKRVDRIE AATHRVQVV WLGIPIYMKA KLDGQMRYLD
251 KLLSEHLKGI IILPTHTL SGGKDRYTDV VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/g298 94.8% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWNRSGAALQENAY					
g298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWNRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
g298	ALSDGIKTFISGETPPTAQDGGSDMPPEAAASEAAPAGGETEWKQDTEAAAVRSGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVOKSLKQYQYIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
g298	FAGDSLMOGVAPFVOKSLKQYQYIESANLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWFDFPVGKLYLKFASDEWAQEYLKRVDRIEAAHTRVQVVWLGIPIYMKA					
g298	LAVFLGPNDPWFDFPVGKRYLKFASDEWAQEYLKRVDRIEAAHTRVQVVWLGIPIYMKV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLDKLLSEHLKGI IILPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
g298	KLDGQMRYLDKLLSEHLKGI IILPTAQTLSGGKGRYTDVNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
g298	EGQKLLAEKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTGCGCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCCTC GAACCGCTT CCGCCTACGG ATGGTGGCGG
151 AGCGGTGCGG CATTGCAAGA AACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GGCAGGTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAACCTGGC
301 GAAACAGAAT GGAAACAAA CACCGAAGCC GCCCGCTCC GAACAGGGGA
351 CAAAGTCTTT TTCGCGGCG ACTCGCTGAT GCAGGGCGTT GCACCCTTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGAAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT
551 TCCTCGGTCC GAACGACCCG TGGGATTTCC CCGTTGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GGCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC

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751  AAACTGCTTT CGGAATATTT GAAAGGCAAA ATCATCCTGA TCCCCACCGC
801  GCACACCCTG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851  ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901  GAAGGACAAA AACTGCTGGC GGCAAAAATA ATGGAAAAAA TCGTTTTTGA
951  ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298 . pep
  1  MKNFLSLFAS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
 51  SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AAPETAPQTG
101  ETEWKQNTA AAVRTGDKVF FAGDSLMOGV APFVQKSLKQ QYGIESVNLS
151  KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201  KFASDEWAE YLKRVDRIE AAHTHYVQVW WLGIPYMKKA KLDGQMRYL
251  KLLSEYLGK IILIPHTAHL SGGKDRYTD VNVNGKPVRY RSKDGIHFTA
301  EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298 . pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRS	GAALQENAY				
a298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRS	GAALQENAY				
	70	80	90	100	110	120
m298 . pep	ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
a298	ALSDGIKAFISGETPPTAQDGGSDMPSEAAAPETAPQTGETEWKQNTAATAVRTGDKVF					
	130	140	150	160	170	180
m298 . pep	FVGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
a298	FAGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	190	200	210	220	230	240
m298 . pep	LAVFLGPNDPWFDFPVGKLYLKFASDEWAEYLKRVDRIEAAHTHRVQVWVLGIPYMKKA					
a298	LAVFLGPNDPWFDFPVGKRYLKFASDEWAEYLKRVDRIEAAHTHYVQVWVLGIPYMKKA					
	250	260	270	280	290	300
m298 . pep	KLDGQMRYLDKLLSEHLKGKIILIPHTHTLSGGKDRYTDVNVNGKPVRYRSKDGIFHTA					
a298	KLDGQMRYLDKLLSEYLGKIIILIPHTHTLSGGKDRYTDVNVNGKPVRYRSKDGIFHTA					
	310	320				
m298 . pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
a298	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299 . seq
  1  ATGAACCCCA AACACTTCAT CGCATTTTCC GCCCTGTTCC CCGCCACGCA
 51  GGCAGAAGCC CTGCCGTCG CCTCCGTCAG CCCGACACC GTTACCGTTT
101  CCCCCTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151  AACGCGCCCG CCTCGCCTTG GATGAAAAAA CTCCGATCCG TCGCACAAAG
201  CAGCGGCGAG GCCTTCCGCA TCCTGCAAAAT CGGCGACTCG CATACCGCGC
251  GCGACTTCTT TACCGACGCC CTGCGCAAAC GCCTGCAAAA AACATGGGGC
301  GACGCGGCGA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351  GGCGGCGGTC CGTCACAGCG GCAACTGGCA AAGCTTCAAC AGCAGGAACA
401  ATACCGAGA TTTCCCGCTC GGCGGCATCC TCGCCCAAAC CGGACGCGC
451  GGCGGCATGA CCCTGACCGC GTCTGACGGC AAAACCGGCA AACAGCGCGT

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501	TTCCCTGTTT	GCCAAACCGC	TGCTCGCCGA	ACAAACCCCTG	ACCGTCAACG
551	GCAACACCTG	CTCCGCCAAC	GGCGGCGGCT	GGCAGGTACT	GGATACGGGC
601	CGGCGACGTG	CCCTGGCCAT	ACAGACCGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATC	GAAATATCCG	CGCGCGGCAT	TACGTTTTC	CGCATGGGCT
701	TCAACGGCGC	ACAATTGACC	CAGTGGTCGA	AATGGCGTGC	CGACGGGTAC
751	AAACGACTTG	CCCCAACCGG	CGCGGATTTG	GTTATCCTTT	CTACCGGCAT
801	CAAACAAGCC	TTCAACAACA	ACATCGACAT	TGCGGATACC	GAACAAAAAT
851	GGCTGGATAC	CGTCCGCCAA	ATCCGCGACA	GCCTGCCCGC	CGCCGGCATC
901	CTCATCATCG	GTCGCGCCGA	CGCTGTGAAA	AACACGCTCG	CGGTATGCGG
951	CACGCGCCCC	GTCCTCTGA	CCGAAGTCCA	ACAGATGCAG	CGCGCGCTGC
1001	CCCGTCAGGG	GCAGACGATG	TTTTGGTCTT	GCACAAACGC	AATGGGCGGC
1051	ATAATGACGA	TGAAAAATCT	GCTCAACCAA	GGATGGCGCG	CCAAAGACCG
1101	CGTATACCTT	TCCGCCCAAG	GCTACCGCGG	CGCGCGCGGA	ATGCTTGCCG
1151	ACAGCCTCGA	AGAAATCGTC	CGCGCCGCGC	CAATCAGGCA	ATAA

g299.pap

1	<u>MNP</u> KHFI <u>AFS</u>	<u>ALFAATQAE</u> A	LPVASVSPDT	VTVSFSAPYT	DTNGLLTDYG
51	NAAA <u>SP</u> MMWK	LR <u>SVAGQ</u> SGSE	AFRILQIGDS	HTAGDFFDTA	LRKRLQKTHG
101	DGGIGWVYPA	NVKGQRM <u>AAV</u>	RHSGN <u>WQ</u> SFT	SRNNTGDFPL	GGILAQTGSG
151	GGMTLTASDG	KTGKQ <u>RVSLF</u>	AKPL <u>LA</u> EQTL	TVNGNTV <u>SA</u> N	GGGQVQLDTG
201	AALPLAIQTE	MPWDIGFINT	ENPAGGITVS	AMGINGAQLT	QWSKWRADRM
251	NDLQAQTGADL	VILSYGTNEA	FNNNIDIAQT	EQKWLDTVRQ	IRDSLPAAGI
301	LIIGAPESLK	NTLGVC <u>GTRP</u>	VLLTE <u>QDQ</u> MQ	RRVARQGTQM	FWSQWNA <u>MG</u> G
351	ICSMKNWLNQ	GWAAGDGVHF	SAQGYRRAAE	MLADSLEELV	RAAAIRO*

m299.seq

1	ATGAACCCCA	AACACCTCAT	CGCATTTTCC	GCCCTATTCC	CCGCCACGCA
51	GGCAGAGGCC	CTACTGTGCG	CCTCGCTACG	CCTCGACAGC	GTTACCGTTT
101	CCCAGTGGCC	CCCCATACCC	GATACCAACG	GGCTGCTGAC	CGACTACGGC
151	AACCGCTCCG	CCTCGCCTTG	GATGAAAAAA	CTTCAATTCC	TCGCACAAGG
201	CAGCGGCGAG	ACCTTCCGTA	TCCTGCAAAT	CGGCGACTCG	CATACCGCCG
251	GGCACTTCTT	TACCGACAGC	CTGCGCAAA	GCCTGCAAAA	AACCTTGGGGC
301	GACGGCGGCA	TAGGCTGGGT	TTACCCCGCC	AACGCTCAAG	GGCAGGCGAT
351	GGCGGCGCTC	GGCCACAACG	GTAACTGGCA	AGAGCTCAC	ACGAGGAACA
401	ACAACGGAGA	CTTCCCGCTC	GGCGGCATCC	TCGCCCACAC	CGGCAGCGGC
451	GGCAGCATGA	CCCTGACCGC	ATCGGACGGC	ATAGCAACAG	AGCAGCGCGT
501	TTCCCTGTTT	GCCAAACCCC	TGCTTGCCGA	ACAAACCTG	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGCGGCT	GGCAGGTACT	GGATACGGGC
601	GCGGCACCTG	CCCTGACCAT	ACACACCGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATG	GAATAATCCG	CGGGCGGCAT	TATCGTTTCC	CGGATGGGCA
701	TCAACGGGCG	ACAATTAACC	CAGTGGTCGA	AATGGCTTGC	CGACCGTATG
751	AACGACCTCG	CCCAAAACGG	GGCGGATTTG	GTTATCCTTT	CCTACGGCAC
801	CAACGAAGCT	TTCAACAACA	ACATCGACAT	TGCCGACACC	GAACAAAAAT
851	GGCTGGATAC	CGTCGCGCAA	ATCCCGGACA	GCCTGCGCTG	CGCGGCGATC
901	CTCATCATCG	GCGCACCCGA	ATCCCTGAAA	AACACGCTCG	CGGTTATGCG
951	CAACAGCCCC	CTCGCGCTGA	CGCAAGTCCA	ACAGATGCAG	CGGCGCGTCG
1001	CCCGTCAGGG	GCAGACGATG	TTCTGGTCTT	GGCAAAACGC	CATGGGCGGC
1051	ATATGTCAGCA	TGAAAAAAGT	GCTCAACCGA	GGATGGGCGG	CCAAAGACGG
1101	CGTACACTTC	TCGCGCAAA	GCTACCGGGC	CGCGGCGGAA	ATAGTCGCGG
1151	ACAGCGCTCGA	AGAAGCTCGT	CGCTCGGCTG	CAATCAGGCA	ATAA

m299.ppt

1	<u>MNPVKHLIAFS</u>	<u>ALFAATOQAEA</u>	LPVASVSLDT	VTVSPSPAPYT	DTNGLLLTDYG
51	NASASPMPMKK	LQSVAAQGSSE	TPRILQIGDS	HTAGDEFFTDS	LRKLRLQKWTG
101	DGGIGWVYPA	NVKGQRMMAV	RHNGNWQSLT	SRNNTGDFPL	GGILAHTGSG
151	GSMTLTASD	ISAGQRVSFL	AKPLLAEQTL	TVNGNTVSAN	GGGVQVLDTG
201	AALPLTIHTE	MPWDIGFINI	ENPAGGITVS	AMGINGAQLT	QWSKWRADRM
251	NDLAQTGADL	VILSYGTEBA	FNNNIDIADT	EQKWLTVVRQ	IRDSLPAAGI
301	LIIGAPESLK	NTLGVCGTRP	VLRTVEQQMQ	RRLVARQGTQ	PFSWNQAMGG
351	ICSMKNWLNQ	GWAAKDGVHF	SAKGYRRAAE	MLADSLEELV	RSAATRO*

m299.pep MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNTNGLLTDYGNASASPWMKK
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

693

g299	MNPKHFIASFALFAATQAEALPVASVSPDVTVTSPSAPYTDNGLLTDYGNAAASPMWKK
	10 20 30 40 50 60
m299.pep	LQSVAQGSGETFRILQIGDSHTAGDFFTDLSLRKRLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
g299	LRSLVAQGSGEAFRILQIGDSHTAGDFFTDALRKRLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
m299.pep	RHNGNWQSLTSRNTGDFPLGGILAHGTSGGSMILTASDGIASKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
g299	RHSGNWQSFSTRNTGDFPLGGILAHGTSGGSMILTASDGIASKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299.pep	TVNGNTVTSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
g299	TVNGNTVTSANGGGWQVLDTGAAALPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299.pep	LIIGAPESLKNLTGVCGRTPVRLTEVQQMQRVARQGGQTFWSWQAMGGICSMKNWLNQ
	310 320 330 340 350 360
g299	LIIGAPESLKNLTGVCGRTPVLLTEVQQMQRVARQGGQTFWSWQAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299.pep	GWAAKDGVFHSAKGYRRAAEMLADSLEELVRSAAIRQX
	370 380 390
g299	GWAAKDGVFHSAQGYRRAAEMLADSLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

a299.seq

1	ATGAACCCCA	AACACCTCAT	CGCATTTTCC	GCCCTATTTCG	CCGCCACGCA
51	GGCAGAAGCC	CTACCTGTCG	CCTCAGTCAG	CCTCGACACC	GTTACCGTTT
101	CCCCGTCCGC	CCCCTACACC	GATACAAACG	GGCTGCTGAC	CGACTACGGC
151	AACGCCTCCG	CCTCGCCTTG	GATGAAAAAA	CTCCAATCCG	TCGCACAAGG
201	CAGCGGCGAG	ACCTTCCGTA	TCCTGCAAAT	CGGCGACTCG	CATACCGCCG
251	GCGACTTCTT	TACCGACAGC	CTGCGCAAAC	GCCTACAAA	AACTTGGGGC
301	GACGGCGGCA	TAGGCTGGGT	TTACCCCGCC	AACGTCAAAG	GGCAGCGCAT
351	GGCGGCCGTC	CGGCACAACG	GTAACCTGGCA	AAGCCTCACC	AGCAGGAACA
401	ACACCGGAGA	CTTCCCGCTC	GGCGGCATCC	TCGCCCACAC	CGGCAGCGGC
451	GGCAGCATGA	CCCTGACCGC	ATCGGACGGC	ATAGCAAGCA	AGCAGCGCGT
501	TTCCCTGTTT	GCCAAACCCC	TGCTTGCCGA	ACAAACCCTG	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGCGGCT	GGCAGGTACT	GGATACGGGC
601	GCGGCACTGC	CCCTGACCAT	ACACACCGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATC	GAAAATCCCG	CCGGCGGCAT	TACCGTTTCC	GCGATGGGCA
701	TCAACGGCGC	ACAATTAACC	CAGTGGTCGA	AATGGCGTGC	CGACCGTATG
751	AACGACCTTG	CCCAAACCGG	CGCCGATCTA	GTCATCCTTG	CCTACGGTAC
801	CAACGAAGCC	TTCGGCGACA	ACATCGACAT	TGCCGATACC	GAACAGAAAT
851	GGCTGGATAC	CGTCCGCCAA	ATCCGCGACA	GCCTACCTGC	CGCCGGCATC
901	CTCATCATCG	GCGCGCCCGA	ATCCCTGAAA	AACACGCTCG	GCGTATGCGG
951	CACACGCCCC	GTCCGCCTGA	CCGAAGTCCA	ACAGATGCAG	CGGCGCATCG
1001	CCCGTCAGGG	GCAGACGATG	TTCTGGTCTT	GGCAAAACGC	GATGGGCGGC
1051	GTTTGCAGCA	TGAAAACTG	GCTCAACCAC	GGATGGGCGC	CCAAAGACGG
1101	CGTACACTTT	TCCGCCAAAG	GCTACCAACG	GTCGGCGGAA	ATGCTCGCCG
1151	ACAGCCTCGA	AGAACTCGTC	CGCTCCGCTG	CAATCAGGCA	ATAA

This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
  1  MNPKHLLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
 51  NASASPWMKK LQSAQGSSE TFRILQIGDS HTAGDFFTDS LKRRLQKTWG
101  DGGIGWVYPA NVKGQORMAAV RHNGNWQSLT SRNNTGDFPL GGILAHGSG
151  GSMTLTASDG IASKQVSLF AKPLLAQTL TVNGNTVSAN GGGWQVLDTG
201  AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251  NDLAQTGADL VILAYGTNEA FGDNIDIADT EQKWLDTVRQ IRDSLPAAGI
301  LIIGAPESLK NTLGVCGRP VRLTEVQOMQ RRIARQGQTM FWSWQAMGG
351  VCSMKNLNLH GWAADGVHF SAKGYQSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

m299.pep	10	20	30	40	50	60
	MNPKHLLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
a299	MNPKHLLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
	10	20	30	40	50	60
m299.pep	70	80	90	100	110	120
	LQSAQGSSETFRILQIGDSHTAGDFFTDSLKRRLQKTWGDGGIGWVYPANVKGQORMAAV					
a299	LQSAQGSSETFRILQIGDSHTAGDFFTDSLKRRLQKTWGDGGIGWVYPANVKGQORMAAV					
	70	80	90	100	110	120
m299.pep	130	140	150	160	170	180
	RHNGNWQSLTSRNNTGDFPLGGILAHGSGGSMTLTASDGIASKQVSLFAKPLLAQTL					
a299	RHNGNWQSLTSRNNTGDFPLGGILAHGSGGSMTLTASDGIASKQVSLFAKPLLAQTL					
	130	140	150	160	170	180
m299.pep	190	200	210	220	230	240
	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
a299	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
	190	200	210	220	230	240
m299.pep	250	260	270	280	290	300
	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI					
a299	QWSKWRADRMNDLAQTGADLVILAYGTNEAFNGNIDIADTEQKWLDTVRQIRDSLPAAGI					
	250	260	270	280	290	300
m299.pep	310	320	330	340	350	360
	LIIGAPESLKNTLGVCGRPVRRLTEVQOMQRRVARQGQTMFWSWQAMGGICSMKNWLNQ					
a299	LIIGAPESLKNTLGVCGRPVRRLTEVQOMQRRRIARQGQTMFWSWQAMGGVCSMKNLNLH					
	310	320	330	340	350	360
m299.pep	370	380	390			
	GWAADGVHFSAGGYRRAEMLADSLEELVRSAAIRQX					
a299	GWAADGVHFSAGGYQSAEMLADSLEELVRSAAIRQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
  1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
 51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101  TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151  GCCTCTGCCG TCGGTGCGTA TTTTCGACTA TCCGTCCCCG ATCCGCGTCC
201  TGTGTTGGGCG AAAGGACGTG CCGATGACGG TTTGATTACG GTTGTCAGCC
251  TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301  TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGTTTCTT TATTGGGCGT
```

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351  GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401  TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451  ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501  GTCCGCCGTC ATCTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551  CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCCGGCAA TCTGTTCTTA
601  GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651  CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAATGCG TTTTATATGG
701  CAGCCAGTAC GTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751  ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGT CACAAGAAGA
801  AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851  TAATTGGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901  AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCTGAAA CAGGATTGGT
951  TGCCGGTTCG CCGTTTTTAA AATCGATTGT TGTTTTTATT TTCTGTGTGT
1001 TTGCGCTGCC GGCATTGTT TATGGCCGGA TAACCCGAAG TTTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTGGTTC ATCATCTTTT TTGCCGCACA GTTGTGCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG TGTGTTGTTT ATCGGTTTAA TTTTAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCGCGCAA TGGGCGGTAA
1301 CTGCGCGGAT TTTCGTCCCT ATGCTGATGT TGGCCGCTA CGCGCCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTCG GGCTGATTAT GGCACGGTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATT CTATGATGTT GCCGTATTCC
1501 GCTTCTTCT TAATTGCATG GATCGCCTTA TTCTGCATT GGTATTGT
1551 TTTGGGCTG CCCGTCGGT CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1  MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAVGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLISALM RLLLTSPRK LTTFMVFTG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLALI TQQAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGV FVALSALLAW
301 SIVPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVNVAMAE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGAVFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAO WAVTAPIFVP MLMLAGYAPQ
451 VIQAAYRIGD SVTNITPMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
501 AFFLIANIAL FCIWVFLGL PVGPGTPTFY PVP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCCGACTA TCCGTCGCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGGTTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCCGGCAA TCTGTTCTTA
601 AGCACAATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTGCT
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTACG TTTGTGATTG
701 CTTTGATTGG TTATTTTGTG ACTGAAAAAA TCGTCGAACC GCAATTGGGC
751 CCTTATCAAT CAGATTGTG ACAAGAAGAA AAAGACATTC GGCATTCCAA
801 TGAAATCACG CCTTTGGAAT ATAAAGGATT AATTGGGCT GCGGTGGTGT
851 TTGTTGCCCT ATCCGCCCTA TTGGCTTGGA GCATCGTCCC TCCGACGGT
901 ATTTTGCCTC ATCCTGAAAC AGGATTGGTT TCCGGTTCGC CGTTTTTAAA
951 ATCGATTGTT GTTTTATTTT TCTGTGTTG TGCATGyCG GGCmTTGTTT
1001 ATGGmCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

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1051 ATGGCCGAAT CGATGAGTAC TCTGGsGCTT TmTTTGswCA kcATCTTTTT
1101 TGCCGCACAG TTTGTCGCAT TTTTAAATTG GACGAATATT GGGCAATATA
1151 TTGCCGTTAA AGGGGCGACG TTCTTAAAAG AAGTCGGCTT GGGCGGCAGC
1201 GTGTTGTTTA TCGGTTTTAT TTTAATTGT GCTTTTATCA ATCTGATGAT
1251 AGGCTCCGCC TCCGCGCAAT GGGCGGTAAC TCGCGCGATT TTCGTCCCTA
1301 TGCTGATGTT GGCCGGCTAC GCGCCCGAAG TCATTCAAGC CGCTTACCGC
1351 ATCGGTGATT CCGTTACCAA TATTATTACG CCGATGATGA GTTATTTCCG
1401 GCTGATTATG GCGACGGTGA TCAAATACAA AAAAGATGCG GCGGTGGGTA
1451 CGCTGATTTC TATGATGTTG CCGTATTCCG CTTTCTTCTT GATTGCGTGG
1501 ATTGCCTTAT TCTGCATTG GGTATTGTT TTGGGCCTGC CCGTCGGTCC
1551 CGGCGCGCCC ACATTCTATC CCGCACCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:

m302.pep

```

1  MHSIYFFKEK QMSQTDTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAVGAYFGL SVPDRPVGA KGRADDGLIY IVSLLNADGF IKILTHTVKN
101 FTGFAPLGTV LVSLGVGIA EKSGLISALM RLLLTSPRK LTTFMVVFTG
151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 STIDPLLACI THQAAVVGPE ANWFFMVAST FVIALIGYFV TEKIVEPQLG
251 PYQSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVFVALSAL LAWSIVPADG
301 ILRHPETGLV SGSPFLKSIV VFIFLLFALX GXVYGRVTRS LRGEQEVVNA
351 MAESMSTLXL XLXIFFFAAQ FVAFFNWTNI QYIAVKGAT FLKEVGLGGS
401 VLFIFGILIC AFINLMIGSA SAQWAVTAPI FVPMMLAGY APEVIAQAYR
451 IGDSTNIIT PMMSYFGLIM ATVIKYKDA GVGLISMML PYSAFFLIAW
501 IALFCIWVTV LGLPVGPGAP TFYPAP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 302 shows 94.0% identity over a 533 aa overlap with a predicted ORF (ORF 302.ng)

from *N. gonorrhoeae*:

m302/g302

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTDTRDGRFLRTVEWLGNNMLPHPVTLFIIIFIVLLLIASAVGAYFGL					
g302	MHSIYFFKEKQMSQTDARRSGRFLRTVEWLGNNMLPHPVTLFIIIFIVLLLIASAVGAYFGL					
	10	20	30	40	50	60
m302.pep	SVPDRPVGAAGKGRADDGLIYIVSLLNADGFIKILTHTVKNFTGFAPLGTVLVSLGVGIA					
g302	SVPDRPVGAAGKGRADDGLIHVSLDADGLIKILTHTVKNFTGFAPLGTVLVSLGVGIA					
	70	80	90	100	110	120
m302.pep	EKSGLISALMRLLLTSPRKLTTFMVVFTGILSNTASELG YVVLIPLSAII FHSLSGRHPL					
g302	EKSGLISALMRLLLTSPRKLTTFMVVFTGILSNTASELG YVVLIPLSAII FHSLSGRHPL					
	130	140	150	160	170	180
m302.pep	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVASTFVI					
g302	AGLAAAFAGVSGGYSANLFLGTIDPLLACITQAAQIIHPDYVVGPEANWFFMAASTFVI					
	190	200	210	220	230	240
m302.pep	ALIGYFVTEKIVEPQLGPGYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVVALSALLAW					
g302	ALIGYFVTEKIVEPQLGPGYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVVALSALLAW					
	250	260	270	280	290	300
	300	310	320	330	340	350

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

a302.ppep

1 MHSIYFFKEK QMSQTDQTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI

51 ASAAGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN

101 FTGFAPLGTV LVSLLLGVGIA EKSGLISALM RLLLTKSPRK LTTFMVVFTG

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151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQAAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMEA SMSTLGLYLVI IFFAAQFVA FFWNTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIIIPMM SYFGLIMATV IKYKKGAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

```

m302/a302 96.1% identity in 533 aa overlap

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTD	QDRGFLRTV	EWLGNNMLPH	PVTLFII	FIVLLLIAS	AVGAYFGL
a302	MHSIYFFKEKQMSQTD	QDRGFLRTV	EWLGNNMLPH	PVTLFII	FIVLLLIASA	AAGAYFGL
	70	80	90	100	110	120
m302.pep	SVPDPRPVGAKGRADD	GLIYIVSLLN	ADGFIKILTHT	VKNFTGFAP	LGTVLVSL	LGVGIA
a302	SVPDPRPVGAKGRADD	GLIHVSVLLD	ADGLIKILTHT	VKNFTGFAP	LGTVLVSL	LGVGIA
	130	140	150	160	170	180
m302.pep	EKSGLISALMRLLLT	TKSPRKLTTF	MVVFTGILS	NTASELGY	VVLIPLSA	IFHSLGRHPL
a302	EKSGLISALMRLLLT	TKSPRKLTTF	MVVFTGILS	NTASELGY	VVLIPLSA	IFHSLGRHPL
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYS	ANLFLSTID	PLLACITHQAA	-----	VVGPEANW	FFMVASTFVI
a302	AGLAAAFAGVSGGYS	ANLFLGTID	PLLAGITQAA	QIIHPDYV	VVGPEANW	FFMVASTFVI
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEP	QLGPIQSD	LSQEEKDIR	SNEITPLE	YKGLIWAG	VVFVALSALLAW
a302	ALIGYFVTEKIVEP	QLGPIQSD	LSQEEKDIR	SNEITPLE	YKGLIWAG	VVFVALSALLAW
	300	310	320	330	340	350
m302.pep	SIVPADGILRHPET	GLVSGSP	PFLKSIVV	FIFLLFAL	GXVYGRV	TRSLRGEQEVVNAMEA
a302	SIVPADGILRHPET	GLVSGSP	PFLKSIVV	FIFLLFAL	PGIVYGR	TRSLRGEQEVVNAMEA
	360	370	380	390	400	410
m302.pep	SMSTLXLXLXXIFF	AAQFVAFF	NWNTNIGQY	IAVKGAT	FLKEVGL	GGSVLFIFIGFILICAFI
a302	SMSTLGLYLVIIF	FAAQFVAFF	NWNTNIGQY	IAVKGAT	FLKEVGL	GGSVLFIFIGFILICAFI
	420	430	440	450	460	470
m302.pep	NLMIGSASAQWAVT	APIFVPM	MLLAGYAPE	VIQAAYR	IGDSVTN	IIIPMMSYFGLIMATV
a302	NLMIGSASAQWAVT	APIFVPM	MLLAGYAPE	VIQAAYR	IGDSVTN	IIIPMMSYFGLIMATV
	480	490	500	510	520	
m302.pep	IKYKKGAGVGT	TLISMMLP	YSAFFLIA	WIALFCI	WVFLGL	PVPGAPTFYPAPX
a302	IKYKKGAGVGT	TLISMMLP	YSAFFLIA	WIALFCI	WVFLGL	PVPGAPTFYPAPX
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

g305.seq

```

1  ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTG
101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CGGTTTGGC GGTAGTGTG GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT
301 GACAAACAAA TCAAAGAGTA TCTGTTTAA CCGTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAATTTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GTGTGCCCCA AGTGTGTTGCA CTGGTTCCGG GTACGTCCCG
501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGCCG TTCCGATGAT GGTTCAGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATAGGCT TTATTGCCG TTTTGTTCG GGTGTTGGTAG
701 CCGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCGTTT
751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGTTGTC
801 GGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAI AF IPAAVMGLLF
101 DKQIKEYLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TVMGGMLWGI ERKTATEFSF FLAVPMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALK FVSKKNYIPF
251 AYYRIVFGIV IILWLSGWI SWE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)

```

1  AtGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTG
101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CAGTTTGGC GGTAGTGTG GAATACCGGC AACGTTTCAG
201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT
301 GGCAWACAAA TCAAAGAGyA TCTGTTTAA CCGTTGAGTG TTGCAGTCAT
351 GCTGGTTyTG GCGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAATTTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GCGTTGCCCA AGTGTGTTGCA CTGGTTCCGG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAA
551 CTGCGACAGA ATTCTCGTTT TTCTTGCGTG TGCCGATGAT GGTGCGCGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CCGTTTGATT CTGATAGGCT TTATTGCTGC CTTTGTTCa GGCTTGGTAG
701 CCGTAAAAGC GTTGCTGAGG TTTGTTTCGG GTAC...

```

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFNSVL HGLGKDRKAN RFVLNLAI AF IPAAVMGLLF
101 GXQIKEXLFN PLSVAVMLVL XGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

	10	20	30	40	50	60
g305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
m305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
	10	20	30	40	50	60

700

	70	80	90	100	110	120
g305.pep	EYRQRFNSVLHGVGKDRKANRFVNLNLAIAFIPAAVMGLLFDKQIKEYLFNPLSVAVMLVL					
	:					
m305	EYRQRFNSVLHGLGKDRKANRFVNLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g305.pep	GGFFILWVEKQRSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTMGGMLWGI					
	:					
m305	XGFXILWVEKQRSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTMGGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
g305.pep	ERKTATEFSFFLAVPMMVAATAVDLKHRYFFTLHDVGLILIGFIAAFVSGLVAVKALLK					
	:					
m305	ERKTATEFSFFLAVPMMVAATAVDLKHRYFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
	190	200	210	220	230	240
	250	260	270			
g305.pep	FVSKKNYIPFAYRIVFGIVIIILWLSGWISWEX					
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1   ATGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCC
101 GCAATCTGAT TGATTTTCAC AGCAATCACA AGGTTTTTGA AATTACCATC
151 CAGCTCGGTG CGGTTTTGGC GGTAGTGTTC GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT
301 GGCAACAAA TCAAAGAGTA TCTGTTTAA CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAATTTGTC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GCGTTGCCCA AGTGTTTGCA CTGGTTCCAG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGGCCG TTCCGATGAT GGTGTCAGCA
601 ACGGCTTATG ATGTCCTGAA GCATTACCGG TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTTGTTTCA GGCTTGGTGG
701 CGGTCAAAGC GTTGCTGAGG TTTGTTTCCA AGAAAAATTA TATTCCTTTT
751 GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
801 AGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1   MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIDFH SNHKVFEITI
51  QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVNLNLAIAF IPAAVMGLLF
101 GKQIKEYLFN PLSVAVMLVL GGFFILWVEK QRSRAEPKIV DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHRY FFTLHDVGLI LIGFVAAFVS GLVAVKALLR FVSKKNYIPF
251 AYYRIVFGIA IILWLSGWI SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHNKVFETIAIQLGAVLAVVF					
	:					
a305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIDFHSNHNKVFETITQLGAVLAVVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m305.pep	EYRQRFNSVLHGLGKDRKANRFVNLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	:					
a305	EYRQRFNSVLHGVGKDRKANRFVNLNLAIAFIPAAVMGLLFGKQIKEYLFNPLSVAVMLVL					

701

	70	80	90	100	110	120
	130	140	150	160	170	180
m305.pep	XGFXILWVEKRSRAEPKIADVLDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
a305	GGFFILWVEKRSRAEPKIVDVALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m305.pep	ERKTATEFSFFLAVPMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	ERKTATEFSFFLAVPMVAATAYDVLKHYRFFTLHDVGLILIGFVAAAFVSGLVAVKALLR					
	190	200	210	220	230	240
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFGIAIILWLSGWISWEX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

g306.seq

```

1 ATGTTTATGA ACAAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTCTT
51 CTTCGGTTTG ATACTGGCAA CGGTCATTAT TGCCGGTATT TTGCTTTATC
101 TGAACCAGGG CGGTCAAAT CCGTTCAAAA TCCCGGCTCC GTCGAAGCAG
151 CCTGCAGAAA CGGAAATCCT GAAACTGAAA AACCAGCCTA AGGAAGACAT
201 CCAACCTGAA CCGGCCGATC AAAACGCCCT GTCCGAACCG GATGTTGCGA
251 AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT
301 GCCGACAAAG CCGACGAGGT TGAAGAAAAG GCGGCGAGC CGGAACGGGA
351 AGAGCCGGAC GGACAGGCAG TCGCAAGAA AGCACTGACT GAAGAGCGTG
401 AACAAACCGT CAGGGAAGAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
451 AAAAAAGCGG TAAACCGTC TAAAGAAACA GAGAAAAAG CTTCAAAAGA
501 AGAGAAAAAG GCGGCGAAAG AAAAAGTTGC ACCCAAACCG ACCCCGGAAC
551 AAATCCTCAA CAGCCGAGT ATCGAAAAAG CGCGTAGTGC CGCTGCCAAA
601 GAAGTGCAGA AATGAAAAA CTTTGGGCAA GCGGGAAGCC AACGCATTAT
651 CTGCAAATGG GCGCGTATGC CGAACCCCG AGCGCGGAAG GGCAGCGTGC
701 CAACTGGCA ATCTTGGGCA TATCTTCCGA AGTGGTCGGC TATCAGGCGG
751 GACATAAAAC GCTTTACCGC GTGCAAAGCG GCAATATGTC CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

g306.pep

```

1 MFMNKFSQSG KGLSGFFFL ILATVIIAGI LLYLNQGGON AFKIPAPSKQ
51 PAETEILKLK NPKEDIQPE PADQNALSEP DVAKEAEQSD AEKAADKQPV
101 ADKADEVEEK AGEPEREEDP GQAVRKALT EEREQTVREK AQKKDAETVK
151 KKA VKPSKET EKKASKEKK AAKEKVAPKP TPEQILNSRS IEKARSAAAK
201 EVQKMNFGQ GGSQRIICKW ARMPNPGARK GSVPNWQSWA YLPKWSAIRR
251 DIKRFTACKA AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

m306.seq (partial)

```

1 ..GGTTTGTCT TCGGTTTGAT ACTGGCGACG GTCATTATTG CCGGTATTTT
51 GTTTTATCTG AACAGAGCG GTCAAAATGC GTTCAAAATC CCGGCTTCGT
101 CGAAGCAGCC TGCAGAAACG GAAATCCTGA AACCGMAWAA CCAGCYTAAG
151 GAAGACATCC AACCTGAWCC GGCCGATCAA AACGCCTTGT CCGAACCGGA
201 TGCTGCGACA GAGGCAGAGC AGTCGGATGC GGAAGAAWGT GCCGACAAGC
251 AGCCCGTTGC CGATAAAGCC GACGAGGTTG AAGAAAAGGC GGGCGAGCCG
301 GAACGGGAAG AGCCGGACGG ACAGGCAGTG CGTAAGAAAG CGCTGACGGA
351 AGAGCGTGAA CAAACCGTCA GGGAAAAAGC GCAGAAGAAA GATGCCGAAA
401 CGGTTAAAW ACAAGCGTGA AAACCGTCTA AAGAAACAGA GAAAAAGCT
451 TCAAAAGAAG AGAAAAAGGC GGCGAAGGAA AAAGTTGCAC CCAAACCAAC
501 CCCGGAACAA ATCCTCAACA GCGGCAGCAT CGAAAAAGCG CGCAGTGCCG
551 CCGCCAAAGA AGTGCAGAAA ATGAAAACGC CGACAAGGCG GAAGCAACCG

```

702

601 ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG
 651 CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA
 701 GGCGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG
 751 ATGCGGTGA

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

m306.pep (partial)
 1 ..GLFFGLILAT VIIAGILFYL NQSGQNAFKI PASSKQPAET EILKPXNQXK
 51 EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP
 101 EREEPDQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA
 151 SKEEKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR
 201 IICKWARMPT VRARKGSPVN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP
 251 MR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

m306/g306

m306.pep	10	20	30	40
	GLFFGLILATVIIAGILFYL NQSGQNAFKI PASSKQPAET EILKPX			
g306	MFMNKFSQSGKLSGFFGLILATVIIAGILLYLNQGGQNAFKI PPSKQPAET EILK			
	10	20	30	40
	50	60	70	80
m306.pep	NQKKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREED			
g306	NQPKEIDIQEPADQNALSEPDAEAEQSDAEXAADKQPVADKADEVEEKAGEPEREED			
	70	80	90	100
	110	120	130	140
m306.pep	GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKAAKEKVAPKP			
g306	GQAVRKKALTEEREQTVREKAQKKDAETVKKAVKPSKETEKKASKEEKAAKEKVAPKP			
	130	140	150	160
	170	180	190	200
m306.pep	TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSPVNWQSWA			
g306	TPEQILNSRSIEKARSAAAKEVQKMNFGQGSQRIICKWARMPTNGARKGSPVNWQSWA			
	190	200	210	220
	230	240	250	
m306.pep	YLPRWSVIRRDIKRFTGCKAAICLPMRX			
g306	YLPKWSAIRRDIKRFTACKAAICPPMRX			
	250	260		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

a306.seq
 1 ATGTTTATGA ACAATTTTC CCAATCCGGA AAAGGTCTGT CCGTTTITTT
 51 CTCGGTTTG ATACTGGCGA CGGTCATTAT TGCCGGTATT TTGTTTATC
 101 TGAACAGAG CGGTCAAAAT GCGTTCAAAA TCCCGTTCC GTCGAAGCAG
 151 CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCCTA AGGAAGACAT
 201 CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA
 251 AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT
 301 GCCGACAAAG CCGACGAGGT TGAGGAAAAAG GCGGACGAGC CGGAGCGGGA
 351 AAAGTCGGAC GGACAGGCAG TGCGCAAGAA AGCACTGACG GAAGAGCGTG
 401 AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
 451 AAACAAGCGG TAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAGA
 501 AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCCGGAAC
 551 AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

601 GAAGTGCAGA AAATGAAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
 651 CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
 701 ACTGGCAATC TTGGGCATAT CTTCCAAGGT GGTCGGTTAT CAGGCGGGAC
 751 ATAAAACGCT TTACCGGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGTG
 801 A

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

a306.pep
 1 MFMNKFSQSG KGLSGFFFL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
 51 PAETEILPKP NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
 101 ADKADEVEEK ADEPEREKSD QQAVRKALT EEREQTVGEK AQKKDAETVK
 151 KQAVKPSKET EKKASKEEK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
 201 EVQKMKTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
 251 IKRFTGCKAA ICLPMR*

m306/a306 93.7% identity in 252 aa overlap

m306.pep	10	20	30	40
	GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX			
a306	MFMNKFSQSGKGLSGFFFLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK			
	10	20	30	40
	50	60	70	80
m306.pep	NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP			
a306	NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEXAADKQPVADKADEVEEKADEPEREKSD			
	70	80	90	100
	110	120	130	140
m306.pep	GQAVRKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKAAEKEKVAPKP			
a306	GQAVRKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETEKKASKEEKAAEKEKVAPKP			
	130	140	150	160
	170	180	190	200
m306.pep	TPEQILNSGSIEKARSAAAEVQKMKTPTRRKQRIICKWARMPTVRARKGSVPNWQSWAY			
a306	TPEQILNSGSIEKARSAAAEVQKMKTPTRRKQRIICKWARMPTAGARKGSVPNWQSWAY			
	190	200	210	220
	230	240	250	
m306.pep	LPRWSVIRRDIKRFTGCKAAICLPMRX			
a306	LPRWSVIRRDIKRFTGCKAAICLPMRX			
	250	260		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

g307.seq
 1 atgaaaacct tcttcaaaac cctttcgacc gcgtcactcg cgctcatcct
 51 cgcagcctgc ggcggtcaaa aagacagcgc gccgcagcc tctgccgcgc
 101 ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcagc
 151 accgtggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
 201 ggagaaaaaa ggctacaccg tcaaattggt cgaatttacc gactatgtgc
 251 gcccgaaatc ggcattggcg gagggcgagt tggacatcaa cgtcttccaa
 301 cacaacacct atcttgacga tttcaaaaaa gaacacaacc tggacatcac
 351 cgaagccttc caagtgcgca ccgcgccttt gggactgtat ccgggcaaac
 401 tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgcccaac
 451 gaccgcgtcca acttcgcacg cgccttggtg atgctgaacg aactgggttg
 501 gatcaaaact aaagacggca tcaatccgct gaccgcatcc aaagccgaca
 551 tcgcggaaaa cctgaaaaac atcaaaatcg tcgagcttga agccgcacaa
 601 ctgccgcgca gccgcgccga cgtggatttt gccgtcgtca acggcaacta
 651 cgccataagc agcggcatga agctgaccga agccctgttc caagagccga

g307.pcp

m307.seq (partial)

m307.pep (partial)

m307/g307

a307.seq

a307.pep

1 MKTFFKTLA AALALILAAC GGOKDSAPAA SASAAADNGA AKKXIVEGTT


```

51  VGDFGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFOH
101 KPYLDDFKKE  HNLDITEVFQ  VPTAPLGLYP  GKLSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLNKI  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEGYKSPAA  WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

m307.pep                               10      20      30
                                      QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
          220      230      240      250      260      270

m307.pep                               39
          AWNEGAAKX
a307      AWNEGAAKX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTCT  GTTTTTCAC  TATAATAGCC  GGTGTCGGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGTGAAGG  CTTTGGAAC
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGCGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301 TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CCGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTGT  TCGATGCGGA
401 CGCTTGCTC  TGTCGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAGCCGCGA
601 ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVFYRIL  GVADNLYPCL  SDFCFFTIIA  GLPLQAVLWE  RMMVRRLLI
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLLTRA
151 ADVVLKERRR  LVLVRETPLE  NLAHLNMR  VTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSI  AHTLSLFGID  TPDLAEWQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTCT  GTTTTTCAC  TATAATAGCC  GGTGTCGGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGTGAAGG  CTTTGGAAC
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTCGGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301 TTGGCGGACT  TCGTGATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CCGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTC  TGTCGCGCAC  GGCTTCGGCG  ACAATCTGCT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GWAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGT  GCACACGCT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  gCG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

m308.pep (partial)

706

```

1  MLNRVFYRIL  GVADNLYPRL  SDFCFFTTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNLMKR  XTEMGGVFP  PVPAMYRKQP
201 TADDIVAHSV  AHALSLFGID  TPDSAEOQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPCLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLNLMKR					
g308	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLNLMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVFPVPVPAMYRKQPQTADDIVAHVAHALSLFGIDTPDSAEOQGM					
g308	VTEMGGVFPVPVPAMYRKQPQTADDIVAHSLAHTLSLFGIDTPDLAEOQGMAD					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTGTTGCCG
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GGCGTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGTGCGCG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTTC  GGTGCTGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCCCT  CGATGTACCG  CAAACGCGAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNLMXR  VTEMGGVFP  PVPAMYRKQP
201 TADDIVAHSV  AHALSLFGID  TPDSAEOQGM  AD*

```

m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308 . pep	MLNRVYRILGVADNLYPRLSDFCFFTTIAGLPQAVLWERRMMVRRLLIIGISGASGFQY					
a308	MLNRIFYRILGVADNLYPRLSDFCFFTTIAGLPQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
m308 . pep	GVKALELLRAQDVETHLVVSKGAEMARASEYARDEVYALADVFVHPIGNIGACIASGTF					
a308	GVKALXLLRAQDIETHLVVSKGAEMARASEXYARDXVYALADXVHPIGNIGACIASGTF					
	70	80	90	100	110	120
m308 . pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
a308	KTDGMLVAPCSMRTLASVVGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR					
	130	140	150	160	170	180
m308 . pep	KTDGMLVAPCSMRTLASVVGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR					
a308	KTDGMLVAPCSMRTLASVVGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR					
	130	140	150	160	170	180
m308 . pep	XTEMGGVVFPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSEWQGM					
a308	VTEMGGVVFPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSEWQGMAD					
	190	200	210	220	230	
m308 . pep	XTEMGGVVFPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSEWQGM					
a308	VTEMGGVVFPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSEWQGMAD					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGTTGTTA TCGGATTCTT GTTTTTCAC  TATAATAGCC GGTTCGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CCGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT  TCGATGCGGA
401 CGCTTGCCCTC TGTGCGGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGCGGCGCG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAGCCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRVYRIL GVADNLYPCL SDFCFFTTIA GLPLQAVLWE RMMVRRLLI
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADVFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
151 ADVVLKERRR LVLNVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTCTT GTTTTTCAC  TATAATAGCC GGTTCGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCAATC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CCGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCCTC TGTGCGGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGCGGCGCG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAACCCGAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRVYRIL GVADNLYPRL SDFCFFTTIA GLPLQAVLWE RMMVRRLLI

```

708

51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA
 101 LADVFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
 151 ADVVLKERRR LVLVRETPL NLAHLNMMKR VTEMGGVVFP PVPAMYRKPO
 201 TADDIVAHSV AHALSIFGID TPDSAEOQGM AD*

m308-1/g308-1 97.0% identity in 232 aa overlap

	10	20	30	40	50	60
m308-1.pep	MLNRV	FYRIL	GVADN	LYPRL	SDFCF	FTIIAGL
	10	20	30	40	50	60
g308-1	MLNRV	FYRIL	GVADN	LYPCL	SDFCF	FTIIAGL
	10	20	30	40	50	60
m308-1.pep	GVKALE	LLRAQ	DVETH	LVVSK	GAE	MA
	70	80	90	100	110	120
g308-1	GVKALE	LLRAQ	DVETH	LVVSK	GAE	MA
	70	80	90	100	110	120
m308-1.pep	KTDGML	VAPCS	MRTL	ASVA	HGFG	DN
	130	140	150	160	170	180
g308-1	KTDGML	VAPCS	MRTL	ASVA	HGFG	DN
	130	140	150	160	170	180
m308-1.pep	VTEMGG	VFPVP	AMYRK	PQTAD	DIVAH	SV
	190	200	210	220	230	
g308-1	VTEMGG	VFPVP	AMYRK	PQTAD	DIVAH	SV
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
 51 TCCGATTATTA TCGGATTTCT GTTTTTCAC TATAATAGCC GGTTCGCCGT
 101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
 151 GGCATCAGTG GGGCGAGCGG TTTCGAATAC GGCCTGAAGG CTTTGGANCT
 201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
 251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC
 301 TTGGCGGACT TNGTGATCC GATCGGCAAT ATCGGGGCGT GCATTGCGAG
 351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
 401 CGCTTGCTTC GGCTGTCAC GGCTTCGGCG ACAACCTCTT GACGCGTGG
 451 GCGGATGTGG TTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
 501 AACGCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAAACGGAA
 551 TGGCGGCGGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAACCGCAG
 601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTGCTGTT
 651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

This corresponds to the amino acid sequence <SEQ ID 1288; ORF 308-1.a>:

a308-1.pep

1 MLNRIFYRIL GVADNLYPYL SDFCFFTIIA GLPLQAVLWE RRMVRRLLI
 51 GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA
 101 LADKVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVVAH GFGDNLLTRA
 151 ADVVLKERRR LVLVRETPL NLAHLNMMKR VTEMGGVVFP PVPAMYRKPO
 201 TADDIVAHSV AHALSIFGID TPDSAEOQGM AD*

a308-1/m308-1 96.1% identity in 232 aa overlap

	10	20	30	40	50	60
a308-1	MLNRIF	YRIL	GVADN	LYPYL	SDFCF	FTIIAGL
	10	20	30	40	50	60
m308-1	MLNRV	FYRIL	GVADN	LYPRL	SDFCF	FTIIAGL
	10	20	30	40	50	60
a308-1	GVKAL	XLLRA	QDIET	HLVVS	KGA	EM
	70	80	90	100	110	120
m308-1	GVKALE	LLRAQ	DVETH	LVVSK	GAE	MA
	70	80	90	100	110	120
a308-1	KTDGML	VAPCS	MRTL	ASV	VHG	FG
	130	140	150	160	170	180
m308-1	KTDGML	VAPCS	MRTL	ASV	VHG	FG
	130	140	150	160	170	180

```

m308-1      KTDGMLVAPCSMRTLASVAHGFCDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNDNMRK
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVVFPPVPAMYRKQTADDIVAHSAHALSLFGIDTPDSAEWQGMADX
              |||
m308-1      VTEMGGVVFPPVPAMYRKQTADDIVAHSAHALSLFGIDTPDSAEWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

g311.seq

```

1   atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgcgtgccg gcgcgctttg ggggtgtttgg
101 gtttggaaac gcaaatacaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggcg gcattctgat tgaacagtc agggcgggcg gtaaacagg
201 tgccgtggtc ggtatcggca tcaatttcgt gctgcccaag gaagtggaaa
251 acgcccgttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaaacattg cttgcggaac tgggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgctggt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggtaaaggc gtggacggac gaggcgttct
501 gcacttgga acggcagaag gcgaacagac ggtcgtcagc ggcgaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccgattcg
601 gaacgttttt tgctgttgga agcggggaac agccggctca agtgggcgtg
651 ggtggaaaaa ggcacgttcg caaccgtggg cagcgcgcgg taccgcgatt
701 tgcgcctttt gggcgcggag tggcggaaaa aggcggatgg aaatgtcccg
751 atcgtcggtt gcgcgctgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgca caggctttgg
851 gcatacgcaa ccactaccgc caccgccgaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgtcgt
951 cagttgcggc acggcggtaa cggttgacgc gtcaccgat gacggacatt
1001 atctcggcgg aaccatcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggttt
1151 gcggctcgat aatgatgatg cagggccgtt tgaaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggcgcgcgcg cgaagtcgc
1251 cgaagccctg ccgctgcgat ttttggcgga aaataccgtg cgcggtggcg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaagcgggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

g311.pep

```

1   MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGILITV RAGGKTAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLET LAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGTVKG VDGRGVHLHE TAEGEQTVVS GEISLRPDNR SVSVKRPDS
201 ERFLLEGGN SRLKWAVEN GTFATVGSAP YRDLSPGAE WAKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRFRS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRP AGKRYFPPTT TGNVAVSGMM DAVCGSIMMM HGRLKEKNGA
401 GKPDVVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

m311.seq (partial)

```

1   ATGTTTCAGTT TTGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTCGCCT GTTGCggCAG TGGCGTGTCT GCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCArATTAAg TGGCCCAATG ATTTGGTTGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAACCGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAAT
351 CAGCCTGCCG TCCGACnACA GGCCGTTTC CGTnCGAAG CCGCGGGATT

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710

```

401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAA ACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTGCGCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TCGGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCGACC
701 GCTGGTTCAA CGCCTTGGGC AGCCGCCGCT TCAGCCGCAA CGCyTGCCTC
751 GTCGTCAGTT GCGGCACGGC GGTAACGGTT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrgGAACCA TCATGCCCGG TTTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTCGCGC TCGTTATGA TGATGCACGG GCGTTTGAAA GAAAAAACCG
1001 GGGCGGGCAA GCCTGTCGAT GTCATCATT CCGGCGGCGG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTGG GCGGAAAAATA CCGTGCCTGT
1101 GCGGACAAC CTCGTCATT ACGGGTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGGAATA TGAACAT....

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
  1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
 51 KLGGLIETV RTGGKTAVAV GIGINFLPX EVENAASVQS LFTASRRGN
101 ADAAVLLXXX XXXXEISLR SDXRPVSVXK RRDSEFLLL DGGNSRLKWA
151 WVNGTFATV GSAPYRDLSP LGAWEAKAD GNVRIVGCAV CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPPEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPTTTGNAV ASGMDAVCG SVMMMHGRLK EKTGAGKPD VIITGGGAAK
351 VAEALPPAFL AENTVRVADN LVIYGLNMI AAEGREYEH....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

m311/g311

	10	20	30	40	50	60
m311.pep	MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGLIETV					
g311	MFSFGWAFDRPQYELGSLSPVAAALACRRALGCLGLETQIKWPNDLVVGRDKLGGLIETV					
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTAVAVVGIGINFLPXEVENAASVQSLFQTASRRGNADAVALLLXXX-----					
g311	RAGGKTAVAVVGIGINFLPKEVENAASVQSLFQTASRRGNADAVALLETLAELGAVLEQ					
	70	80	90	100	110	120
m311.pep	-----XXXX					
g311	YAEFGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTGKVDGRGVLHLETAEGEQTVVS					
	130	140	150	160	170	180
	120	130	140	150	160	170
m311.pep	XEISLRSDXRPVSVXKRRDSEFLLLDDGGNSRLKWAVVNGTFATVGSAPYRDLSPLGAE					
g311	GEISLRPDNRSVSPKRPDSEFLLLEGGNSRLKWAVVNGTFATVGSAPYRDLSPLGAE					
	190	200	210	220	230	240
	180	190	200	210	220	230
m311.pep	WAEKADGNVRIVGCAVCGEFKKAQVQEQELARKIEWLPSSAQALFGIRNHYRHPPEHGS					
g311	WAEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSSAQAL-GIRNHYRHPPEHGS					
	250	260	270	280	290	

711

```

      240      250      260      270      280      290
m311 .pep  WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR
          |||
g311       WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR
      300      310      320      330      340      350

      300      310      320      330      340      350
m311 .pep  HAGKRYFPFPTTGNASGMMDAVCGSVMMHGRLEKKTGAGKPVDVITGGGAAKVAEA
          |||
g311       PAGKRYFPFPTTGNASGMMDAVCGSIMMHGRLEKKTGAGKPVDVITGGGAAKVAEA
      360      370      380      390      400      410

      360      370      380      389
m311 .pep  LPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEH
          |||
g311       LPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHAX
      420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311 .seq
1   ATGTTCA GTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTT
51  GCTGTCGCCT GTTGCGGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTGAAAC GCAAATCAAG TGGCCAAACG ATTTGGTCGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTCGT GCTGCCAAG GAAGTGGAAA
251 ACGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGAAAT
301 GCCGATGCCG CCGTGTTGCT GGAACGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTGCAA TATGCGCGGG ACGGATTTGC GCCTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGGCGG TATTGCTGTT GCGCGACGGC
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGC GTGGACGGAC AAGGCGTTCT
501 GCACTTGGAA ACGGCAGAGG GCAACAGAC GGTCTGCAGC GCGGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTTCCG TGCCGAAGCG GCGGGATTCTG
601 GAACGTTTTT TGCTGTTGGA CGGCGGCAAC AGCCGCTCA AGTGGGCGTG
651 GGTGAAAAC GGCACGTTCT CAACCGTCGG TAGCGCGCGG TACCGCGATT
701 TGTCGCCTTT GGGCGCGGAG TGGCGGAAA AGGTGGATGG AAATGTCCGC
751 ATCGTCGGTT GCGCCGTGTG CGGAGAATTC AAAAAGGCAC AAGTGCAGGA
801 ACAGCTCGCC CGAAAATCG AGTGGCTGCC GTCTCCGCA CAGGCTTTTG
851 GCATACGCAA CCACTACCGC CACCCGAGG AACACGGTTC CGACCGCTGG
901 TTCAACGCCT TGGGAGCGCG CCGCTTCAGC CGCAACGCCT GCGTCGTCGT
951 CAGTTGCGGC ACGGCGGTAA CCGTTGACGC GCTCACCGAT GACGGACATT
1001 ATCTCGGGG AACCATCATG CCCGTTTCC ACCTGATGAA AGAATCGCTC
1051 GCCGTCGAA CCGCCAACCT CAACCGGCAC GCCGTAAGC GTTATCCTTT
1101 CCCGACCACA ACGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 GCGGCTCGGT TATGATGATG CACGGCGGTT TGAAAGAAAA AACCGGGGCG
1201 GGCAAGCCTG TCGATGTCAT CATTACCGGC GCGCGCGCGG CAAAAGTTGC
1251 CGAAGCCCTG CCGCTGCAT TTTTGGCGGA AAATACCGTG CGCGTGGCGG
1301 ACAACCTCGT CATTACGGG CTGCTGAACC TGATTGCCCG CGAAGGCGGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311 .pep
1   MFSFGWVDR PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
51  KLGGILIEIV RTGKTVAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLET LAELDAVLLQ YARDGFAPFV AEYQANRDH GKAVLLLRD
151 ETVFEGTVKG VDGQGVHLLE TAEGKQTVVS GEISLRSDDR PVSVPKRRDS
201 ERFLLLDGGN SRLKWAVVEN GTFATVGSAP YRDLSP LGAE WAEKVDGNVR
251 IVGCAVCGEF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRRFS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRH AGKRYFPFPT TGNASGMM DAVCGSVMM HGRLEKKTGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIH LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

712

	10	20	30	40	50	60
m311.pep	MFSFGWVFD RPQYELGSLSPVAACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV					
a311	MFSFGWVFD RPQYELGSLSPVAACRRALSRLGLKTQIKWPNDLVVGRDKLGGILIETV					
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTVAVVGIGINFLVLPKEVENAASVQSLFQTASRRGNADA VLLXXXXXXXXX-----					
a311	RTGGKTVAVVGIGINFLVLPKEVENAASVQSLFQTASRRGNADA VLLLETLAELDAVLLQ					
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGV DQGVLHLETAEGKQTVVS					
	130	140	150	160	170	180
	120	130	140	150	160	170
m311.pep	-EISLRSDXRPVSVXKRRDSEFLLLDGGSRLKWAVVENGTFATVGSAPYRDLSP LGAE					
a311	GEISLRSDDRPVSPKRRDSEFLLLDGGSRLKWAVVENGTFATVGSAPYRDLSP LGAE					
	190	200	210	220	230	240
	180	190	200	210	220	230
m311.pep	WAEKADGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNHYPHEHGS DR					
a311	WAEKVDGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQAL-GIRNHYPHEHGS DR					
	250	260	270	280	290	
	240	250	260	270	280	290
m311.pep	WFNALGSRFRSNACVVVSCGTAVTV DALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
a311	WFNALGSRFRSNACVVVSCGTAVTV DALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTTGNASGMMDAVCGSVMMHGR LKEKTGAGKPDVVIITGGGAAKVAEA					
a311	HAGKRYPFPTTTGNASGMMDAVCGSVMMHGR LKEKTGAGKPDVVIITGGGAAKVAEA					
	360	370	380	390	400	410
	360	370	380	389		
m311.pep	LPPAFLAENTVRVADNLVIYGLLN MIAAEGREYEH					
a311	LPPAFLAENTVRVADNLVIHGLLN LIAAEGGESEHTX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTTCGG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGCG GCGAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGCC TATGTTTCA GTTCGGCTGGG CGTTTGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTCGCC TGTTCGCGCA CTTGCGTGCC GCGCGCCTTT
501 GGGGTGTTG GGTTTGGA ACGAAATCAA GTGGCCAAAC GATTTGGTCG
551 TCGGACGCGA CAAATTGGG GGCATTCTGA TTGAACAGT CAGGCGGGCG
601 GGTAAACGG TTGCGTGGT CCGTATCGGC ATCAATTTCT TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCT CCGTGCAGTC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGCAA TGCCGATGCC GCCGTATTGC TGGAACATT GCTTGGCGAA
751 CTGGGCGCGG TGTGGAACA ATATGCGGAA GAAGGTTTCG CGCCATTTT

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801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGC CGCAGCG CGAAACCGTG TGC GAAGGCA CGGTAAAGG CGTGGACGGA
901 CGAGGCGTTC TGC ACTTGA AACGGCAGaa ggCGAACAGA cggtcGtcag
951 cggcGaaaTC AGcctTGGGc CCgacaacag gtcggtttcc GTgccgaagc
1001 gGccggatTC GgaacgttTT tTGCTgttgg aaggcgggaa cagccggctc
1051 aAGTGGgcgt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGCgCC
1101 gtaCCGCGAT TTGTGCGCTT TGGGCGCGGA GTGGCGCGAA AAGCGCGATG
1151 GAAATGTCCG CATCGTCGGT TGC GCGTGT GCGGAGAATC CAAAAAGGCA
1201 CAAGTGAAG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCGAGC GCCGCTTCAG CCGCAACGCC
1351 TGC GTCTGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACC GA
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCGTCCGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCCCT TCCCGACCAC AACGGGCAAC GCCGTCGCA GCGGCATGAT
1551 GCAGCGCGGT TCGGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCG GCGCGCGCGG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1 MTVLKPSHWR VLAELADGLP QHVSQAREA DMKPQQLNGF WQMPAHIRG
51 LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTLKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWAFDRPQY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGRDKLG GILIETVRAG
201 GKTAVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVVDG
301 RGVHLHLETAE GEQTVVSGEI SLRPDNRVS VPKRPDSERF LLLEGGNSRL
351 KWAWVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAL GIRNHYRHPE EHGSDRWANA LGSRRFSRNA
451 CVVVSCTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRPAKG
501 RYPPFTTGN AVASGMDAV CGSIMMHGR LKEKNGAGKP VDVITGGGA
551 AKVAELPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1 ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51 CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGCGGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAGTAAAG GGCAGGGGCG GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTGTTGACG GCCGAGTAT
451 GAGTTGGGTT CGCTGTGCGC TGTGCGGCA GTGGCGTGTG GCGCGCCTT
501 GTCGCGTTTA GGTGTTGATG TGCAGATTAA GTGGCCCAAT GATTGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCGGTGGT CCGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGAA
751 CTGGACGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCATTGGA AACGGCAGAG GGCAACAGA CGTCTGTCAG
951 CCGCGAAATC AGCCTGCGGT CCGACGACAG GCCGTTTCC GTGCCGAAGC
1001 GCGCGGATTG GGAACGTTT CTGCTGTTGG ACGCGGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCCTGTGT GCGGAGAAT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCGAGC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCTGTC TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACC GA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTT CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGG GGGCAAGCCT GTCGATGTCA TCATTACCG GCGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTTACGG GTTGTGTAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTAA

This corresponds to the amino acid sequence <SEQ ID 1298; ORF 311-1>:

m311-1.pep

```

1  MTVLKLSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVFDROPY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILIETVRTG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLVE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVGD
301 QGVHLHLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQLARKI EWLPSSAQAL GIRNHYRHPE EHGSDFWNA LGSRRFSRNA
451 CVVVSCTAV TVDALDDGH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTTCN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*

```

m311-1/g311-1 93.9% identity in 591 aa overlap

	10	20	30	40	50	60
m311-1.pep	MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR					
g311-1	MTVLKPSHWRVLAELADGLPQHVSQALAREADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR					
	10	20	30	40	50	60
m311-1.pep	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
g311-1	LVRPLAVFDAEGLRDLGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
	70	80	90	100	110	120
m311-1.pep	GRGRQGRKWSHRLGECLMFSFGWVFDROPYELGSLSPVAACRRALSRLGLDVQIKWPN					
g311-1	GRGRQGRKWSHRLGECLMFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPN					
	130	140	150	160	170	180
m311-1.pep	DLVVGRDKLGGILLETVRTGGKTAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
g311-1	DLVVGRDKLGGILLETVRTGGKTAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
	190	200	210	220	230	240
m311-1.pep	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGD					
g311-1	AVLLETLLAELGAVLEQYAEEGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVGD					
	250	260	270	280	290	300
m311-1.pep	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSERFLLLDGGNSRLKWAUVENGTF					
g311-1	RGVLHLETAEGEQTVVSGEISLRPDNRSVSVPKRPDSERFLLLEGGNSRLKWAUVENGTF					
	310	320	330	340	350	360
m311-1.pep	ATVGSAPYRDLSPPLGAEWAEKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQAL					
g311-1	ATVGSAPYRDLSPPLGAEWAEKADGNVRIVGCAVCGESKKAQVQEQLARKIEWLPSSAQAL					
	370	380	390	400	410	420
m311-1.pep	GIRNHYRHPPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALDDGHYLGGTIMPGF					
g311-1	GIRNHYRHPPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALDDGHYLGGTIMPGF					
	430	440	450	460	470	480
m311-1.pep	HLMKESLAVRTANLNRHAGKRYFPFTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
g311-1	HLMKESLAVRTANLNRHAGKRYFPFTTTGNAVASGMMDAVCGSIMMHGRLEKKNAGGKP					
	490	500	510	520	530	540
m311-1.pep						
g311-1						
	550	560	570	580	590	

m311-1.pep VDVIITGGGAARVAEALPPAFLAENTVRVADNLVIYGLLNMAAEGREYEHIX
 |||||:|||||
 g311-1 VDVIITGGGAARVAEALPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHAX
 550 560 570 580 590

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

a311-1.seq
 1 ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
 51 CGGTTTGGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
 101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
 151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
 201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
 251 CCGCATTTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
 301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGTG TGACCCACCT
 351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
 401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTTGACCG GCCGCGATAT
 451 GAGTTGGGTT CGCTGTCGCC TGTTCGGGCA GTGGCGTGCC GGCAGCGCTT
 501 GTCGCGTTTG GGTGTGAAAA CGCAAATCAA GTGGCCAAAC GATTGGGTCT
 551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
 601 GCGAAAACGG TTGCCGTGGT CCGTATCGGC ATCAATTTCG TGCTGCCCAA
 651 GGAAGTGGAA AACGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
 701 GCGCGGGAAT TGCCGATGCC GCCGTGTTGC TGGAAACGCT GTTGGCGGAA
 751 CTTGATGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
 801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
 851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
 901 CAAGCGCTTC TGCATTGGA AACGGCAGAG GGCAACAGA CGGTCGTCAG
 951 CCGCGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
 1001 GCGGGGATTG GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
 1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
 1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGTGGATG
 1151 GAAATGTCCG CATCGTCGGT TGGCGCGTGT GCGGAGAAAT CAAAAAGGCA
 1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
 1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
 1301 CCGACCGCTG GTTCAACGCC TTGGGACGCC GCCGCTTACG CCGCAACGCC
 1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
 1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
 1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
 1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA CGGGCATGAT
 1551 GGATGCGGTT TGGCGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
 1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
 1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
 1701 GCGCGTGGCG GACAACCTCG TCATTACCGG GCTGCTGAAC CTGATTGCCG
 1751 CCGAAGCGCG GGAATCGGAA CATACTTAA

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

a311-1.pep
 1 MTLVKPSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
 51 LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQTLKHEC ASSNDEILEL
 101 ARIAPDKAHR TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVDFRPOY
 151 ELGSLSPVAA VACRRALSRL GLKTQIKWPN DLVVGRDKLG GILLETVRTG
 201 GKTVAUVVIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLAE
 251 LDAVLLQYAR DGFAPFVAEY QANRDHGKA VLLLRDGETV FEFTVKGVDG
 301 QGVLLHLETA GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
 351 KWAVVENGTF ATVGSAFYRD LSPLGAEMAE KVDGNVRIVG CAVCGEFKKA
 401 QVQEQLARKI EWLPSAQAAL GIRNHYRHPE EHGSDFWFNA LGSRRFSRNA
 451 CVVVSCTGAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
 501 RYFPPTTGN AVASGMMDAV CGSVMMHGR LKERTGAGKP VDVITGGGA
 551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

a311-1/m311-1 98.5% identity in 591 aa overlap

	10	20	30	40	50	60
a311-1.pep	MTVLKPSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR					
m311-1	MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a311-1.pep	LVRPLAVFDAEGLRELTERS GFQTLKHECASSNDEILELARIAPDKAHTICVTHLQSK					
m311-1	LVRPLAVFDAEGLRELTERS GFQTLKHECASSNDEILELARIAPDKAHTICVTHLQSK					
	70	80	90	100	110	120

716

a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGECLMFSFGWVFDPRQYELGSLSPVAACRRALSRLGLKTQIKWPN					
m311-1	GRGRQGRKWSHRLGECLMFSFGWVFDPRQYELGSLSPVAACRRALSRLGLDQIKWPN					
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGILITVRTGGKTVAVVGIGINFLPKKEVENAASVQSLFQTASRRGNADA					
m311-1	DLVVGRDKLGGILITVRTGGKTVAVVGIGINFLPKKEVENAASVQSLFQTASRRGNADA					
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
m311-1	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
a311-1.pep	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVSGEISLRSDDRPSVSPKRRDSEFLLLDGGNSRLKWAWVNGTF					
m311-1	QGVHLHLETAEGKQTVVSGEISLRSDDRPSVSPKRRDSEFLLLDGGNSRLKWAWVNGTF					
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSPGAEWAEEKVDGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAAL					
m311-1	ATVGSAPYRDLSPGAEWAEEKADGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAAL					
a311-1.pep	430	440	450	460	470	480
	GIRNHYRHPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDAITDDGHYLGGTIMPGF					
m311-1	GIRNHYRHPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDAITDDGHYLGGTIMPGF					
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
m311-1	HLMKESLAVRTANLNRHAGKRYFPPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
a311-1.pep	550	560	570	580	590	
	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAEGGESEHTX					
m311-1	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNLMIAEGGREYEHIX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1  atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTAccat cggcaTTgaT ttgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggtcg gcaaagactT GGTGGCAacg Gcgaaacacc tTTccgcCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgcAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTGCGCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGGCTGCG
551 CAAAATCGT CGTGTCTGTC AACCGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTCC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGTCCA GCGTGGTCA AAGCCGCGCT GGAAAATTCG GACGCGGTCA
701 GCCTGACCGA GGTGCGCGAA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTGT CGTGGCACC GACCCCGCC GTCGCGACT
851 CCGTGGCGCG CATTCTGAA GAAATGGGCT TGAGCGTCTG CGGTACGCAC

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901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAGGCAGG CGTGTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCGGTC TGCTCCGTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTC GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATTCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTTGGG TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
1301 TGTTTCGTC CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1 MSIQSGEILE TVKMVADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51 TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1 ATGAGTATCC AATCCGCGCA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51 CCAGAAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACCTCAGCGT GCGCGAAACT
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAAGGGA TGTGCGcTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGcWG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACcGTC AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAATAATTGT CGTGTTCTGC AACCGCGTGG AAGACAACCC GTTTWTGGCG
601 GGCGCGTTTC ATGGTTCCGG CGATGCCGTT ATCAATGTCT GCGTATCCGG
651 CCCAGGTGTC GTAAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAAACTG CTTTCAAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCGCGCA AGCcTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTGCGCGA CCCC GCCCGT CGGCGACTCA GTGGCACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCCGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCCGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCGGC CATCATTGCC GACGAAGCCG
1151 CCATCGGCAt GATCAACAGC AAAACCACTG CCGTGCGCAT TATCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CAcGGTCGAG TTCGGCGGCT TGTGGGgCTA
1251 CGCGCCTGTG ATGCCGGTCA AAGAAGGTTT GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
51 TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCX SIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGCAKIVVFC NAVEDNPFXA
201 GAFHGS GDV INVGVSGPGV VKAALENS DA TTLTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCGTHGTTA
301 ALALLNDAVK KGGMMASSAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGGLLGYPV MPVKEGSCFV FVNRGGRI PA PVQSMKN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

	10	20	30	40	50	60
m312.pep	MSIQSGEILETVKMVADQNFVVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT					
g312	MSIQSGEILETVKMVADRNFDVVRTITIGIDLHDCISTDIDVNLQNIYNKITTVGKDLVAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m312.pep	AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVVAQTLDKAAKAIGVSFIGGFSALV					
g312	AKHLSAKYGVPIVNQRISVTPIAQIAAATKADSYVSVVAQTLDKAAKAIGVSFIGGFSALV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m312.pep	QKGMSPSPDEVLRISPEAMKTTDIVCXSNIGSTRAGINMDAVKLAGETVKRTAEITPEG					
g312	QKGMSPSPDEVLRISVPEAMKTTDIVCSSINIGSTRAGINMDAVKLAGETIKRTAEITPEG					
	130	140	150	160	170	180
	190	200	210	220	230	
m312.pep	FGCAKIVVFCNAVEDNPFKAGAFHGSG--DAVINVGVS GPGVVKAALENS DATTLTEVAE					
g312	FGCAKIVVFCNAVEDNPFMAGAFHGSGEADAVINVGVS GPGVVKAALENS DAVSLTEVAE					
	190	200	210	220	230	240
	240	250	260	270	280	290
m312.pep	VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH					
g312	VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCGTH					
	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDVAVKKGMMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
g312	GTTAALALLNDVAVKKGMMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
g312	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRRGGRIAPVQSMKNX					
g312	YAPVMPAKEGSCEVFVNRRGGRIAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

```

1  ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51  CCAGAATTTC GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAC CGACATCGAC GTGTTGAACC AAAATATTTA CAACAAAATT
151 ACCACGGTCG GCAAAGACTT GGTGGCGACA GCAAATATC TGTCTGCCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCTGTCACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAAC

```

a312.pep

1	MSIQSGEILE	TVKMDADQNF	DVRTITIGID	LHDCISTDID	VLNQNIYNKI
51	TTVGKDLVAT	AKYLSAKYGV	PIVNQRISVT	PIAQIAAATH	ADSYVSVAQT
101	LDKAAKAIGV	<u>SFIGGFSALV</u>	QKGMSPSDEV	LIRSIPEAMK	TTDIVCSSLN
151	IGSTRAGINM	DAVRLAGETI	KRTAEITLEG	FGCAKIVVFC	NAVEDNPFMA
201	GAFHSGSEAD	AVINUVGSGP	GVVKAALENS	DATTLTEVAE	VVKKTAFTKI
251	RVGELIGREA	SKMLNIPFGI	LDLSLAPTPA	VGDSVARILE	EMGLSVCGTH
301	GTTAALALLN	DAVKKGGGMA	SSAVGGLSGA	FIPVSEDEGM	IAAAEAGVLT
351	LDKLEAMTAV	<u>CSVGGLDMIAV</u>	PGDTPAHTIS	GIIADEAAIG	MINSKTTAVR
401	IIPVTGKTVG	DSVEFGGLLG	YAPVMPVKEG	SCEVFVNRGG	RIPAPVQSMK
451	N*				

m312/a312 96.7% identity in 451 aa overlap

	10	20	30	40	50	60
m312.pep	MSIQSGEILETVK	MVADQNF	DVRTITIGID	LHDCISSD	INVLNQNI	YNKITTVGKDLVTT
a312	MSIQSGEILETVK	MVADQNF	DVRTITIGID	LHDCISTD	IDVLNQNI	YNKITTVGKDLVAT
	10	20	30	40	50	60
	70	80	90	100	110	120
m312.pep	AKYLSAKYGVPI	VNQRI	SVTPIAQIAA	AATHADSYV	SVAQTLDKA	AKAIGVSFIGGFSALV
a312	AKYLSAKYGVPI	VNQRI	SVTPIAQIAA	AATHADSYV	SVAQTLDKA	AKAIGVSFIGGFSALV
	70	80	90	100	110	120
	130	140	150	160	170	180
m312.pep	QKGMSPSDEVL	LIRSI	PEAMKTTD	IVCX	SINIGSTR	AGINMDAVKL
a312	QKGMSPSDEVL	LIRSI	PEAMKTTD	IVCSS	SINIGSTR	AGINMDAVRL
	130	140	150	160	170	180
	190	200	210	220	230	
m312.pep	FGCAKIVVFC	NAVEDNP	FXAGAFHGS	G--DAVIN	VGVS	SGPGVVKAA
a312	FGCAKIVVFC	NAVEDNP	FMAGAFHGS	GEADAV	INVGVS	SGPGVVKAA
	190	200	210	220	230	240
	240	250	260	270	280	290
m312.pep	VVKKTAFKIT	RVGELIG	REASKMLN	IPFGILD	LS--PT	PPVGDS
a312	VVKKTAFKIT	RVGELIG	REASKMLN	IPFGILD	LSLAPT	PAVGDS

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	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRRGGRIPAPVQSMKNX					
a312	YAPVMPVKEGSCEVFVNRRGGRIPAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

g313.seq

```

1  atggacgacc  cgcgcaccta  cggatcgggc  aatcccgggc  cgaccaatgt
51  tttagcgagc  ggcaaaaaaa  aggcggccgc  gctgacgctc  ttggcgcatg
101 cgcgcaaagg  tttggttgcc  gttttgcttg  cacgcgtgct  tcaagaaccg
151 ctcggtttat  cgcacagcgc  aatcgccgcc  gtcgcactcg  ccgcgctggt
201 cgggcatatg  tggccggtgt  ttttcggatt  taaggcgggc  aaaggcgtgg
251 caacggcatt  gggcgtgctt  ctggcactct  ctcccgcaac  tgccttggtc
301 tgcgcgttga  tttggcttgt  gatggcattc  ggcttcaaag  tatcctccct
351 tgccgcgctg  gtcgccacaa  ccgccgcccc  ccttgccgca  ctgtttttta
401 tgccgcatac  ttcttggtat  ttccgaaccc  tcgcaatcgc  catattgggtg
451 ttgctccgcc  ataagagcaa  catcctcaac  ctgattaaag  gcaaagaaa
501 caaaatcggc  gaaaaacgct  ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

g313.pep

```

1  MDDPRTYGS NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL VATTAAPLAA LFFMPHTSWI FATLAAILV
151 LLRHKSNILN LIKGKESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

m313.seq

```

1  ATGGACGACC  CGCGCACCTA  CGGATCGGGC  AATCCGGGGG  CAACCAATGT
51  TTTACGCAGC  GGCAAAAAAA  AGGCGGCCGC  GCTGACGCTC  TTGGCGCATG
101 CCGCCAAAGG  TTTAGTTGCC  GTTTTGCTTG  CACGCGTGCT  TCAAGAACCG
151 CTCGGTTTAT  CCGACAGCGC  AATCGCGGCC  GTCGCACTCG  CCGCGCTGGT
201 CGGGCATATG  TGGCCGCTGT  TTTCGGATT  TAAAGCGGCG  AAAGGCGTGG
251 CAACGGCATT  GGGCGTGCTT  CTGGCACTCT  CTCCCGCAAC  TGCCTTGGTC
301 TGCGCGTTGA  TTTGGCTTGT  TATGGCATT  GGCTTCAAGG  TGTCTCCCT
351 TGCCGCATTA  ACCGCCACAA  TCGCCGCACC  GGTCCGCGCA  TCCTTCTTTA
401 TGCCGCACGT  CTCGTGGGTT  TGGCGGACCG  TCGCCATTGC  TTTGCTGGTG
451 TTGTTCCGCC  ACAAAGTAA  TATCGTCAAG  CTGCTCGAAG  GCAGAGAAAG
501 CAAAATCGGC  GGCAGCCGCT  GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

m313.pep

```

1  MDDPRTYGS NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL TATIAAPVAA SFFMPHVSUV WATVAIALLV
151 LFRHKSNIIVK LLEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNGPATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
g313	MDDPRTYGSNGPATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
g313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVSWWATVAIALLVLRHKSNIIVKLLEGRESKIGGSRX					
g313	VATTAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNIILNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

a313.seq

1	ATGGACGACC	CGCGCACCTA	CGGATCGGGC	AATCCGGGGG	CAACCAATGT
51	TTTACGCAGC	GGCAAAAAAA	AGGCGGCCGC	GCTGACGCTC	TTGGGCGATG
101	CCGCCAAAGG	TTTGGTTGCC	GTTTGTCTTG	CACGCGTGCT	TCAAGAACCG
151	CTCGGTTTAT	CCGACAGCGC	AATCGCGGCC	GTCGCACTCG	CCGCGCTGGT
201	CGGGCATATG	TGGCCGGTGT	TTTTCGGATT	TAAAGGCGGC	AAAGGCGTGG
251	CAACGGCATT	GGCGGTGCTT	CTGGCACTCT	CTCCACAAC	TGCCTTGGTC
301	TGCGCGTTGA	TTTGGCTTGT	GATGGCATTG	GGCTTCAAGG	TGCTCTCCCT
351	TGCCGCATTA	ACCGCCACAA	TGCGCGCCCC	CCTTGCCGCA	CTGTTTTTTA
401	TGCCGCATAC	TTCTTGGATT	TTCGCAACCC	TCGCAATCGC	CATATTGGTG
451	TTGCTCGGCC	ATAAGAGCAA	CATCCTCAAC	CTGATTAAAG	GCAAAGAAAG
501	CAAAATCGGC	GAAAAACGCT	GA		

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

a313.pep

1	MDDPRTYGS	NGPATNVLR	S	GKKKAAALT	L	LGDAAKGLV	A	VLLARVLQEP
51	LGLSDSAIA	A	VALAALVGH	M	WPVFFGFKG	G	KGVATALGV	L
101	CALIWLVMF	A	GFKVSSLA	L	TATIAAPLA	A	LFMPHTSWI	F
151	LLRHKSNI	L	NLIKGESKIG	E	KR*			

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNGPATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
a313	MDDPRTYGSNGPATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
a313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVSWWATVAIALLVLRHKSNIIVKLLEGRESKIGGSRX					
a313	TATIAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNIILNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```
g401.seq
  1  atgaaattac aacaattggc tgaagaaaaa atcggcggttc tgatttgtgtt
 51  cacgctgctt gtagtcagtg tcggtctggt gattgaagtt gtgcccttgg
101  cctttaccaa ggcggcaaca cagccggcgc cgggctgtaa gccttacaat
151  gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacaa
201  ctgccactct caaatgattc gtccgttccg tgcggaaacc gagcggttacg
251  gtcattactc tgttgccgga gtagtcggtt acgaccatcc gttccaatgg
301  ggttccaaac gtaccgggtc tgatttggca cgtgtgggcg gccgctattc
351  cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
401  agtccaatat gccggcattc ccgtggcttg cacgcaataa agtcgatgtc
451  gatgcaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501  cagtgatgag gaaattgcca aagcgctga ggctttggca aacaaatccg
551  agctggatgc tgtagtcgcc tatctgcaag gattgggtct ggctttgaaa
601  aacgtaaggt aa
```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```
g401.pep
  1  MKLQQLAEEK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201  NVR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```
m401.seq
  1  ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
 51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101  CCTTTACCAA GGC GGCAACA CAGCCGGCGC CGGGCTGAA GCCTTACAAT
151  GCCCTGCAGG TTGCCGGACG CGATATTAC ATCCGTGAGG GCTGTACAA
201  CTGCCACTCG CAAATGATTC GTCCGTTCG TCGGAAACC GAGCGTTACG
251  GTCATTACTC TGTGCGGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301  GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351  CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401  AGTCCAATAT GCCGGCATT CCGTGGCTTG CACGCAATAA AGTCGATGTC
451  GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501  CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551  AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601  AACGTAAGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```
m401.pep
  1  MKLQQLAEEK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201  NVR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

m401/g401

	10	20	30	40	50	60
m401.pep	MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY					
g401	MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m401.pep	IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW					

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```

g401      |||||
          IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
          .70      80      90      100      110      120

          130      140      150      160      170      180
m401 . pep HRIHLLNPRDVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
g401      HRIHLLNPRDVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130      140      150      160      170      180

          190      200
m401 . pep NKSELDAVVAYLQGLGLALKNVRX
          |||||
g401      NKSELDAVVAYLQGLGLALKNVRX
          190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401 . seq
1  ATGAAATTAC AACAAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GCGGCAACA CAGCCGGCGT CGGGCGTGAA GCCTTACAAT
151 GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCCG TCGGGAACC GAGCGTTACG
251 GTCATTACTC TGTGCCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATTG CCGTGGCTTG CACGCAATAA AGTCGATGC
451 GATGCAACCG TTGCCAATAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401 . pep
1  MKLQQLAEEK IGV LIVFTLL VSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

          10      20      30      40      50      60
m401 . pep MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||
a401      MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
          10      20      30      40      50      60

          70      80      90      100      110      120
m401 . pep IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
          |||||
a401      IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
          70      80      90      100      110      120

          130      140      150      160      170      180
m401 . pep HRIHLLNPRDVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
a401      HRIHLLNPRDVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130      140      150      160      170      180

          190      200
m401 . pep NKSELDAVVAYLQGLGLALKNVRX
          |||||
a401      NKSELDAVVAYLQGLGLALKNVRX
          190      200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

g402.seq

```

1  ATGGATATGG TGAACACTAA Accgaatact agtgtgatta atatgctttc
51  tttccttacc ggaTATTGA GCTTGGGTat agaagtCtTg tGGGTAAGGA
101 TGtttttcgTT CGCagcAcag tccgtgcctc aggCATTtTC atttattcctt
151 gcctGttttc tgACCGgtat cgcgcgtcggc gCgTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCctT TATCGGGCAG TgcttcttgT
251 GGGCGGGTAT TgccgaTttt ttgatTTTGG GTGCTGCGTG GTTGTGACG
301 GGTtTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
351 CGtcGTCAGG GGGTTGATTT TCCCACtTGT ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCAGTGCAAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATttgtt
501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTtCT GCTGctgtcc
551 cTTGTTTTg tacaCTGtTC CAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTc
651 TGCTTTTCAA AATATTGCTG GCCGTCCGGA TAGGTTGATT GAAAACAAAC
701 ACGGCATTGT TCGGTTTAC CATAGAGATG GTGATAAGGT TGTtTATGGG
751 GCGAATGTAT ACGACGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCC GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGT CGTGGGCGCG CGTCTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGCATA
951 CCGTAGCCTT ATCGCGGAcg agcgcgCAAT CGCACCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATTCGACTT GGTACTGGCG
1101 TGCTATTCC ACTAACCTGT TGAGTGCgGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATgctTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCctt AATAAAGAAC
1301 TGCTCaagca aCGCCTTcc cgGTTGATTT GGCCGAAAG CGGCAGgcac
1351 gtATTGTACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGtctctCG
1401 TATGCTGATT CGGATGACGG AacctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

g402.pep

```

1  MDMVNTKPNT SVINMLSFLT GLLSLGIEVL WVRMFSFAAQ SVPOAFSFLI
51  ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLIT
101 GFSGFVHHAG IPITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIAGRPRDLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DIFNSVNGIE RAYLLPSLKS GIRRI FVVGL STGSWARVLS
301 AIPMQSMIV ABINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSSTDAA AQKVSRMLI RMTEPSAGAE VIITDDNMIVE YKYGRGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

m402.seq

```

1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGcNtTC
51  TTTCTTtagc GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTtTC ATTtACCCTT
151 GCCTGTTTTc TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTtTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAsA sGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAmCGTTGCC
451 GGCAGTGCAAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTtCTT
501 GTCCACCCAA CAGATTtACC TGCTCATCTG TwTGATTtCT GCTGCTGTCC
551 CTTTGTtTTG TACACTGTTT CAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTcYtAC TGCCGGATTc

```

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651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTATTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CCGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAACTCT GGCATACGCC
851 GCATTTTCGT CGTTGGACTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCGCAAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGGCGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCTT AATAAAGAAC
1301 TCGTCAAGCA ACGTCTCTCC CGTTTGATTG GGCCGAAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG aAcCTTCGGC TGGGGCGGAA GTTATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1322; ORF 402>:

m402.pep

```

1 MDIVNTKPNT SLIYMXSFLS GLLSLGIEVL WVRMFSPAAQ SVPQAFSFTL
51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAWLLT
101 GFSGFVHHAG IFITLSAVVX XLIFPLVHHV GTDGNKSGRQ VSNVYFAXVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICKIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFVVGL STGSWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDA AOKVVSRLMI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/g402

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSPAAQSVPQAFSFTLACFLTGIAVG					
	: : :					
g402	MDMVNTKPNTSVINMLSFLTGLLSLGIEVLWVRMFSPAAQSVPQAFSFTLACFLTGIAVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAWLLTGFSGFVHHAGIFITLSAVVX					
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQIYLLICKIS					
g402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDLSTQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIAGRDRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFVVGLSTGSWARVLS					

726

g402	HRDGDGVVYGANVYDGAYNTDIFNSVNGIERAYLLPSLKSIGIRRFVVGLSTGSGWARVLS
	250 260 270 280 290 300
m402.pep	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHRPDEKFDLILM
g402	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHRPDEKFDLILM
	310 320 330 340 350 360
m402.pep	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
g402	NSTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
	370 380 390 400 410 420
m402.pep	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSTVDAAQKVVSRMLIQMTEPSAGAE
g402	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSTVDAAQKVVSRMLIRMTEPSAGAE
	430 440 450 460 470 480
m402.pep	VITDDNMIVEYKYGRGIX
g402	VITDDNMIVEYKYGRGI
	490

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402.seq
1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATT TATATGCTTTC
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTAAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTGTTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAGA GGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TTTGATTTCT GCTGCTGTCC
551 CTTTGTTTTG TACACTGTTT CAAAAAAGTC TCCGACTGAA TGCAGTGTCTG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTC
651 TGTCTTTCAA AATATTGCTG ACCGTCGGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATTGT TGCAGTTTAC CATAGAGATG GTGATAAGGT TGTATTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTAAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCGGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCCT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAAG CGGCAGGCAC
1351 GTATTTGACA GCAGACCGGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTGCGGAA GTCATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

```

a402.pep
1  MDIVNTPKNT SLIYMLSFLS GLLSLGIEVL WVRMFSEFAQ SVPOAFSFTL

```

51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
 101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
 151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
 201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
 251 ANVDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSGWARVLS
 301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
 351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
 401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
 451 VFDSSTVDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

m402/a402 99.0% identity in 497 aa overlap

	10	20	30	40	50	60
m402. pep	MDIVNTKPNSTLIYMXSFLSGLLSLGIEVLWVRMFSAQSVPAQAFSFTLACFLTGIAVG					
a402	MDIVNTKPNSTLIYMLSFLSGLLSLGIEVLWVRMFSAQSVPAQAFSFTLACFLTGIAVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402. pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
a402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402. pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQOIYLLICXIS					
a402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQOIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402. pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
a402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402. pep	HRDGDKVYGANVDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSGWARVLS					
a402	HRDGDKVYGANVDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSGWARVLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m402. pep	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHPDEKFDLILM					
a402	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHPDEKFDLILM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m402. pep	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
a402	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m402. pep	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTVDAAAQKVSRMLIQMTEPSAGAE					
a402	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTVDAAAQKVSRMLIQMTEPSAGAE					
	430	440	450	460	470	480
	490					
m402. pep	VITDDNMIVEYKYGRGIX					
a402	VITDDNMIVEYKYGRGIX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTGCGGCG GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGGGAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGLTG LTTSLSLINA PALSRQSDG SGRSSLGLN
151 IGGMDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSKEIK PTEGLMVDPS DIQPYGNHTG NSAPSV EADN
301 SHEGYGSDE AVRQHRQGP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTGCTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACGGAAG GATTAATGGT CGATTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGGGAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK

```



```

51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYET AETTSGLTG LTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFF DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGP *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAANKMDLQALHGR					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAANKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPREYETTAETTSGLTG					
m406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPREYETTAETTSGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406.pep	LTSLSTLNAPALSRQSDGSGSRSSGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
m406	LTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFFSDIRPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFFSDIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406.pep	SHEGYGYSDEAVRQHRQGPX					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

a406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGCGCG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

```

730

```

501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT CGAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGGLTG LTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVP ANADTDVFIN
201 IDVEGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSCKGIK PTEGLMVD FS DIQPYGNHMG NSAPSVEADN
301 SHEGYGYSDE AVRRHRQGP *

```

m406/a406 98.8% identity in 320 aa overlap

	10	20	30	40	50	60
m406.pep	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKMDLQALHGR					
a406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKMDLQALHGR					
	10	20	30	40	50	60
m406.pep	KVALYIATMGDQSGSLTGGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
a406	KVALYIATMGDQSGSLTGGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
	70	80	90	100	110	120
m406.pep	KVALYIATMGDQSGSLTGGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
a406	KVALYIATMGDQSGSLTGGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
	70	80	90	100	110	120
m406.pep	LTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
m406.pep	LTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
m406.pep	FLRGIDVVPANADTDVFINIDVEGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVPANADTDVFINIDVEGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
m406.pep	FLRGIDVVPANADTDVFINIDVEGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVPANADTDVFINIDVEGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
m406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTTEGLMVD FS DIRPYGNHMG NSAPSVEADN					
a406	IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTTEGLMVD FS DIQPYGNHMG NSAPSVEADN					
	250	260	270	280	290	300
m406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTTEGLMVD FS DIRPYGNHMG NSAPSVEADN					
a406	IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTTEGLMVD FS DIQPYGNHMG NSAPSVEADN					
	250	260	270	280	290	300
m406.pep	SHEGYGYSDEVVRQHRQGPX					
a406	SHEGYGYSDEAVRRHRQGPX					
	310	320				
m406.pep	SHEGYGYSDEVVRQHRQGPX					
a406	SHEGYGYSDEAVRRHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
1  atggtcggac ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
51  ggcaggcgga gatggcaaga tgcagcatca ctttgacggc agggttgcgt

```

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101  tcgtcaaacg attcggacac caagccgctg tctcggctga ggccgagggg
151  cagctgggtc atgtcggtcg agccgatgga gaagccgctc aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggt cagacccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcctg cggttcgtat acgctgccgc
501  cgaccaggtt ggcgatttcg ttggatttga agtcggacat acggacgatg
551  gttttacgcy gataaaccga tgcggcaagc gttgccacgc cttcggcgat
601  tttatcgacy tagaagtcga caggggatgc gtaaccggcg atgcggcgga
651  taatttcgcy tttcagttcg tcgtcttggt tgtcaaattc caacaaggct
701  ttcgggtgga tgcgatttg gcggtgatg ataaattcca tacgcgccaa
751  gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801  tcgcgacgtt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgacatcgg taattttgac gtccagcagg ccggcataga taaagccggt
901  atcgccttcg gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggtcgcatt gccgcagccg acgacggcag gaatacccag ttcgcgcgcg
1001 atgatggcgg cgtggcaggt gcgtccgccg cggttggtca cgatggcgga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcgat tcggttaacca
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgcacaa
1201 gacggttttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttgga tttgacggtt tcggggcggg cttgcaggat gtagagtttg
1301 ccgtccaggc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagcgcgt agtgtccaa ctcggtgatt tcttcgtcgg
1401 taatggagaa gcggttgccg tcttcttcgg gaacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 acccatggtc ttgcgcagga tggcggtttt gcttgccttg agcgtgggtt
1551 tgaacacata aaattcgtcc ggggtgaccg cgccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

g501.pep

```

1  MVGRTLADT DIFVLLAAGG DGKMQHHFDG RFAFVKRFGH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAADQV GVFVGFEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVVKF QQGFVRDADL AVDDKFHTRQ
251 ADAFAQIGIE AECEFGIADV HHDGFCFWH IVQGDIGNLY VQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHDDG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHALTD FLTDGTTFAQ
401 DGFFAVDQVA AQVAAFFLG FDGFGAGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQRVVQC LGDFFVNGE AVAVFFGDFD VGYRFAGGFP VGENHFDVFR
501 THGLAQDGGF ACFERGFEBI KFVRVDRALY DVFAQTVRGG NKDDLVVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

m501.seq

```

1  atggtcggac sggccttgac cgcagatgcc gacatatttg ttctgcttgc
51  ggcaggcgga gatggcaagg tgcagcatca ctttgacggc agggttgcgt
101 tcgtcaaacg attcggatac caagccgctg tcgcggctga gaccgagggg
151 cagttgggtc atgtcggtcg agccgatgga gaagccgctc aagtattgca
201 ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggtttt
301 gacaacggmt tcggttcgc ccaaagtgcg gacgaacgga atcatgattt
351 caacgttggy caacccatt tcatcgcgga cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451 acggaagccc aacatcgggt tttcttcctg cggttcgtat acgttgccgc
501 cgaccaggtt ggcgatttcg ttggatttga agtcggacat acggacgatg
551 gttttacgcy gataaaccga tgcggccaat gtcgccacgc cttcggcgat
601 tttatcgacy tagaagtcga caggggacgc gtaaccggcg atacggcggg
651 taatttcgcy ttttaattcg tcgtcttggt tgtcaaattc caacaargct

```

732

```

701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca ggttggcgaa gctgaatgcg agttcgggat
801 tgccgacgtt catcatgact tttacagggtg ctttaggcat attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgcccttcg gcacaggata cggtaacttc ttgaccgttt ttcagcaatt
951 cggttgcatt gccgcagccg acaacggcag gaatgcccaa ttcacgcgcg
1 001 atgatggcgg cgtggcaggt acggccgccc cggttggtta cgatggcaga
1 051 agcacgtttc atcacgggtt cccaatccgg atcggtcatg tcggtaacga
1 101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc tttaatcagg
1 151 cgcaccttgc cctgaccgac tttctgaccg atggcgccgg cttcgcataa
1 201 tacggttttg tcgccgttga tggcgaaagcg gcgcagggtt cggttgccct
1 251 cttcttggga ttttacgggt tcgggacggg cttgcaggat gtagagtttg
1 301 ccgtccaagc cgtcgcgccc ccattcgata tccatcgggc ggccgtagtg
1 351 tttttcgatg gtcagtgcgt aatgcgcaa ctcagtaatt tcttcgctcg
1 401 taatggagaa gcggttgccg tcttcctcgg ggacatcgac gttggttacg
1 451 gatttaccgg cttctgcttt gtcggtaaaa atcatattga tgtgttttga
1 501 acccatggtt ttacgcagga tggcgggcgt gcccggtttg agcgtggggt
1 551 tgaacacatr aaattcgccc gggttgaccg caccttgtag gacgttttcg
1 601 cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggatgc
1 651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

```

m501.pep
1  MVGXALTADA DIFVLLAAGG DGKVQHFFDG RFAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFVGFVGVH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR FXFVVLVVKF QXFGVDIDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH IVXGDIGNLY VQQTGIDKAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAVGNDRGR
351 STPHHGFPPIR IGHVGNEYVA GFDGIHLGSI FNQAHALTD FLTDGAFAFX
401 YGFVAVDGEA AQVAVALFLG FYFGFTGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQCVMRQ LSNFFVGNGE AVAVFLGDI VGYGFTGFCF VGKNHFDVFX
501 THGFTQDGLL ARFERGFEXH KFRVRDRTLY DVFAQTVRGG NKDDLIVXGF
551 GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

m501/g501

```

              10      20      30      40      50      60
m501.pep  MVGXALTADADIFVLLAAGGDGKVQHFFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG
          ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      MVGRTLTAADTDIFVLLAAGGDGKMQHFFDGRVAFVKRFGHQAAVSVEAEGQLGHVVRADG
              10      20      30      40      50      60

              70      80      90     100     110     120
m501.pep  EAVEVLQELFRQYRVARQLAHHNQAAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      EAVEVLQELFRQYRVARQLAHHNQAAVFAAFQAVFFQCLNHCFGFAQSADERNHDFDVG
              70      80      90     100     110     120

              130     140     150     160     170     180
m501.pep  QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFVGFVGVH
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      QTHFVTNAFQGFQGETVFEALGNITRRTTEAQHRVFFMRVYVAADQVGVFVGFVGVH
              130     140     150     160     170     180

              190     200     210     220     230     240
m501.pep  TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXFGVDIDL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTDGAADNFRFQFVVLVVKFQQGFVRVDADL
	190 200 210 220 230 240
m501 . pep	250 260 270 280 290 300
	AVDDKPFHTRQADAFAGQVGEAECEFGIADVHHD FYRCFRHIVXGDI GNLYVQQTGIDKAG
g501	AVDDKPFHTRQADAFAGQI GEAECEFGIADVHHD FDGCFWHIVQGDIGNLYVQQAGIDKAG
	250 260 270 280 290 300
m501 . pep	310 320 330 340 350 360
	IAFGTGYGNFLT V FQ QFGC IAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPPIR
g501	IAFGTGYGNFLT V FQ EFGRIAAADDGRNTQFARDDGGVAGASAAVGHDDGGSTFHHGFPPIR
	310 320 330 340 350 360
m501 . pep	370 380 390 400 410 420
	IGHVGN EYVAGFDGIHLGSI FNQ AHLALTD FLTDGA AFAXYGFVAVDGEAAQVAVALFLG
g501	IGHVGNQYVAGFDGIHLGSI FNQ AHLALTD FLTDGTTFAQDGF FAVDGVAAQVAAAFVLG
	370 380 390 400 410 420
m501 . pep	430 440 450 460 470 480
	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGGQCVMRQLSNFFVGNGEAVAVFLGDID
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDGGQRVVQC LGDFFVGNGEAVAVFFGDFD
	430 440 450 460 470 480
m501 . pep	490 500 510 520 530 540
	VGYGFTGFCFVGKNHFDVFXTHGFTQDGG LARFERGF EHXK FVRVDR TLYDVFAQTVRGG
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGF EHIK FVRVDRALYDVFAQTVRGG
	490 500 510 520 530 540
m501 . pep	550
	NKDDLIVXGFGVGEHHT
g501	NKDDLIVVAGFGVGEHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501 . seq (partial)

1	ATGGTCGGAC	GGGCCTTGAC	CGCAGATGCC	GACATATTTG	TTCTGCTTGC
51	GGCAGGCCGA	GATGGCAAGG	TGCAGCATCA	CTTTGACGGC	AGGGTTGCGT
101	TCGTCAAACG	ATTCGGATAC	CAAGCCGCTG	TCGCGGTCGA	GACCGAGGGT
151	CAGTTGGGTC	ATGTCGTTTC	AGCCGATGGA	GAAGCCGTCG	AAGTATTGCA
201	GGAATTGTTC	CGCCAATACC	GCGTTGCTCG	GCAGCTCGCA	CATCATAATC
251	AGGCGCAGGC	CGTTTTTGCC	GCGTTCCAAG	CCGTTTTCTT	TCAGGGCTTT
301	GACAACGGCT	TCGGCTTCGC	CCAAAGTGCG	GACGAACGGA	ATCATGATTT
351	CAACGTTGGT	CAACCCCAT	TCATCGCGGA	CGCGTTTCAA	GGCTTTGCAT
401	TCCAAGGCGA	AACAGTCTTT	GAAGTTGTCG	GCGACATAAC	GCGCCGCACC
451	ACGGAAGCCC	AACATCGGGT	TTTCTTCATG	CGGTTCTGAT	ACGTTGCCGC
501	CGACCAGGTT	GGCGTATTCG	TTGGATTTGA	AGTCGGACAT	ACGGACGATG
551	GTTTTACGCG	GATAAACCGA	TGCGGCCAAT	GTCGCCACGC	CTTCGGCGAT
601	TTTATCGACG	TAGAAGTCGA	CAGGGGACGC	GTAACCGCGC	ATACGGCGGG
651	TAATTTCCGC	TTTTAATTCG	TCGTCTTGTT	TGTCAAATTC	CAACAAGGCT
701	TTGGGGTGGA	TACCGATTTG	GCGGTTGATG	ATAAATTCCA	TACGCGCCAA
751	CCGATGCCT	TCGCTGGGCA	GGTTGGCGAA	GCTGAATGCG	AGTTCCGGAT
801	TGCCGACGTT	CATCATGACT	TTTACAGGTG	CTTAGGCAT	GTTGTCCAAA
851	GCAACATCGG	TAATTTGTAC	GTCCAGCAGG	CCGGAGTAGA	TGAAGCCGGT
901	ATCGCCTTCG	GCACAGGATA	CGGTAACCTC	TTGACCGTTT	TTACGCAATT
951	CGGTTGCATT	GCCGACGCCG	ACAACGGCAG	GAATACCCAG	TTGCGCGCGG

734

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1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCCC CTGTTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCAGGT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCGTACCGAC TTTCTGACCG ATGGCGCGGC CTTCCGACAA
1201 GACGGTTTTT TCGCCGTTGA TAGAAAAGCG GCGCAGGTTG CGGTCGCTT
1251 CTTCTGGGA TTTGACGGTT TCGGGACGGG CTTGCAGGAT GTAGAGTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTGATG TCCATCGGGC GGCCGTAGTG
1351 TTTTTCGATG GTCAGTGCCT AATGCGCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGGTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGTT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGAC GACGTTTTCG
1601 CCCAGACCGT AGGATGAAGT GACAAAGAC ACTTGTCGT AACCGGATTC
1651 GGTATCGAGG GTGAACATCA C

```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

a501.pep

```

1 MVGRALTADA DIFVLLAAGG DGKVQHFDG RFAFVKRFGY QAAVAVETEG
51 QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNNG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFGFVEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNER F*FVVLVVKF QQGFVDTDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDYFRCFRH VVQSNIGNLY VQAGVDEAG
301 IAFGTGYGNF LTVFQFGCI AAADNGRNTQ FARDDGGVAG TSAVGHDDGG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAFAAQ
401 DGFFAVDRKA AQVAAFFLG FDGFGTGLQD VEFVAVQAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFFVNGE AVAVFFGDID VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVFAQTVG*S DKDDLVTGTF
551 GIEGEHH

```

m501/a501 90.3% identity in 557 aa overlap

m501.pep	10	20	30	40	50	60
	MVGXALTADADIFVLLAAGGDGKVQHFDGRFAFVKRFGYQAAVAVETEGQLGHVVRADG					
a501	MVGRLTADADIFVLLAAGGDGKVQHFDGRFAFVKRFGYQAAVAVETEGQLGHVVRADG					
m501.pep	70	80	90	100	110	120
	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNNG					
a501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNNG					
m501.pep	130	140	150	160	170	180
	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGFVEVGH					
a501	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGFVEVGH					
m501.pep	190	200	210	220	230	240
	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXFGVDTDL					
a501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQGFVDTDL					
m501.pep	250	260	270	280	290	300
	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDYFRCFRHVVQSNIGNLYVQAGVDEAG					
a501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDYFRCFRHVVQSNIGNLYVQAGVDEAG					
m501.pep	310	320	330	340	350	360
	IAFGTGYGNFLTIVFQFGCIAAADNGRNTQFARDDGGVAGTAAAVGNDGRSTFHHGFPIR					
a501	IAFGTGYGNFLTIVFQFGCIAAADNGRNTQFARDDGGVAGTSAPVGHDDGGSAPVGHHRFPIW					

g502.seq

1	atgatgaaac	cgcacaacct	gttccaattc	ctcgcggttt	gctccctgac
51	cgtcgcgctc	gcttcgcgac	aggcggggcg	ggtaggacgc	ctcaagcaat
101	tcaacaacga	tgccgacggt	atcagcggca	gcttcaccca	aaccgtccaa
151	agcaaaaaga	aaacccaaac	cgcgcacggc	acgttcaaaa	tctgtcgccc
201	ggcgctcttc	aaatgggaat	acactttgcc	ctacagacag	actattgtcg
251	gcgacggtca	aacggtttgg	ctctacgatg	ttgatttggc	acaagtgcac
301	aagtcgtccc	aagaccaggc	catcggcgcg	agccccgcgc	ccatcctgtc
351	gaacaaaacc	gccctcgaaa	gcagttacac	gctgaaagag	gacggttcgt
401	ccaacggcat	cgattatgtg	cggggcaacg	cccaaacgca	acaacgcggg
451	ctaccaatac	atccgcgacg	gcttcaaagg	cggcaacctc	gcgcgcatgc
501	acgtctaa				

g502.pcp

1 MMKPHNLFQF LAVCSLTAV ASAQAGAVDA LKQFNNDADG ISGSFTQTQV
51 SKKKTQTAHG TFKILRPLGF KWEYTLPYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNTK ALESSYTLKE DGSSNGIDYV RGNAAQTQORR
151 LPIHPHRLOR ROPRRHAA*

m502.seq

1	atgatgaaac	cgcacaacct	gttccaattc	ctcgccggtt	gctccctgac
51	cgtcgcgctc	gcttcgcgac	aggcggggcg	ggtagacgcg	cttaagcaat
101	tcaacaacga	tgccgacggt	atcagcggca	gcttcaccca	amccgtccaa
151	wgcaaaaaga	aaacccaaac	cgcgcacggc	acgttcaaaa	tcttcgcgacc
201	gggccttttc	aaatgggaat	acaccaaact	t.acaggcaa	accatcgctcg
251	gcgcaggtca	aacygtttgg	ctmtacgatg	tyagtctggc	acaagtgacc
301	aagtcgtccc	aagaccaggc	cataggcgsc	agccccggc	ccatcgtgtc
351	gaacaaarcc	gccttcgaaa	gcagctacac	gctgaaagag	gacggttcgt
401	ccaacggcat	cgattatgtg	ggcaacgccc	aaacgcaaca	acgccgggcta
451	ccaatacatc	cgcacgcggt	tcaaaggcgg	caacctcgcc	gccatgcagc
501	ttaa				

m502 . pep

```

1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
51  XXXKTQTAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGX SPAAILSNKX ALESSYTLKE DGSSNGIDYV GNAQTQORRL
151 PIHPHRLQRR OPRRHAAX

```

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502 . pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502 . pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502 . pep	ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502 . seq

1	ATGATGAAAC	CGCACAACT	GTTCCAATTC	CTCGCGTTT	GCTCCCTGAC
51	CGTCTCCGTC	GCTTCCGCAC	AGGCGGGCGC	GGTGGACGCG	CTCAAGCAAT
101	TCAACAACGA	TGCCGACGGT	ATCAGCGGCA	GCTTCACCCA	AACCGTCCAA
151	AGCAAAAAGA	AAACCCAAAC	CGCGCACGGC	ACGTTCAAAA	TCCTGCGCCC
201	GGGCCTCTTT	AAATGGGAAT	ACACTTCGCC	TTACAAACAG	ACTATTGTCG
251	GCGACGTCA	AACCGTTGG	CTCTACGATG	TCGATTGGC	ACAAGTGACC
301	AAGTCGTCCC	AAGACCAGGC	CATAGGCGGC	AGCCCCGCGC	CCATCCTGTC
351	GAACAAAACC	GCCCTCGAAA	GCAGCTACAC	GCTGAAAGAG	GACGGTTCGT
401	CCAACGGCAT	CGATTATGTG	GGCAACGCCC	AAACGCAACA	ACGCCGGCTA
451	CCAATACATC	CGCATCGGCT	TCAAAGGCGG	CAACCTCGCC	GCCATGCAGC
501	TTAA				

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502 . pep

1	MMKPHNLFQF	LAVCSLTVSV	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVQ
51	SKKKKTQTAHG	TFKILRPGLF	KWEYTSPIKQ	TIVGDGQTVW	LYDVLDAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	GNAQTQQRRL
151	PIHPHRLQRR	QPRRHAA*			

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502 . pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVASQAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502 . pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSPIKQQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502 . pep	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAAX					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAAX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

g502-1.seq

```

1  ATGatGAAAc  cgcaCaacct  gttccaaTtc  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTGGACGCG  CTCAGCAAT
101  TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151  AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGCCC
201  GGGCCTCTTC  AAATGGGAAT  ACACTTTGCC  CTACAGACAG  ACTATTGTCG
251  GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATTTGGC  ACAAGTGACC
301  AAGTCGTCCC  AAGACCAGGC  CATCGGCGGC  AGCCCCGCGC  CCATCCTGTC
351  GAACAAAACC  GCCCTCGAAA  GCAGTTACAC  GCTGAAAGAG  GACGGTTCGT
401  CCAACGGCAT  CGATTATGTG  CGGGCAACGC  CCAAACGCAA  CAACGCCGGC
451  TACCAATACA  TCCGCATCGG  CTTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501  GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GCGGTTTGA
551  ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAA
601  GCGGTGGACG  TGTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

g502-1.pep

```

1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51  SKKKTQTANG TFKILRPGLF KWEYTLPYRQ TIVGDGQTVW LYDVDLAQVT
101  KSSQDQAIIG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RATPKRNNAG
151  YQYIRIGFKG GNLAAMQLKD SFGNQTSSIF GGLNTNPQLS RGAFKFTPPK
201  GVDVLSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

m502-1.seq

```

1  ATGATGAAAC  CGCACAACT  GTTCCAATC  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTAGACGCG  CTTAAGCAAT
101  TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151  AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGACC
201  GGGCCTTTTC  AAATGGGAAT  ACACCAAACC  TTACAGGCAA  ACCATCGTCG
251  GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATCTGGC  ACAAGTGACC
301  AAGTCGTCCC  AAGACCAGGC  CATAGGCGGC  AGCCCCGCGC  CCATCCTGTC
351  GAACAAAACC  GCCCTCGAAA  GCAGCTACAC  GCTGAAAGAG  GACGGTTCGT
401  CCAACGGCAT  CGATTATGTG  CTGGCAACGC  CCAAACGCAA  CAACGCCGGC
451  TACCAATACA  TCCGCATCGG  CTTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501  GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GCGGTTTGA
551  ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAA
601  GCGGTGGACG  TGTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

m502-1.pep

```

1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51  SKKKTQTANG TFKILRPGLF KWEYTKPYRQ TIVGDGQTVW LYDVDLAQVT
101  KSSQDQAIIG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151  YQYIRIGFKG GNLAAMQLKD SFGNQTSSIF GGLNTNPQLS RGAFKFTPPK
201  GVDVLSN*

```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVO	SKKKTQTANG				
g502-1	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVO	SKKKTQTANG				
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPYRQ	TIVGDGQTVWLYDVDLAQVT	KSSQDQAIIGGSPAAILSNKT			
g502-1	TFKILRPGLFKWEYTKPYRQ	TIVGDGQTVWLYDVDLAQVT	KSSQDQAIIGGSPAAILSNKT			
	70	80	90	100	110	120
m502-1.pep	TFKILRPGLFKWEYTKPYRQ	TIVGDGQTVWLYDVDLAQVT	KSSQDQAIIGGSPAAILSNKT			
g502-1	TFKILRPGLFKWEYTKPYRQ	TIVGDGQTVWLYDVDLAQVT	KSSQDQAIIGGSPAAILSNKT			
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYV	LATPKRNNAGYQYIRIGFKG	GNLAAMQLKDSFGNQTSSIF			
g502-1	ALESSYTLKEDGSSNGIDYV	LATPKRNNAGYQYIRIGFKG	GNLAAMQLKDSFGNQTSSIF			
	130	140	150	160	170	180
m502-1.pep	ALESSYTLKEDGSSNGIDYV	LATPKRNNAGYQYIRIGFKG	GNLAAMQLKDSFGNQTSSIF			
g502-1	ALESSYTLKEDGSSNGIDYV	LATPKRNNAGYQYIRIGFKG	GNLAAMQLKDSFGNQTSSIF			
	130	140	150	160	170	180

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```

                190      200
m502-1.pep      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||||
g502-1          GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACTT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT AACTTTCGCC TTACAAACAG ACTATTGTCTG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCGC CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAA
601 GGCCTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51  SKKKTQTAHG TFKILRPLGF KWEYTSPIKQ TIVGDGQTVW LYDVLQVVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTISIF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

                10      20      30      40      50      60
a502-1.pep      MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG
                |||||
m502-1          MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG
                10      20      30      40      50      60

                70      80      90      100     110     120
a502-1.pep      TFKILRPLGFKWEYTSPIKQIVGDGQTVWLYDVLQVTKSSQDQAIGGSPAAILSNKT
                |||||
m502-1          TFKILRPLGFKWEYTKPYRQIVGDGQTVWLYDVLQVTKSSQDQAIGGSPAAILSNKT
                70      80      90      100     110     120

                130     140     150     160     170     180
a502-1.pep      ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
                |||||
m502-1          ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
                130     140     150     160     170     180

                190     200
a502-1.pep      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||||
m502-1          GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgctcgcatc ggtaatcatt ttgttccatg ccgcttcgat
51  ttccgcatcg agctgttcgg ggaagggcgt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcgaaa cgtcttcgac atccaatttt
151 gccagagcgg cggaaatgcg ttcgttcaga ccgttgtgtg cgagaaatgc
201 gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSTSNF
51  ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

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m503.seq
 1 atgtccgcac cgccggcatc ggcaaccatt ttgttccatg ccgcttcgat
 51 ttcggcatcg agctgttcgg ggaaaggcgt atccaaaatc cattggcgga
 101 tttctttgcc gacgcgtgcc agttcggcaa cgtcttcgac atccaatttt
 151 gccagtgcgg cggaaatgcg ttcgctcaga ccgttgtgtg cgaggaatgc
 201 gcggtag

This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:

m503.pep
 1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
 51 ASAAEMRSLR PLCARNAR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

m503/g503

	10	20	30	40	50	60
m503.pep	MSAPPASATILFHAASISASSCSGKGVSKIHWISLPTRASSATSSTSNFASAAEMRSLR					
	:: :					
g503	MSAPSASVILFHAASISASSCSGKGVSKIHWISLPTRASSETTSSTSNFARAAEMRSFR					
	10	20	30	40	50	60
	69					
m503.pep	PLCARNAR					
g503	PLCARNAR					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

a503.seq
 1 ATGTCCGCGC CGCCGGCATC GGCAACCATT TTGTTCATG CCGCTTCGAT
 51 TTCGGCATCG AGCTGTTCGG GGAAGGGCGT GTCCAAAATC CATTGGCGGA
 101 TTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT
 151 GCCAGTGGG CCGAAATGCG TTCGCTCAGA CCGTTGTGTG CGAGGAATGC
 201 GCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

a503.pep
 1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
 51 ASAAEMRSLR PLCARNAR*

m503/a503 100.0% identity in 68 aa overlap

	10	20	30	40	50	60
m503.pep	MSAPPASATILFHAASISASSCSGKGVSKIHWISLPTRASSATSSTSNFASAAEMRSLR					
a503	MSAPPASATILFHAASISASSCSGKGVSKIHWISLPTRASSATSSTSNFASAAEMRSLR					
	10	20	30	40	50	60
	69					
m503.pep	PLCARNARX					
a503	PLCARNARX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

g503-1.seq
 1 ATGGCGCGGT CGTTGTACAG GGAGGCGAAA ACGTGGCGCA TCGCTTTTTT
 51 AACGTTATCC AAGCCATTGA TATTCAGGAA GGTTTCCTGT TGGCCGGCAA
 101 ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG
 151 GAAATGTCCG CGCCGTCGGC ATCGGTAATC ATTTGTGTTT ATGCGGCTTC
 201 GATTTCCGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC
 251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG AAACGTCTTC GACATCCAAT
 301 TTTGCCAGAG CGGCGGAAAT GCGTTCGTTT AGACCGTTGT GTGCGAGAAA
 351 TGCGCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

g503-1.pep

```

1  MARSLYREAK TWRIAFLLS KPLIFRKVSC WPANDASGRS SAVAEERTAT
51  EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSETSSTSN
101 FARAAMRSL RPLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

m503-1.seq

```

1  ATGGCAGCGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT
51  AACGTTATCC AAGCCGTTGA TGTTCAAGAA GGTTTCCTGT TGCCAGCGA
101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAACG TACGGCAACG
151 GAAATGTCGG CACCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTTCGCA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCCAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

m503-1.pep

```

1  MARSLYREAN TWCIASLTLK KPLMFKKVSC CPANDASGRS SAVAEERTAT
51  EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRIAFLLSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPSASVI					
m503-1	MARSLYREANTWCIALTLKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCSGKGVSKIHWRISLPTRASSETSTSNFARAAMRSLRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRISLPTRASSETSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

a503-1.seq

```

1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT
51  AACGTTTTCC AAGCCGTTGA TATCAGGAA GGTTTCCTGT TGGCCGGCAA
101 ATGATGCGTC GGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG
151 GAAATGTCCG CGCCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTTCGCA TCGAGCTGTT CGGGGAAAGG CGTGTCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCTAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

a503-1.pep

```

1  MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAEERTAT
51  EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRIASLTFSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPPASAT					
m503-1	MARSLYREANTWCIALTLKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKIHWRISLPTRASSETSTSNFASAAEMRSLRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRISLPTRASSETSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

g504.seq

```

1 atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51 cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggt gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacagg catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttgga
301 atcggcaaac acaaatatcg tottgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgcgcgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccacgtgtga cgcacccgt gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattattttt
551 ggtgaccggg cagcgcgagc ggcttgacag agcaataacc ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaac
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttggatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgaccggtt cgcgggtgct gcttttggtc tatctcggct cggatttgtt
1101 gggtttgggt acagtattta tgttttatgt gcccaaaaaa cggcggtggg
1151 tattgttttc aaacdgcata atccgttttg ctatgtcttc ggcccgcagc
1201 gaacgggatt tgcagaagga atttccaaaa cagtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

g504.pep

```

1 MLVQDLPEFV KLKPFHIDFY NTGMPDRFAS DIEVTDKATG EKLERTIRVN
51 HPLTLHGITI YQASFADGGS DLTFKAWNLR DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTOEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPAEI REQFMLAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQODKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLHLS MDAYTGLTEY PAPMLQLDQ FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPKK RAWVLFNSKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

m504.seq..

```

1 atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51 cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggt gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacagg catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttgga
301 attggcaaac acaaatatcg tottgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccggtttt gcaggacag gattattttt
551 ggattaccgg cagcgcgagc ggcttgacag agcaataacc ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaac
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttggatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcgtttcct
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgctc gggtttgcag

```

1051 atgaccggtt ccccggtg cgttttggtc tatctcggct cgggtgctgtt
 1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg
 1151 tattgttttc agacggcaaa atccgttttg ccatgtcttc ggcccgagc
 1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg
 1251 gctcggcaag gacttgaatc atga

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

m504.pep..

1 ILVQDLPPFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
 51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQYRWLR
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
 251 TLNIFAQKGY LGLDEFITSN IPKEQDKMQ GYFYEMLYGV MNAALDETIR
 301 RYGLPEWQQD EARNRFLHLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
 401 ERDLQKEFPK HVESLQRLGK DLNHD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng)
 from *N. gonorrhoeae*:

m504/g504

	10	20	30	40	50	60
m504.pep	ILVQDLPPFEV KLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLEKERTIRVNHPLTLHGITI					
	: : : : : :					
g504	MLVQDLPPFEV KLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLEKERTIRVNHPLTLHGITI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m504.pep	YQASFADGGS DLTFKAWN LGDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	: : : : :					
g504	YQASFADGGS DLTFKAWN LRDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m504.pep	MSEGAREKSLKSTLXDVR AVTQEGKKYTNIGPSIVYRIRDAAGQAVEYK NYMLPVLQEQ					
	: : : : :					
g504	MSEGAREKSLKSTLNDVR AVTQEGKKYTNIGPSIVYRIRDAAGQAVEYK NYMLPILQDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m504.pep	DYFWITGTRS GLQQYRWLR IPLDKQLKADTFMALREFLK DGEGRKRLVADATKGAPAEI					
	: : : : :					
g504	DYFWLTGTRS GLQQYRWLR IPLDKQLKADTFMALREFLK DGEGRKRLVADATKDAPAEI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m504.pep	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQDKMQGYFYEMLYGVMNAALDETIR					
	: : : : :					
g504	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKGQDKMQGYFYEMLYGVMNAALDETIR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m504.pep	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQ MTRSPGALLV					
	: : : : :					
g504	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQ MTRSPGALLV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m504.pep	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK					
	: : : : :					

743

g504 YLGSVLLVLGTVFMFYVPIKRAWVLSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK
 370 380 390 400 410

m504 . pep DLNHD
 |||||
 g504 DLNHD
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504 . seq

```

1 ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAAGTGAATA AATTCCATAT
51 CGATTTTAC AATACGGGTA TGCCGCGCGA TTTTGCCAGT GATATTGAAG
101 TAACGGATAA GGCAACCGGT GAGAACTCG AGCGCACCAT CCGCGTGAAC
151 CATCCTTTGA CCTTGCACGG CATCACGATT TATCAGGCGA GTTTTGCCGA
201 CGGCGGTTTC GATTGTGACAT TCAAGGCGTG GAATTTGGGT GATGCTTCGC
251 GCGAGCCTGT CGTGTGGAAG GCAACATCCA TACACCAGTT TCCGTTGGAA
301 ATTGGAACAA ACAAAATATCG TCTTGAGTTC GATCAGTTTA CTCTATGAA
351 TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GGAAAAAGC CTGAAATCCA
401 CGCTGAACGA TGTCCGCGCC GTTACTCAGG AAGGTAAAAA ATACACCAAT
451 ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATGCGGCAG GCGAGGCGGT
501 CGAATATAAA AACTATATGC TGCCGGTTTT GCAGGAACAG GATTATTTTT
551 GGATTACCGG CACGCGCAGC GGCTTGCAGC AGCAATACCG CTGGCTGCGT
601 ATCCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTGCGTGA
651 GTTTTGTAAA GATGGGGAAG GCGCAAAACG TCTGGTTGCC GACGCAACCA
701 AAGGCGCACC TGCCGAAATC CGCGAACAAT TCATGCTGGC TCGGAAAAAC
751 ACGCTGAACA TCTTTCACAA AAAAGGCTAT TTGGGATTGG ACGAATTTAT
801 TACGTCCAAT ATCCCGAAAG AGCAGCAGGA TAAGATGCAG GGCTATTTCT
851 ACGAAATGCT TTACGGCGTG ATGAACGCTG CTTTGGATGA AACCATACGC
901 CGGTACGGCT TGCCCGAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCCT
951 GCTGCACAGT ATGGATGCGT ACACGGGTTT GACCGAATAT CCCGCGCCTA
1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TGCGTTCGTC GGGTTTGCAG
1051 ATGACCCGTT CCCCGGGTGC GCTTTTGGTC TATCTCGGCT CGGTGCTGTT
1101 GGTATTGGGT ACGGTATTGA TGTTTTATGT GCGCGAAAAA CGGGCGTGGG
1151 TATTGTTTTT AGACGCAAAA ATCCGTTTTG CCATGTCTTC GGCCCGCAGC
1201 GAACGGGATT TGCAGAAGGA ATTTCCAAAA CACGTCGAGA GTCTGCAACG
1251 GCTCGGCAAG GACTTGAATC ATGACTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504 . pep

```

1 ILVQDLPEFV KLKKEHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51 HPLTLHGITI YQASFADGGS DLTFFKAWNLG DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREEKS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQQD EARNRFLLS MDAYTGLTEY PAPMLQLDQ FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401 ERDLQKEFPK HVESLQRLGK DLNHD*
  
```

m504/a504 99.8% identity in 425 aa overlap

```

m504 . pep 10 20 30 40 50 60
ILVQDLPEFV KLKKEHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN HPLTLHGITI
|||||
a504 10 20 30 40 50 60
ILVQDLPEFV KLKKEHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN HPLTLHGITI

m504 . pep 70 80 90 100 110 120
YQASFADGGS DLTFFKAWNLG DASREPVVLK ATSIHQFPLE IGKHKYRLEF DQFTSMNVED
|||||
a504 70 80 90 100 110 120
YQASFADGGS DLTFFKAWNLG DASREPVVLK ATSIHQFPLE IGKHKYRLEF DQFTSMNVED

m504 . pep 130 140 150 160 170 180
MSEGAREEKS LKSTLNDVRA VTQEGKKYTN IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ
  
```

a504	MSEGAEREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ
	130 140 150 160 170 180
m504.pep	190 200 210 220 230 240
	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
a504	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
	190 200 210 220 230 240
m504.pep	250 260 270 280 290 300
	REQFMLAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
a504	REQFMLAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
	250 260 270 280 290 300
m504.pep	310 320 330 340 350 360
	RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV
a504	RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV
	310 320 330 340 350 360
m504.pep	370 380 390 400 410 420
	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
a504	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
	370 380 390 400 410 420
m504.pep	DLNHDX
a504	DLNHDX

g505.seq

g505.pap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

745

m505.seq (partial)

```

1   GGCATGTTTC GTTTACAATT CAGGCTGTTT CCCCCTTTGC GAACCGCCAT
51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
151 TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCCGAC CCCAAAACGG TCAAAGCCGT TTTGCGGAA ACGGCAAAAG
251 GCGGTTTGA ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301 ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
351 CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGCTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTCCCGCT GACCGCCATG
451 TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTTCGCGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
601 ACGTCCCCTC CCCTCAAGAA GCGGGGGAAG GCGTATGGGT GGATTCTTTC
651 GGCAAACCTG CCTATACCAT GACGCTGGCG GCAAATTGG CACACGTCAA
701 AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GCGGACAAG
751 GTTTCGATT GCACATCCGC CCCGTCCAAG GGGAATTGAA CGGCGACAAA
801 GCCCATGATG CCGCCGTGTT CAACCGCAAT GCCGAATATT GGATACGCCG
851 TTTCCGACG CatATC....

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

m505.pep (partial)

```

1   MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGHlafYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDIE T
101 MPKAVHGWEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAM Y
151 KPPKIKAIKIMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFGKPA YMTLAAXLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPFTHI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHlafYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHlafYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDIETMPKAVHGWEHVQALDKHEG					
g505	MRQAGLNPDQTQTVKAVFAETAKGGLLELAPAFKKPEDIETMPKAVHGWEHVQALDKHEG					
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDIETMPKAVHGWEHVQALDKHEG					
g505	MRQAGLNPDQTQTVKAVFAETAKGGLLELAPAFKKPEDIETMPKAVHGWEHVQALDKHEG					
	70	80	90	100	110	120
m505.pep	LLFITPHIGSYDLGGYISQQLPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYTMTLAAXLAHVKGVKTLFF					
g505	VKQIIKALRAGEATIIIPDHVPSPQEGG-GVWADFFGKPAYTMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYTMTLAAXLAHVKGVKTLFF					
g505	VKQIIKALRAGEATIIIPDHVPSPQEGG-GVWADFFGKPAYTMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	
m505.pep	CCERLPGGQGFDLHIRPVQELNGDKAHDAAVFNRNAEYWIRRFPTH					
g505	CCERLPGGQGFVLRPVQELNGDKAHDAAVFNRNTEYWIRRFPTHQYLFMYNRYKTP					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

```
a505.seq
1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAAGGCG
251 GTTTGGAAGT TGCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAACCG CGCTACCAG CATAAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GGCGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAGAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGTC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

```
a505.pep
1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSCSLHTLGN RLGHlafYLL
51  KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLELAPA FFRKPEDiet
101 MFKAVHWEH VQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVGRK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTQYLF MYNRYKMP*
```

m505/a505 99.0% identity in 287 aa overlap

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHlafYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHlafYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDietMFKAVHWEHVQQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDietMFKAVHWEHVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDietMFKAVHWEHVQQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDietMFKAVHWEHVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAIKIMQAGRVGRKGKTAPTSIQG					
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAIKIMQAGRVGRKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAIKIMQAGRVGRKGKTAPTSIQG					
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAIKIMQAGRVGRKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF					
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF					
	190	200	210	220	230	240
m505.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRNAEYWIRRFPTHI					
a505	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCCAGCCCC AAAACGGTCA AAGCCGTTT TCGCGAAACG GCAAAAGGCG
251 GTTTGGAACT TGCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGCAAAA GGA AAAACCG GCGCTACCAG CATAAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GCGGAAGCAA CCATCGTCTT GCCCGACCAC
601 GTCCTCTCCC CTCAAGAAGG GGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATGGGCA CACGTCAAAG
701 GCGTGA AAC CCTGTTTTC TGCTGGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTTGC ACATCCGCCC CGTCCAAGGG GAATGGAACG GCGACAAAGC
801 CACGATGCC GCGGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSC LHTLGN RLGH LAFYLL
51  KEDRARIIVAN MRQAGLN PDP KTVKAVFAET AKGGL ELAPA FFRK PED IET
101 MFKA VHGWEH VQALDKHEG LLFITPHIGS YDLGG RYISQ QLPF PLTAMY
151 KPPK IKAIDK IMQAGRVRGK GKTAPT SIQG VKQII KALRS GEATI VLPDH
201 VPSPQEGGEG VWVDFFGKPA YMTLA AKLA HVKG VKTLPF CCERLP GGQ
251 FDLH IRPVQG ELNGDKA HDA AVFN RNAEYW IRRFP TQYLF MYNRY KMP*

```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIIVAN					
	10	20	30	40	50	60
m505-1.pep	MRQAGLN PDKPTVKAVFAETAKGGL ELAPAF FRKPED IETMFKA VHGWEHVQALDKHEG					
g505	MRQAGLN PDKPTVKAVFAETAKGGL ELAPAF FRKPED IETMFKA VHGWEHVQALDKHEG					
	70	80	90	100	110	120
m505-1.pep	MRQAGLN PDKPTVKAVFAETAKGGL ELAPAF FRKPED IETMFKA VHGWEHVQALDKHEG					
g505	MRQAGLN PDKPTVKAVFAETAKGGL ELAPAF FRKPED IETMFKA VHGWEHVQALDKHEG					
	70	80	90	100	110	120
m505-1.pep	LLFITPHIGSYDLGG RYISQQLPFP LPLTAMYKPPK IKAIDKIMQAGRVRGKGKTAPT SIQG					
g505	LLFITPHIGSYDLGG RYISQQLPFP LPLTAMYKPPK IKAIDKIMQAGRVRGKGKTAPT SIQG					
	130	140	150	160	170	180
m505-1.pep	LLFITPHIGSYDLGG RYISQQLPFP LPLTAMYKPPK IKAIDKIMQAGRVRGKGKTAPT SIQG					
g505	LLFITPHIGSYDLGG RYISQQLPFP LPLTAMYKPPK IKAIDKIMQAGRVRGKGKTAPT SIQG					
	130	140	150	160	170	180
m505-1.pep	VKQIIKALRSGEATI VLPDHVPSPQEGG VWVDFFGKPAYTMTLA AKLAHVKG VKTLPF					
g505	VKQIIKALRSGEATI VLPDHVPSPQEGG VWVDFFGKPAYTMTLA AKLAHVKG VKTLPF					
	190	200	210	220	230	240
m505-1.pep	VKQIIKALRSGEATI VLPDHVPSPQEGG VWVDFFGKPAYTMTLA AKLAHVKG VKTLPF					
g505	VKQIIKALRSGEATI VLPDHVPSPQEGG VWVDFFGKPAYTMTLA AKLAHVKG VKTLPF					
	190	200	210	220	230	
m505-1.pep	CCERLP GGQGF DLH IRPVQGE LNKGDKA HDA AVFN RNAEYW IRRFP TQYLF MYNRY KMPX					
g505	CCERLP GGQGF DLH IRPVQGE LNKGDKA HDA AVFN RNAEYW IRRFP TQYLF MYNRY KMPX					
	240	250	260	270	280	290
m505-1.pep	CCERLP GGQGF DLH IRPVQGE LNKGDKA HDA AVFN RNAEYW IRRFP TQYLF MYNRY KMPX					
g505	CCERLP GGQGF DLH IRPVQGE LNKGDKA HDA AVFN RNAEYW IRRFP TQYLF MYNRY KMPX					

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIIVAN					
	70	80	90	100	110	120
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIIVAN					

748

m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMPKAVHGWHEHVQQALDKHEG
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMPKAVHGWHEHVQQALDKHEG
	70 80 90 100 110 120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTISIQQ
a505	LLFITPHIGSYDLGGYISQQLPPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTISIQQ
	130 140 150 160 170 180
m505-1.pep	VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
a505	VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
	190 200 210 220 230 240
m505-1.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRNAEYWIRRPPTQYLFMYNRYKMPX
a505	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRNAEYWIRRPPTQYLFMYNRYKMPX
	250 260 270 280 290 299

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

g506.seq

```

1  ATGCGCGTAT  TTGATGAAGT  CGGGCGCATC  GCCCATGGCT  GCGGCGGTGT
51  TGTCAAACAA  AGCCTGTTTC  TGCGCGTCGT  TCATCAGGTT  GAACAAGGCG
101 CGCGGTTGGC  TGAAGTAGTC  GTCATCGTCT  TGGCGGTAGT  CCCAGTGTGC
151 CGCGTCGCCG  TTGATTTTCA  AAGGCGGTTT  GCGCAAGTCG  GGTGTGTGCT
201 GCCATTGGCC  GAAGCTGTTG  GGTTCGTAGT  GCGGCAGGCT  GCCGTAGTTG
251 CCGTCGGCGC  GGCCTTGTC  GTGCGCTGG  TTGCTGTGAA  CAGGGCAACG
301 CGGACGATTG  ACGGGGATTT  GCGGGAAGTT  CACACCCAAG  CGGTAACGTT
351 GCGCGTCGGC  GTAATTGAAC  AAACGGGCTT  GCAACATTTT  ATCCGGGCTC
401 GCGCCGATAC  CGGGAACGAG  GTTGCTCGGT  GCGAAGGCGG  ATTGTTCCAC
451 ATCGGCGAAG  AAGTTTTTCG  GATTGCGGTT  CAACTCGAAT  TCGCCCACTT
501 CAATCAGCGG  ATAGTCTTTT  TTCGGCCAAA  CTTTGGTCAA  GTCAAACGGA
551 TGATAAGGCA  CTTTTTCGGC  ATCGGCTTCA  GGCATGACTT  GGATGTACAT
601 CGTCCATTTC  GGGAACTCGC  CGCGCTCGAT  GGCTTCGTAC  AGGTCGCGCT
651 GATGGCTTTC  GCGGTCGTCG  GCGATGATTT  TTGCAGCTTC  TTCGTTGGTC
701 AGGTTTTTAA  TCCCTTGCTG  GCTGCGGAAA  TGGAATTTCA  CCCAAAAACG
751 TTCGCCGCT  TCGTTCAGAG  AGCTGTAGGT  ATGCGAACCG  AAGCCGTGCA
801 TATGGCGGTA  GCTGGCGGGA  ATACCGCGGT  CGCTCATCAC  GATGGTAACT
851 TGGTGCAGGG  CTTGGGCGAG  CAGCGTCCAG  AAGTCCCATG  TGTGTTGGCG
901 GGAACGCATA  TTGGTGCGCG  GATCGCGTTT  GACGGCTTTG  TTCAGGTCGG
951 GGAATTGCG  CGGGTCGCGC  AGGAAGAACA  CGGGCGTGTT  GTTGCCGACC
1001 ACATCCAGT  TGCCTTCTTC  GGTATAGAAT  TTCAACGCAA  AACCGCGGAT
1051 GTCGCGTCC  GCATCGGCTG  CGCCGCGCTC  GCCTGCCACG  GTGGTGAAC
1101 GGGCGAACAT  CTCGGTTTTT  TTGCCGACTT  CGCTGAAAAT  TTTGGCGCGG
1151 GTGTATTTGG  TGATGTCGTG  TGTACGGTA  AACGTACCGA  ACGCGCCCGA
1201 ACCTTTGGCG  TGCATACGGC  GTTCGGGGAT  GACTTCGCGC  ACGAAGTCGG
1251 CGAGTTTTTC  ATTCAAGCAC  AAATCTTGCG  TCAGCAGGGG  GCCGCGCGGG
1301 CCGGCGGTCA  GGCTGTTTTG  ATTGTCGGCA  ACGGGCGCGC  CGTTGTTTCA
1351 GGTCAGATGG  GTTACGGGGC  ATTTGGAGGT  AGTCATCGCT  CTTGTTCCCT
1401 TTCTCAGGTT  GGTCAAATGG  GGGGCAAACG  GCTTACAGTA  CGATTTGGCG
1451 GAAAGCGTAT  TCGTAACCGG  TTTCTTGATT  GTAATAAATT  TCTTGAATCG
1501 ACATTTTATT  TTCCTTTTGC  AAAAATATG  GATGCGATTA  TACGCCAAGA
1551 TTTTCGTTAT  TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

g506.pep

```

1  MAVFDEVGRI  AHGCGGVVKQ  SLFLRVVHGV  EQGARLAEV  VIVLAVVPVC
51  RVAVDFORRF  GEVGLLLPLA  EAVGFVVRQA  AVVAVGAALS  VALVAVNRAT
101  RTIDGDLAEV  HTQAVTLRVG  VIEQTGLQHF  IRARADTGNE  VARCEGGLFH
151  IGEVFVGI  AV  QLEFAHFNQR  IVFFRPNFGQ  VKRMIRHFFG  IFRHDLVDV

```

m506.seq

1	ATGGCGGTAT	TTGATGAAGT	CGGGCGCGTC	GCCCATTGCG	GCGGCGGTGT
51	TGCCGAACAA	TGCTGTTC	TGCGCGTCGT	TCATCAGGTT	GAACAGGGCG
101	CGCGTTGGC	TGAAATAGTC	GTCATCGTCT	TGGCGGTAGT	CCCAGTGTGC
151	CGCGTCGCCG	TTGATTTTCA	AAGCGGGTTC	GGCGAAtCGg	GGTTGTTGCT
201	GCCATTGGCC	GAAGCTGTyG	GGTTCGTAGT	GCGGCAGGGT	GCCGyAGTTG
251	CCGTCCGGCG	GGCTTGACTT	gTyGCCsTgr	TtGTCTgAA	CasGGCAACG
301	CGGACGATTG	ACGGGAATTT	GTCGGAAGTT	TACGCCCAAA	CGGTAGCGTT
351	GTGCGTCGGC	GTAATTGAAC	AAACGCGCTT	GCAGCATTTT	ATCTsGGCTG
401	GCGCCGACAC	CGGGAACGAG	GTTGCTCGGT	GCGAAGGCGG	ATTGTTCCAC
451	ATCGCGAAG	AAGTTTTTCGg	GATTGCGGTT	CTCAAACGGA	TGATAAGGTA
501	CTTTTTCCCG	GTCGTCTTCA	GGCATGACTT	GGATGTACAT	CGTCCATTTC
551	GAAACTCGC	CGCGTTCGAT	GGCTTCsTAT	AAGTCGCGCT	GATGGCTTTC
601	GCGGTCGTG	GCGATGATT	TGGCGGCTTC	TTCGTTGGTC	AGGTTTTTAA
651	TGCCTTGTG	GGTGCGGAAA	TGGAATTTCA	CCCCAAACG	CTCGCTGCTG
701	TCGTTCCAGA	AGCTGTAGGT	ATGCGAACCG	AAGCCGTGCA	TATGCCGGTA
751	GCCGGCGGG	ATGCCGCGGT	CGCTCATCAC	GATGGTAACT	TGGTGCAGTG
801	CTTCGGGCAG	CAGCGTCCAG	AAGTCCCAGT	TGTTTGTGGC	AGAGCGCATA
851	TTGGTGCGCG	GGTCGCGTTT	GACGGCTTTG	TTCAGGTCGG	GGAACTTACG
901	CGGGTCGCGC	AGGAAGAACA	CGGGCGTGTT	GTTGCCGACC	ACATCCCAGT
951	TGCTTCTCT	GGTATAAAAT	TTCAAGGCAA	AACCCGGAT	GTCGCGTTCT
1001	GCATCGGCTG	CGCCGCGTTC	GCCTGCCACG	GTTGTGAAAC	GGGCGAATC
1051	CTCGGTTTTT	TTGCCGACTT	CGCTGAAGAT	TCCTTTGGCG	TGCATACGGC
1101	GTTCCGGGAT	GACTTCGCGC	ACGAAGTCGG	CGAGTTTTTC	AGTCATCGCT
1151	CTTGTTCTCT	TTCTCAGGTT	GGTCAAATGG	GGGTAAACGG	CTTACAGTAC
1201	GATTTGGCGG	AAAGCGTATT	CGTAACCGGT	TTCTTGATTG	CAATAAATTT
1251	CTTGAATCGA	CATTTTATTT	CCCTTTTGTA	AAAACATGG	ATGCGACTAT
1301	ACGCGAAGAT	TTTCGCTATT	AA		

m506.ppt

1	MAVFDEVGRV	AHCGGGVAEQ	CLFLRVVHVQ	<u>EQGARLAEIV</u>	<u>VIVLAVVPVC</u>
51	<u>RVAVDQRRF</u>	GESGLLLPLA	<u>EAVGVVVRQA</u>	<u>AXVAVGAALP</u>	<u>VAXXAVNXT</u>
101	RTIDGNLAEV	YAQTVALCVG	<u>VIEQTRLQHF</u>	<u>IXAGADTGNE</u>	<u>VARCEGGFLH</u>
151	IGEEVFGIAV	QLEFAHFNQR	IVFFRPNFGQ	VKRMIRYFFR	VCFRHDLDVH
201	<u>RPFKLAAFD</u>	<u>GFXXVALMAF</u>	<u>AVVGDDPFGF</u>	<u>FVGQVFNALL</u>	<u>GAEMEFHPKT</u>
251	LACFVPEAVG	MRTEAVHMAV	AGGDAVAHH	DGNLVQCFQG	QRPEVPVVC
301	RAHIGARVAF	DGFVQVGELT	RVAQEEHGRV	VADHIVPAFF	GIKFQKGTAD
351	VAFICIGAAF	ACHGGETGEH	LGFFADFAED	FGAGVFGDVV	RYGKRTERAR
401	TFGVHTAFGD	DFAHEVGEFF	IQPQILRQQR	AARTGGQAVL	IVGNRRRAVVH
451	GQMGYTRAFGG	SHRSCFSFSQ	QOMGGKRLTV	RFGGKRIRNR	FLDCNKFLES
501	TFYFPFVKTM	DATRQDREY	*		

Homology with a predicted ORF from *N. gonorrhoeae*

m506/q506

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      10          20          30          40          50          60
m506.pep  MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRAVDFFRRF
           |||||:::||:||||:||||:||||:||||:||||:||||:||||:||||:
g506       MAVFDEVGRIAHGCGGVVKQSLFLRVVHQVEQGARLAEVVVIVLAVVPVCRAVDFFRRF
           10          20          30          40          50          60

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750

	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
g506	GEVGLLLPLAEAVGFVVRQAADVAVGAALSVALVAVNRATRTIDGDLAEVHTQAVTLRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
g506	VIEQTGLQHFIRARADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVCFRHDLVHRPFRKLAALDGFXXVALMAFAVVGDDFGGFFVGVFNALL					
g506	VKRMIRHFFGIGFRHDLVHRPFRRELAALDGFVQVALMAFAVVGDDFCSEFFVGVFNPLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLACFVPEAVGMRTAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVCG					
g506	AAEMEFHPKTFARFVPEAVGMRTAVHMAVAGGNTAVAHHDGNLVQGFQQRPEVPVVCG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVADHIPVAFFGIKFQKGTADVAFICIGCAAF					
g506	GTHIGARIAFDGFVQVGEFARVAQEEHGRVADHIPVAFFGIEFQKGTADVAFRIGCAAL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
g506	ACHGGETGEHLGFFADFAENFGAGVFGDVVCYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQQRARTGGQAVLIVGNRAVHVGQMGYAFGGSHRSCSFSQVGMGGKRLTV					
g506	IQPQILRQQGAARAGGQAVLIVGNRAVHVGQMGYAFGGSHRSCSFSQVGMGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFKTMDAIRQDFRY					
g506	RFGGKRIRNRFLDCNKFLESTFYFPFAKTMDAIRQDFRY					
	490	500	510	520		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1379>:

```

a506.seq
1  ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT
51  TGCCGAACAA TGCCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAGGGCG
101 CGCGGTTGGC TGAATAGTCT GTCATCGTCT TGGCGGTAGT CCCAGTCCGC
151 CGCGTCGCCG TTGATTTTCA AAGCGGTTTC GGCGAAGTCG GGCTGCTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGGCGC GTCCTTGTCG GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGGTTG ACAGGGATTG GCGGAAGTT CACGCCCAAG CGGTAGCGTT
351 GCGCGTCGGC GTAATTGAAC AAACGCGCCT GCAACATTTT ATCTGGGCTG
401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCCG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATACGGCA CTTTTCCGCG ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTC GGAAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTCGCGCT

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751

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651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTGTTG GGTGCGGAAA TGGAAATTCA CCCAAAAACG
751 CTCGCCTGCT TCGTTCCAGA AGCTGTAGGT ATGCGAACC G AAGCCGTGCA
801 TATGGCGGTA GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCACTG CTTCCGGGAG CAGCGTCCAG AAGTCCAGT TGTTTGTGGC
901 AGAGCGCATA TTGGTGCGCG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGT GTTGCCGACC
1001 ACATCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACC GCGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACAGGCGCGC CGTTGTTTAT
1351 GGTCAGATGG GTTACAGGGC ATTTGGAGGT ANTCATCGCT CTTGTTCTCT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```
a506.pep
1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHVQ EQGARLAEIV VIVLAVVPVR
51 RVAVDFQRRF GEVGLLLPLA EAVGVFVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQVALRVG VIEQTRLQHF IWAGADTNE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRHDLVDH
201 RPFRLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVC
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRKTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQOR AARTGGQAVL IVGNRRVAVH
451 GQMGYRPFGR XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFVKTM DATIRQDFRY *
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m506/a506 94.8% identity in 520 aa overlap

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQEQGARLAEIVVIVLAVVPVCRVAVDFQRRF					
a506	MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQEQGARLAEIVVIVLAVVPVRRVAVDFQRRF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGVFVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
a506	GEVGLLLPLAEAVGVFVRQAAXVAVGASLSVALVAVNRATRTVDRDLAEVHAQVALRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIXAGADTNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
a506	VIEQTRLQHFIWAGADTNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVCFRHDLDVHRPFRKLAALDFGFXVALMAFAVVGDDFGGFFVGQVFNALL					
a506	VKRMIRHFFRIGFRHDLDVHRPFRKLAALDGFVQVALMAFTVVGDDFGGFFVGQVFNALL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHH DGNLVQCFGQQRPEVPVVC					
a506	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHH DGNLVQCFGQQRPEVPVVC					
	250	260	270	280	290	300

752

	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVDHIPVAFFGIKFQGKTADVAFICIGCAAF					
a506	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVDHIPVAFFGIELQKRTADVAFICIGCAAF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQORAARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCFSQVGMGGKRLTV					
a506	IQPQILRQORAARTGGQAVLIVGNRRRAVVHGMGYRAFGGXHRSCFSQVGMGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFFLESTFYFPFVKTMDATIRQDFRYX					
a506	RFGGKRIRNRFLDCNKFFLESTFYFPFVKTMDATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq
 1 ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
 51 TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTTTCCTG CTTCAGACGG
 101 CCTTTGCGCT CTTGCTGCTT GGCAACGGTT TGTTTCGGCAT GGGCAAGCTG
 151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCTGCT
 201 GGGTTTGAA GGCAGCGTTG AGCGTGGCTT GGACTTCTTC CAATTCGGGC
 251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCATTCCG CCAATTCGGT
 301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTC CTCAAGCTGC ACGCGGATTT
 351 GCTGCTGCTC CTGCCGGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
 401 TCGCGTTCGA TCGGTGGTG CAGGTTTTCG CGGTGGCGGA TTTGTTCTTC
 451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCGT
 501 GTACTGCCTG CTGCTGCGAC TGTTCCGGCAG TCTGCAAGGC GTGTACTTCG
 551 TTATTTAA

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep
 1 MLLPALQQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNGLFGMGKL
 51 LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
 101 LLFFDLQLVF LKLHADLLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
 151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq
 1 ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
 51 TTTCGGCTTC GTCGGGCAGG TTTAAGGCTT GGTTTTCCTG TTTCAGACGA
 101 CCTTTGCGCT CTTGCTGCTT GGCAATCGTT TGTTTCGGCAT GGGCAAGCTG
 151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCTGCT
 201 GGGTTTGAA GGCAGCGTTG AGCGTGGCTT GGGCTTCTTC CAATTCGGGC
 251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCATTCCG CCAGCTCGGT
 301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATTT
 351 GCTGCTGCTC TTGATGAATG CGTTGTAACT GCGCCTGCGC TGCCTGCTTG
 401 TCGCGTTCGA TCGGTGGTG CAGGTTTTCG TGATGCGGGA TTTGTTCTTC
 451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCAT
 501 GCACTGCCTG CTGCTGCGAC TGTTCCGGCAG TCTGCAAGGC GTGTACTTCG
 551 TCGTTTAA

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep
 1 MLLLTQQGG CFLRGGGFGF VGQVXGLVFL FQTFALFVL GNRLFGMGKL

51 ILLQRFQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLVFG NLHRPFRQLG
 101 LFFFDLQLVF FKLHADLLLL LMNALXLRRLR CLLVAFDALV QVLLMADLFF
 151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng) from *N. gonorrhoeae*:

m507/g507

	10	20	30	40	50	60
m507.pep	MLLLTLQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNRLFQGMGKLLLLLQRFQFAAD					
	: : : : : :					
g507	MLLPALQGGGFLSGGGFGLVGVQVGLVFLFQTTAFALFVLGNRLFQGMGKLLLLLQRFQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m507.pep	AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL					
	: : : : :					
g507	AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQFGLLFFDLQLVFLKLHADLLLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m507.pep	LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTNLLAQHAALVAQFMHCLLLRLFGSLQG					
	: : : : :					
g507	LPDALQLRLRCLLVAFDALVQVLPVADLFFQTNLLAQHAAFVAQFVYCLLLRLFGSLQG					
	130	140	150	160	170	180
m507.pep	VYFVV					
	:					
g507	VYFVI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

a507.seq

1	ATGCTCTTGC	TGGCTTTGCA	ACAAGGCGGC	AGCTTCCTGC	GCGGCGGCGG
51	TTTCGGCTTC	GTCAGGCAGA	TTCAGGGCTT	GGTTTCCTG	TTTCAGACGA
101	CCTTTGCGCT	CTTCGTGCTT	GGCAACGGTT	TGTTCCGCAT	GGGCAAGCTG
151	CTGCTGCTTC	AACGCCAGTT	CGCGGCGGAT	GCGGTTTGCC	TCGTCCTGCT
201	GGGTTTGGA	GGCGGCATTG	AGTGTGGCTT	GGGTTTCTTC	CAATTCCGGG
251	AGACGCTCTT	CGTGTTCGGC	AACCTGCATC	GCCATTCCG	CCAATTCCGT
301	TTGCTTTTCT	TCCGCCTGCA	ACTCGTTTTC	TTCAAGCTGC	ACGCGGATTT
351	GCTGCTGCTC	CTGATGGATG	CGCTGCATCT	GCGCCTGCGC	CGCCTGCTTG
401	TCGCGTTTCA	TGCGTTGGTG	CAGGTTTTTC	TGATGGCGGA	TTTGTTCCTC
451	CAAACGGGCA	ATCTGTTCGC	GCAACACGCC	GCGTTTGTTC	CCCAATTCGT
501	GCACCGCCTG	CTGCTGCGAC	TGTTCCGGCAG	TCTGCAAGGC	GTGTACTTCG
551	TCGTTTAA				

This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>:

a507.pep

1	MLLLALQGG	SFLRGGGFGF	VRQIQGLVFL	FQTTFALFVL	GNLFGMGKL
51	LLLQRFQFAAD	AVCLVLLGLE	GGIECGLGFF	QFGQTLFVFG	NLHRPFRQFG
101	LLFFRLQLVF	FKLHADLLLL	LMDALHLRLR	RLVAFDALV	QVLLMADLFF
151	QTGNLFAQHA	AFVAQFVHRL	LLRLFGSLQG	VYFVV*	

m507/a507 89.7% identity in 185 aa overlap

	10	20	30	40	50	60
m507.pep	MLLLTLQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNRLFQGMGKLLLLLQRFQFAAD					
	: : : : :					
a507	MLLLALQGGGFLRGGGFGFVRQIQGLVFLFQTTFALFVLGNLFGMGKLLLLLQRFQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

754

```

m507.pep  AVCLVLLGLEGGVERGLGFFQFGQTLFVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL
          |||||||||||:| |||||||||||:|||||||||:|:| |||||||||||
a507       AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLHRPFRQFGLLFFRLQLVFFKLHADLLLL
          70      80      90      100     110     120

          130     140     150     160     170     180
m507.pep  LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG
          ||:| ||| |||||||||||:|||||||||:|:| |||||||||||
a507       LMDALHLRLRLLVAFDALVQVLLMADLFFQTGNLFAQHAALVAQFVHRLLLRLFGSLQG
          130     140     150     160     170     180

m507.pep  VYFVVX
          |||||
a507       VYFVVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCCTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGGCAGCT TGGTTTGAGG GGTTCGTACG
101 CGGGCGTATT GCTCCCTGCC CTGTTCTCTG ATCTGCGCGA GTTTTCTCTG
151 CACGGCGATG TATTCTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTTTGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCCGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCGAGCCG
301 GGCGATTTGC TGCCGGTAGT TTTGTTTTTG CGGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

```

g508.pep
1  MVAFGVDQGL LLLQQGGLGG GLKLRQLGLQ GLYAGVLLPA LFLNLRFFFL
51  HGVVFFVQRV YGFGQLVELD VLLVVLELGF IGEGKLLPAF LPVQGLLFEP
101 GDLLFPVVLFL RVEFVDGDFG KPVLA VG FQQ GKLR L FQTAL LLLA AVRGGL
151 LLVFEFGGGF LQSSDVV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```

m508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGGCAGCT TGGTTTGAGG GGTTCGCACT
101 TTAGCGTATT GCTCCCTGCC CTGTTCTCTG ATCTGCGCGA GTTCTCTCTG
151 CACAACAATA TATTCTTCGT CCAAGGTCTG TACGGCTTCG CTTAATTCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTTTGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCG AGGGTTTGCT GTTCAAGCTG
301 GGCGATTTGC TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA ACGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

```

m508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLHFSVLLPA LFLNLRFFLL
51  HNNIFVQGL YGFAXFFKLD VLLVVLELGF IGEGKLLAF LPVEGLLFKL
101 GDLLFPVVLFL LVEFVDGDFG KPVLA VG FQQ GKLR L FQTAL LLLA AVRGGL
151 LLVFEFGGGF LQGNVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

755

	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLQGGGLGGGLKLRQLGLQGLHFSVLLPALFLNLRFFLLHNNIFFVQGL					
g508	MVAFGVDQGLLLQGGGLGGGLKLRQLGLQGLYAGVLLPALFLNLRFFLLHGDVFFVQVRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFLKLDLLPVVLFLLVEFVDGDFG					
g508	YGFQQLVELDVLLVVLELGFIGEGKLLPAFLPVQGLLFEFGDLPVVLFLRVEFVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQ QG KLR L FQ TALL LLA A VR GGL L LV FEF GGG F LQ GND VV					
g508	KPVLA VG FQ QG KLR L FQ TALL LLA A VR GGL L LV FEF GGG F LQ SSV DVV					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```

a508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGCAG GGTTTGTACG
101 CGGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTGCGCGA GTTTCCTCTG
151 TACGACAATA TATTCTTCGT CCAAACCTCG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAATCG AAGGTTTGT GTTCAAGCTG
301 GGCAATTTGC TGTGGTAGT TTTGTTTTG CTGGTTGAGC TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAATG GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```

a508.pep
1  MVAFGVDQGF LLLQGGGLGG GLKLRQLGLQ GLYAGVLFPT LLLNLRFFLL
51  YDNIFFVQTL YGFAQLFELD VLLVVLELGF IGEKLLLAFL LPIEGLLFKL
101 GNLLLVVLF LVELVDGDFG KPVLA VG FQ QG KLR L FQ TALL LLA A VR GGL
151 LLVFEFGGGF LQNGDVV*

```

m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLQGGGLGGGLKLRQLGLQGLHFSVLLPALFLNLRFFLLHNNIFFVQGL					
a508	MVAFGVDQGFLLQGGGLGGGLKLRQLGLQGLYAGVLFPTLLNLRFFLLYDNIFFVQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFLKLDLLPVVLFLLVEFVDGDFG					
a508	YGFAQLFELD VLLVVLELGF IGEKLLLAFLPIEGLLFKLGNLLLVVLFLLVELVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQ QG KLR L FQ TALL LLA A VR GGL L LV FEF GGG F LQ GND VVX					
a508	KPVLA VG FQ QG KLR L FQ TALL LLA A VR GGL L LV FEF GGG F LQ GND VVX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509.seq

```

1  atggtcgctg tatgtgatga acgggctgta cagcggacgt tgggtggccca
51  attcgcgcaa caaggcggct tgtttttgct cttcgttcag gctgtttag
101 tcttccaagc ctgctgttg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggctg
251 ccgttgtcga taagggaacg ttgcaatttt ttcaaatacat cgagaaattt
301 ttgggccgaa gcataaggct cgagaaagcc gaatttgcag cccatgcccc
351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
401 gcgcggcggt aagggttcttc ggtgcgggcg atttcttcgt caggcgagag
451 ggctgccagt gccattacgt cgtcgttgac tttgacgcgg cggatggaaa
501 gcggcagttc gcggtaaagt ttgtcgagtt cgctgcggta aaaacggaac
551 acgcgcatcg cggtggcgcg gaaggcaaaag cgcagggttt cgccagaaac
601 aaacggattg ccgtcgcggt cgccgccgat ccagccgccg attttaagga
651 tattcggaac gcggacatcg ggataggccg tctgaaagtc gtgttccatc
701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg ggaagatgga
751 cacgcggttg ttgatttcgt cgttgacgct gagtttgtgg cggcgcggtt
801 cgctggtctg ccacaagccc agaagcacgg tgtcgatttc gcggcgacgc
851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgcgttgcg gcagcagcgc
901 gcggatgcgg cggttgaaat tcaaaacggg ttggcggtgc acttcggctg
951 ggtgcgcggt caaaacggcg gtaacggacg tattgtccaa ctgccgctgc
1001 accgatttgc cgtcggtttt ccccgctttg agcctgcgga cggtttccgt
1051 caggctgcct tctgctgcgt tgtggccggc atcttcgtgg atttggcggc
1101 ggcttctgtg gtgcacgtct tcggcgatat tcagaatctg ggccaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgctgtcgtc ggaagtggac aagagtttga
1251 ccgtttcgac aaccaacggc gaggcttctt cgtgcaggag gttgaacagg
1301 gactgtttca aaaattccgc gtccgccgcc aaagccgcgt ccttcggatt
1351 gttcaggata tgcagttgca tgattttcct ctcatcgccg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcca aaccgttcac actttaacca
1451 ctcattgtccc gaaatgccgt ctgaagtga acgcgcgccg acggcgcgct
1501 tacaatcgcc cgcaactgtt tttttccgaa catcatcatg accgcgacgc
1551 aacacgacaa cgacgacgca ctctgctgct ggtacagccg ccacatcctc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatat
1651 tttggtcgtc ggctgcggcg gattgggcgc cgccgccctt gccctatctc
1701 gccgcctcgg ggtcgggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1  MVAVCDERAV QRTLVAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCOQAFGK QAAAVVDKGT LQFFQIIEKF
101 LGRSIRLEKA EFAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAVAAD PAADFDIRN ADIGIGRLKV VFHLAVEFGQ GFKKAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAFALRQOR
301 ADAAVEIQNG LALHFGRVVRG QNGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVVAG IFVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRADV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLRI
451 VQDMLHDFP LIAVNTVNVP QMPHPCQTVH TLTHVPKCR LKLNAARRRR
501 YNRPLFFSE HHHDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFRRAY
551 FGRLRRIGR RRPCISPPIR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1  ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTGCGCGAA CAGGGCGGTT TGTttttGCT CTTCGTTCAG GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTtt
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGACGGCTG
251 CCCTTGTGCA TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGGCGGT AGGGTCTTTC GCGCGGGGCG ATTTCTTCGT CGGCGCATTT
451 GTCGGACAAC GCCGTTACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTGAGTTC CGCCGCGATA GAAGCGGAAC

```

```

551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAG CGCAGGGTTT CGGCAGAAAC
601 AAACGGATTG CCGTCGCGGT CGCCGCCGAT CCAGCCGCCG ATTTTGAGGA
651 TGTCGGGAAC GCGGACGCCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCGAAA AAGCTCATCG GGAAGATGGA
751 CACGCCGTG TTGATTTCTG CGTTGACGCT GAGTTTGTGG CGGCGGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTtC GCgCGCAGC
851 CGTGCCAGCG CGTCGGCATT GGTGCAGCGT TCgCGTTGCG GCAACAGTGC
901 GCGGATGCGG CGGTGAAGC TTAAGACGGT TTGGCGTTGC ACTTCGGTCG
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATGTCCAA CTGCCGCTGC
1001 ACCGATTTGC CGTCGGCTTT CCCCCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGGTTCTGT GTGCACGTCT TCGGCGATGT TCAAATCTG GCGCAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCTGTTCA ATTGCGGCAA
1201 TACTTTTCA ATCAATGCCG CGCTGTCTGC GGAAGTGGAC AAGAGTTTGA
1251 CTGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCGCG GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAAGTTGCA TGATTTTCT CTCTCTCTG CCGTAAATAT
1401 TGTAATGTA CCCCAAATGC CGCATCCGTG CCAAACCGT CACACTTTAA
1451 CCGCCCGTGT CCCGAAATGC CGTCTGAAGT TGAACGCCGC CCGACGGCAG
1501 CGTTACAATC GCCCGCAACT GTTTTtTTCC GAACATCATC ATGACCACGA
1551 CCGAACACGA CAACGACGAT GCATTCCTGC TCGGTACAG CCGCCACATC
1601 CTCTTGGACG AAATCGGCAT CGAAGGGCAG CAGAACTTT CCGCCGCGCA
1651 TATTTTGGTC GTCGGCTGCG GCGGTTTGGG TGCCGCCGCA CT.GCCCTAC
1701 CTGCGCGCTT CGGTGTGCG CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

m509.pep

```

1  MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVKAEHGYGT DEVCQTAFGK QTAAVVDKGT LQFFQIIQKL
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAVGFF GAGDFFVGRF
151 VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201 KRIAVAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFKAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQDSVDF AAQPCQRVGI GAAPALRQQC
301 ADAAVEAXDG LALHFGVRVG QNGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFDLAAAFV VHVFGDVQNL GEQAAGQGXI VGLLFVQLRQ
401 YFFNQCRVV GSGQEFDCFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LSSAVNIVNV PQMPHPCQTV HTLTARVPKC RLKLNARRQ
501 RYNRPQLFFS EHHHDHRTTR QRRCI PAAVQ PPHPLGRNRH RRAAETFRRA
551 YFGRRLRRFG CRRTXPTLPL RVSAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

m509/g509

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFAVLAQVERH					
g509	MVAVCDERAVQRTLVQAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFAVLAQVERH					
	10	20	30	40	50	60
m509.pep	HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLOFFQIIQKLLCRSIRLEKAEFAAHTQTER					
g509	HVEAEHGHGTDEVCQTAFGKQAAA VVDKGTLOFFQII EKFLGRSIRLEKAEFAAHTQTER					
	70	80	90	100	110	120
m509.pep	ARFAHSARHNVGDGAAVGFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
g509	ARFAHSARHNVGNAAVRFVFFGAGDFFVRRREGQCHYVVVDFDAADGKRQFAVKFEFAAV					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKAQGFGRNKRIVAVAAADPAADFEDVRNADAGIGRLKVVFHFLAVELGQ					
g509	KTEHGIGVAAEGKAQGFARNKRIVAVAAADPAADFDIRNADIGIGRLKVVFHFLAVEFGQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GFKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQDQSVDFAAQPCQRVGIGAAAFALRQQC					
g509	GFKKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQKHGVDFAAQPCQRVGIGAAAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m509.pep	ADAAVEAXDGLALHFGRVGRQNGGNGRIVQLPLHRAVGFPRFEPADGFRQAAAFRAAASG					
g509	ADAAVEIQNGLALHFGRVGRQNGGNGRIVQLPLHRAVGFPRFEPADGFRQAAAFCCVVAG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m509.pep	FFVDLAAAFVHVFGDVQNLGEQAAGQGXIVGLLFVQLRQYFFNQCRVAVGSGQEFDCFD					
g509	IFVDLAAAFVHVFGDIQNLGEQPAQKRQIVGLPFVQLRQYFFNQCRVAVGSGQEFDRFD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m509.pep	NQRRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSSAVNIVNVPQMPHPQCQTV					
g509	NQRRGFFVQVEVEQGLFQKFRVRRQSRVLRIQDMQLHDFPLI-AVNTVNVNVPQMPHPQCQTV					
	430	440	450	460	470	
	490	500	510	520	530	540
m509.pep	HTLTARVPKCRLKLNAARRQRYNRPLFFSEHHHDHRTQRRCIPAAVQPPHPLGRNRH					
g509	HTLTTHVPKCRLKLNAARRRRYNRPLFFSEHHHDDRTQRRTTAAVQPPHPLGRNRH					
	480	490	500	510	520	530
	550	560	570			
m509.pep	RRAAETFRRAYFGRRLRRFGCRRTCPTLPLRV SAR					
g509	RRAAEAFRRAYFGRRLRRIGRRRCPISPGR SAR					
	540	550	560	570		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1397>:

```

a509.seq
1   ATGGTCGCTG TATGTGATGA ACGGACTGTA CAGTGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGCT TGTTTTGTCT CTTGCTTGAG GCTGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTG
151 GCCTGCGTGT TGGCGCAGGT CGAGCGGCAT CATGTGGAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGGCGGCTG
251 CCGTTGTGCGA TAAGGGAATG TTGCAATTTT TTCAAATCAT CGAGAAATTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTGT CCCATAGCGC GCGCCATAAT GTAGGCAATG
401 GCGCGACGGT AGGGTTCTTC GCGCGGGCG GTTCTTCGT CGGGCGATTT
451 GTCGGACAAC GCCATCACAT CGCCGTTGAC TTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGT CGCCACGGTA AAAACGGAAC
551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAA CGCAAGGTTT CGGCAGAAAC
601 GAACGGATTG CCGTCGCGGT CGCCGCGGAT CCAGCCGCCG ATTTTGAGGA
651 TGTCCGGAAC GCGGACATCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCAAAA AAGCTCATCG GAAAGATGGA
751 CACGCCGTTG TTGATTTCTG CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTGATTTT CGGCGCGCAGC
851 CGTGCCAGCG CGTCGGCATT GGTACAGCGT TCGCGTTGCG GCAGCAGCGC

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901 GCGGATGCGG CGGTTGAAAT TCAAGACGGT CTGGCGTTGC ACTTCGGTCCG
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTGTC CGTCGGCTTT CCCCCTTTG AGCCTGCCGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGTTCGTG GTGCACGTCT TCGGCGATGT TCAAAATCTG GCGGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCGTCCA ATTGCGGCAA
1201 TACTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CCGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCGCG GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCT CTCATTGCCG TAAATACTGT
1401 AAATGTACCT CAAATGCCGC ATCCGTGCCA AACCGTTCAC ACTTTAACCG
1451 CCCGTGTCCC GAAATGCCGT CTGAAGTTGA ACGCCGCCCG ACGGCAGCGT
1501 TACAATCGCC CACAACTGTT TTT.TCCGAA CATCATCATG ACCACGACCG
1551 AACACGACAA CGACGATGCA TTCCTGCTGC GGTACAGCCG CCACATCCTC
1601 TTGGACGAAA TTGGCATCGA AGGGCAGCAG AAACCTTCCG CCGCGCATAT
1651 TTTGGTCGTC GGCTGCGGCG GTTTGGGTGC CGCCG.CCCT GCCTATCTC
1701 GCCGCTCCG GCATCGGCAC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

a509.pep

```

1  MVAVCDERTV QWTLMAQFAQ QGGLFLLFVE AVVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGYGT DEVCQTAFGK QAAAVVDKGM LQFFQIIIEKF
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGNGATVGFF GAGGFFVGRF
151 VGQRHHIAVD FDAADGERQF AVEFVEFATV KTEHGIGVAA EGKTQGFGRN
201 ERIA VAAAD PAADFEDVRN ADIGIGRLKV VFHLAVELGQ GFKKAHRKDG
251 HAVVDFVDDA EFVAARFAGL PQAQDSDVDF AAQPCQRVGI GTAFALRQOR
301 ADAAVEIQDG LALHFGRVRG QNGGNGRIVQ LPLHRFVAVG PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQG*I VGLLFVQLRQ
401 YFFNQCRVAV GSGQEFDRFD NQRRGFVQVE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LIAVNTVNVF QMPHPCQTVH TLTARVPKCR LKLNAAARRQ
501 YNRPQLFXSE HHHDHDRTRQ RRCIPAAVQP PHPLGRNWHR RAAETFRRAY
551 FGRLRRFGC RXPCPISPLP ASAR*

```

m509/a509 93.0% identity in 575 aa overlap

m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVVFQACVLEKLGNHIGVFACVLAQVERH
a509	MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVVFQACVLEKLGNHIGVFACVLAQVERH
	10 20 30 40 50 60
m509.pep	HVKAHGYGTDEVCQTAFGKQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAEFAAHTQTER
a509	HVEAEHGYGTDEVCQTAFGKQAAAVVDKGM LQFFQIIIEKFLCRSIRLEKAEFAAHTQTER
	70 80 90 100 110 120
m509.pep	ARFAHSARHNVGDGAAGVFFGAGDFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI
a509	ARFAHSARHNVGNGATVGFFGAGGFFVGRFVGQRHHIAVDFDAADGERQFAVEFVEFATV
	130 140 150 160 170 180
m509.pep	EAEHGIGVAAEGKAQGFGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ
a509	KTEHGIGVAAEGKTQGFGRNERIAVAVAADPAADFEDVRNADIGIGRLKVVFHLAVELGQ
	190 200 210 220 230 240
m509.pep	GFEKAHREDGHAVVDFVDDAEFVAARFAGLPQAQDSDVDFAAQPCQRVGIGAAAFALRQOC
a509	GFKKAHRKDGHAVVDFVDDAEFVAARFAGLPQAQDSDVDFAAQPCQRVGIGTAFALRQOR
	250 260 270 280 290 300
	310 320 330 340 350 360

760

```

m509.pep      ADAAVEAXDGLALHFGRVVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFRAAASG
               |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509          ADAAVEIQDGLALHFGRVVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFRAAASG
               310      320      330      340      350      360

               370      380      390      400      410      420
m509.pep      FFVDLAAAFVVHVFGDVQNLGEQAAGQGXIIVGLLFVQLRQYFFNQCRVVGSGQEFDCFD
               |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509          FFVDLAAAFVVHVFGDVQNLGEQAAGQGXIIVGLLFVQLRQYFFNQCRVVGSGQEFDRFD
               370      380      390      400      410      420

               430      440      450      460      470      480
m509.pep      NQRRGFFVQVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSAVNIVNVPQMPHPCQTV
               |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509          NQRRGFFVQVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSI-AVNTVNVNVPQMPHPCQTV
               430      440      450      460      470

               490      500      510      520      530      540
m509.pep      HTLTARVPKCRLKLNAAARRQRYNRPQLFFSEHHHDHTRQRRICIPAAVQPPHPLGRNRH
               |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509          HTLTARVPKCRLKLNAAARRQRYNRPQLFXSEHHHDHTRQRRICIPAAVQPPHPLGRNWH
               480      490      500      510      520      530

               550      560      570
m509.pep      RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRV SARX
               |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509          RRAAETFRRAYFGRRLRRFGCRXPCFISPLPASARX
               540      550      560      570

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1399>:

```

g510.seq
1   atgccttcgc ggacaccgca gggaaaaagg ggttattcct gccccaaagg
51  ggatagtgcc ttttggcagg cgttgtccat atcggttatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgccgttca gggaggtttt caataggtcg
151 tggacgacgt tgagcgcggc cataatgacg atttttcgc tgtccgcgac
201 gcggccgcct tcgcgcatgg ctteggcttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
301 ggcgtgcatg acttcgatgt agacttggtc gatgttcac ctttaatcct
351 tattgtgcg tttcctgccg ttgggggagg cgcgctgcca gtgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:

```

g510.pep
1   MPSRTPQGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51  WTTLAAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1401>:

```

m510.seq
1   ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTATTCTCT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGCG TGTCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC GGTGAGCCGG
301 GCGGTGCAwG ACTTCAAtGT GGAATTGTTC GATGTTGATC CTTTAATCCT
351 TATTGCTGCG TTTCTGCCA TTGGGGGAGG GCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:

```

m510.pep
1   MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51  WTTLAAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVXDFXVDLF DVHPLILIAA FPAIGGGALP VR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA F WQALSISAILRAKSPIAKSPPFREVFNRSWTTL SAAIMT					
g510	MPSRTPQGKRGYSCPKRDSA F WQALSISVILRAKSPIAKSPPFREVFNRSWTTL SAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLT VSRGVXDFXVDLFDVHPLILIAA					
g510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLT VSRGVHDFD VDLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

```

1  ATGCCTTCGC GGACACCGCA GGGAAAAAGG GGTTATTCCT GCGCCAAGCG
51  GGATAGTGCT TTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTT CAACAGGTCTG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGC TGTCGCGCAC
201 GCGTCCGCCT TCGCGGATGG CTTTCGGCTT GCCGTTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTT TCTTCTGCCG GCGTGTGAC GGTGAGCCGG
301 G.CGTGCATG ACTTCGATGT GGACTGTTC GATGTTGATC CTTTAATCCT
351 TATTGCTGCG TTCCTGCCG TTGGGGGAGG CGCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

```

1  MPSRTPQGKR GYSCAKRDSA F WQALSISAI LRAKSPIAKS PPFREVFNR
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLT VSR
101 XVHDFD VDLF DVHPLILIAA FPAVGGGALP VR*

```

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA F WQALSISAILRAKSPIAKSPPFREVFNRSWTTL SAAIMT					
a510	MPSRTPQGKRGYSCAKRDSA F WQALSISAILRAKSPIAKSPPFREVFNRSWTTL SAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLT VSRGVXDFXVDLFDVHPLILIAA					
a510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLT VSRXVHDFD VDLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

```

1  atgaaagtgc ttgttttagg tgcgggtgtt gccggcgat cctccgtgtg

```

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```

51  gtatctggca gaggccggac atgaagtaac ggtcatcgac cgcaccgagg
101  gtgtggcgat ggaaaccagt tttgccaatg caggccagct ttcttacggc
151  tataccacgc cttgggctgc acccggtatt ccgaccaaag cactgaaacg
201  gctgtttaaa agccatccgc ctttactgtt ccgccctgac ggcggcctgt
251  atcaaataca atggctgtgg cggatgtctg aaaactgcac ggcaacgcgc
301  tatcaaataca ataaagagcg catggtcagg atttccgaat acagccgtga
351  aatgtttccgc cgttttgaag cgcaaaccga catgaatttt gagggacgca
401  aaaaagggac gttgcagatt ttccgccaaa ccgaagaagt cgaagcggca
451  aaacaagaca ttgccgtttt ggaacgctac ggcggtgccg accgccgtct
501  gaagcccga  gaatgcgcag aattcgagcc tgcgttgga  cgcgttaccg
551  caaaaattgt cggcggctctg cacctgcctg cggatgcgac cggcgactgc
601  cgcctcttca ccgaaaacct gtacaaattg tgtcaagaga agggggtagc
651  gttctacttc aaccaaacca tcagccgcac cgaccacaac gggctgcgca
701  tcaaagccgt tgaaacgaaa cagggcggtt tgaacagat gccgttgtct
751  gcgcgctcgg ctgcttcagc aggactgtgt tggcgagtt ggatctcaat
801  ctgcccattt atcccgtcaa aggtatttcc ttga

```

This corresponds to the amino acid sequence <SEQ ID 1406; ORF 512.ng>:

g512.pep

```

1  MKVLVLGAGV AGVSSVWYLA EAGHEVTVID RTEGVAMETS FANAGQLSYG
51  YTTPWAAPGI PTKALKRLFK SHPPLLFRPD GGLYQIEWLW RMLQNCTATR
101  YQINKERMVR ISEYSREMFR RPEAQDTMNF EGRKKGTLOI FRQTEEVAAA
151  KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIVGGL HLPADATGDC
201  RLFTENLYKL CQEKGVRFYF NQTISRIDHN GLRIKAVETK QGGLKQMPLS
251  ARSAASAGLC WRSWISICPF IPSKAIP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1407>:

m512.seq (partial)

```

1  ..GTTTTGGAAC GCTACGGCGT GCCGTACCGC CGTCTGAAAC CCGAAGAATG
51  TGCAGAATTT GAGCCTGCGC TGGCACGCGT TACCGCCAAA ATTGCCGGCG
101  GCCTGCACCT GCCTGCAGAT GCGACCGGCG ACTggCGCCT CTTCACTGAA
151  AACCTATACA AATTGTGTCA GGAAAAGGGC GTACGGTTTC ATTCAACCA
201  AAACATCAGC CGCATCGACC ACAACGGGCT GCGCATCAA ACCGTTGAAA
251  CCAAACAGGG CGGTTTGAAG CAGATGCCGT TGTCTGCGCG CTCGGTTGCT
301  TCAGCAGGAC GGTTTGGCG CAGTTGATC TCAATCTGCC CATTATCCC
351  GTCAAAGGCT ATTCCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1408; ORF 512>:

m512.pep (partial)

```

1  ..VLERYGVFYP RLKPEECAEF EPALARVTAK IAGGLHLPAD ATGDWRLFTE
51  NLYKLCQEKV VRFHFNQNIS RIDHNGRLIK TVETKQGLK QMPLSARVA
101  SAGRFWRWI SICPFIPSKA IP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 512 shows 93.4% identity over a 122 aa overlap with a predicted ORF (ORF 512.ng) from *N. gonorrhoeae*:

m512/g512

```

                                     10      20      30
m512.pep                               VLERYGVFYPYRRLKPEECAEFEPALARVTAK
                                     |||
g512      TDMNFEGRKKGTLOIFRQTEEVAAKQDIAVLERYGVFYPYRRLKPEECAEFEPALARVTAK
          130      140      150      160      170      180

          40      50      60      70      80      90
m512.pep  IAGGLHLPADATGDWRLFTEENLYKLQCEKGVRFHFNQNISRIDHNGRLIKTVETKQGLK
          :|||
g512      IVGGLHLPADATGDCRLFTENLYKLQCEKGVRFYFNQTISRIDHNGRLIKAVETKQGLK
          190      200      210      220      230      240

          100      110      120
m512.pep  QMPLSARSVASAGRFWRWSWISICPFIPSKAIP
          |||
g512      QMPLSARSAASAGLCWRSWISICPFIPSKAIP

```

763

250 260 270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
1  ATGAAAGTGC TTGTTT TAGG TGCTGGTGT GCCGGCGTAT CTTCCGCGTG
51  GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCATCGAC CGCGCCGAGG
101 GCGTGGCGAT GGAACACAGT TTTGCCAACG CAGGCCAGCT TTCTTACGGC
151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GGCGTGCCGT ACCGCGCTCT
501 GAAGCCCGAA GAATGCGCAG AATTTCGAGC TCGCTGGCA CGCGTTACCG
551 CCAAAATTGC CGCGGCCTG CACCTGCCCC CAGACGCGAC CGGCGACTGC
601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAAGAAA AGGGCGTACG
651 GTTTCATTTC AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701 TCAAAACCGT TGAAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGTTT TGGCGCAAGT GGATCTCAAT
801 CTGCCGATT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
1  MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
51  YTPWAAPI PTKALKWLFK SHPPLERPD GSLYQIEWLW QMLQHCTAAR
101 YQINKERMVR MSEYSREMER RFEAQTMNF EGRKKGTLQI FRQTKEVEAA
151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVETK OGGLKQMPPLS
251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

```
m512.pep                                10      20      30
                                VLERYGVYPYRRLKPEECAEFEPALARVTAK
a512      TGMNFEGRKKGTLQIFRQTKEVEAAKQDIAVLERYGVYPYRRLKPEECAEFEPALARVTAK
              130      140      150      160      170      180

              40      50      60      70      80      90
m512.pep  IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNLRLIKTVETKQGGGLK
              |||||
a512      IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQISRIDHNLRLIKTVETKQGGGLK
              190      200      210      220      230      240

              100      110      120
m512.pep  QMPLSARSVASAGRFWRWSWISICPFIPSKAIPX
              |||||
a512      QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
              250      260      270
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
1  ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
51  TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTTGTCGAT ACCATCATCG
101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
201 GCAATGGGGC GCGGTTTCC TCGCGTCAT CCTGTTTATG TTGCGCTTTT
251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
351 GGTCTATTTC GGCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTGTCGC CATCCTGCTG
451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```

764

501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKG DPEFKLSEHP GLKRRIKSDV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq

1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGCAAGGT ATGATTCAA TGCTGGGCGT GTTTGTCGAT ACCATCATCG
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
 151 GATTGAGCG GTGCGGCGCT GACgcAGGCG GCGATTGTCA GCCAAGTGGG
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTGGCGTGG
 351 GGTCTATTTT GCGCGCGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCTGCTG
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
 501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKG DPEFKLSEHP GLKRRIKSDV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

	10	20	30	40	50	60
m513.pep	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
	10	20	30	40	50	60
m513.pep	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
m513.pep	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
m513.pep	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMXLRD Y TAKLKMKG DPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRD Y TAKLKMKG DPEFKLSEHP					
	130	140	150	160	170	180
m513.pep	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMXLRD Y TAKLKMKG DPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRD Y TAKLKMKG DPEFKLSEHP					
	130	140	150	160	170	180
m513.pep	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

```
1 ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51 CGATCCGATG TGGTCATACT TGGTTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACCACGGGC TTTGTCCAAT TCCGCCTGTT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTG TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTTGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCAAGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTGTTCGC CCTGAGCCTG ATTTCTGTT TCGGCTTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTGC CGATACCGTC AAAGCGGCGT
551 GGGGTTGGGA GCCTCATTAT TCGGGCGTGC CCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CGGAAATCGT
651 CGTCCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTGAGAT TTTTTCGGGC
751 GCGTTCAAAT TCGACGCGGC AGCAGGCGGC TTACTCGGCG GTCTGATTTT
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CTGTATTCC AACGAGGCGG
851 GTATGGGTTT CGCGCCGAAC GCCGCCGCCG CCGCCGAAGT GAAACACCCT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTCT ATACCATCAT
951 CGTTTGTCT TGCACCGCCT TCATCATCTT GATTTACCAA CAGCCTTACG
1001 GCGATTGAG CGGTGCGGCG CTGACGCAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGCTT CCTCGCGTCT ATCCTGTTTA TGTTCGCTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAGCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTCGCGG
1201 TGGGTCTATT TCGGCGCGGT TGCCAAATGT CCTTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCCGA GTTCAAACCT TCCGAACATC CGGGCTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```
a513.pep
1 MNENFEWLH GWVGAINDEP WSYLVYXLLG TGLFFTVTG FVQFRLFGRS
51 IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGPGGA
101 VFWMWVTALI GMSSAFVESS LAQLEKVRDY DNHHRFGGPA YYITQGLGQK
151 WLGLVFALSL IFCFGVFEEA VQNTIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVEL MAVLYLFIAL FIILTNIPMI PDVFGQIFSG
251 AFKFDAAAGG LLGGLISQTM MMGIKRGlys NEAGMGSAPN AAAAAEVKHP
301 VSQGMQMLG VFVDTIIVCS CTAFIILYQ QPYGDLGAA LTQAAIVSQV
351 GQWAGFLAV ILEMFASFV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WVFYFVANV PLVWDMADMA MGIMAWINLV AILLSPALF MLLRDYAKL
451 KMGKDPEFKL SEHPGLKRRI KSDVW*
```

m513/a513 100.0% identity in 191 aa overlap

```
m513.pep
10 20 30
MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
|||||
a513
260 270 280 290 300 310
DAAAGGLLGLISQTMGMGIKRGlysNEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD

40 50 60 70 80 90
TIIIVCSCTAFIILYQPYGDLGSAALTQAAIVSQVGQWAGFLAVILFMFAFSTVIGNY
|||||
a513
320 330 340 350 360 370
TIIIVCSCTAFIILYQPYGDLGSAALTQAAIVSQVGQWAGFLAVILFMFAFSTVIGNY

100 110 120 130 140 150
AYAESNVQFIKSHWLITAVFRMLVLAVVYFGAVANVPLVWDMADMAMGIMAWINLVAILL
|||||
a513
380 390 400 410 420 430
AYAESNVQFIKSHWLITAVFRMLVLAVVYFGAVANVPLVWDMADMAMGIMAWINLVAILL

160 170 180 190
LSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX
|||||
```

a51.3

LSPLAFMLLRDYTA KLKMGKDPEFKLSEHPGLKRRIKSDVWX

440

450

460

470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq

```

1 atggttcaaa tacaggttgt gcgcgcgcgc gccgttgccc gtggtctgca
51 ttccgagttt gcgcgcgcgc taactgccga ggaaatagcc ttcgacaatg
101 ccgttttgaa tcacgaagcg cggcgcgcgc gcaacacctt ccgcatcaaa
151 atagctgctg cggaaagagc gggggatgtg cggttcttcg cgcaggttga
201 ggaaatcggg caggactttt ttgccgatgc tgctgatcag gaaactgctt
251 tggcggtaga gcgcgcgcgc ggagagtgtg ccgacgaggt gtccgatcag
301 cccgcccga acggttgtat cgaagaggac ggggtagctg cctgtcggga
351 tgctgcggct gccgagtcgc cgcaaagtgc gccgggcggc ggtttgaccg
401 atggtttcgg ggctgtccat atccggatgg cggcagcggc aatcgtacca
451 gtatgcgcgc tgcattccgt ttcgtcggc gccgacgacg ctgcaggaaa
501 tgctgtggtg cgtgctttgc cgtgtgctgc caaaaccgtg ggtgttgccg
551 taaacgtatt ggtactgtcc ggtttgacc gccgcgcctt cggagttttc
601 gatgcggctg tccgtgtcca acgctgcctg ttgcattgtt ttgccaagc
651 cgacggcggc ttccgtatcc aaatccatt cgtggttaaag gtcggggtcg
701 ccgatgtgtt gcgccatcaa ctccgggtcg gcaagtccgg cgcaaccgtc
751 ttcggcgggtg tggcgggcga tgcggcggc gccgcggacg gtgtcgcga
801 gggcttggtt ggagaagtcg gcggtgcggc cgcggccttt gcgtttgccg
851 acgtaaacgg taatgtccag cgatttgcct tgctggaact cgatttgttc
901 gatttcgccc aagcgcacgc tgacgctttg tccgagcgat tcgctgaagt
951 cggcttcggc gccggtcgcg cccgctgctt ttgccaagtc gacgctgcgg
1001 cggcagaggt cgaggagttc ggaagcgggt tgggtgaaca gcataacaat
1051 ctttcttggg ggagcgttgt ggcattttaa

```

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep

```

1 MVQIQVVRAA GVARGLHSEF ARAVTAEBIA FDNVLNHEA RRGNTFRIK
51 IAAERAGDV RFFAQVEIG QDFFADAVDQ ETALAVERAA GECADDEVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFFVG GDDAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAVEVEF GSGVVEQHNN
351 LSWWSVVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)

```

1 ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC
101 GCGCCGCCGG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCCGAAAC
151 GGTGGTATCG AAGAGGACGG GGTAGCTGCC TGTCCGGATG CTGCGGCTGC
201 CGAGTCGGCG CAAAGTGC GGCGCGCGG TTTGACCGAT GGTTCGCGG
251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG
301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTGCGGTA AACGTATTGG
401 TAATGGCCGG TTTGCACCGC CGCGCCTTCG GAGTTTTCGA TCGGCTCATC
451 CTCGTTTCAGG GCGGCTTGTT CGCATTGTTT TGCCAAGCCG ACGGCGGCTK
501 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CGGGGTCGCC GATGTGTTTT
551 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CCGCGGTGTG
601 GCGGGCGATG TCGATGGCGG CTTTGACGGT GTCTTGACAG GCTTTTTCGG
651 AGAAGTCGGC AGTACTGGCG CGGCCTTTCG GTTTGCCGAC GTAAACGGTA
701 ATGTCCAGCG ACTTGTCCTG CTGGAACCTG ATTTGTTsGA TTsGCCAG
751 CCGCACGCTG ACGCTTTGTC CCAATGATTC GCTGAAATCG GCTTCGGCGG
801 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGCGGCG GCAGAGGTGC
851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA
901 TGCTTGCGG CATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

m515/g515

[illegible]

a515.seq

1	ATGGTTCAAA	TAAAGGTTGT	GCGCGCCGCC	GGCGTTGCCC	GTGGTCTGCA
51	TTCCGAGTTT	GCGCGCGCTG	TAACGTCTGA	GGAAATAGCC	TTCGACAATG
101	CCGTTTTTGA	TCACGAAGCG	CGGTGCGGTG	GCAACGCCTT	CCGCATCAAA
151	ATAGTCTGCT	CGGAAGAAGC	GGGGGATGTG	CGGTTCTTCG	CGCAGGTTGA
201	GGAAATCGGG	CAGCACTTTT	TTGCGCATGC	TTCGCATCAG	GAAACTGCTT
251	TGGCGGTAGA	GCGCTCCGCC	GGAGAGTGCG	CGCCAGGAGT	GTCCGATAAG
301	ACCGCCCGAA	ACGGTGGTAT	CGAAGAGGAC	GGGGTAGTTG	CCTGTCGGGA
351	TGCTGCGGGT	GCGGAGTCCG	CGCAAAAGTC	GGCGGGCGGC	GGTTTGACCG
401	ATGGTTTCGG	GCTGTGCCAT	ATCCGGATGG	CGGCAGGCGG	AATCGTACCA
451	GTAGTCGCGC	TGCATGCCGT	TTTCTGCGGG	GGCAACGACG	CTGCAGGAAA
501	TGCTGTGGTG	CGTGCTTTGC	CGGTGTGCGG	CAAAACCGTA	GGTGTGTGCC

a515.pcp

1	MVQIKVVRAA	GVARGLHSEF	ARAVTAEIEA	FDNAVLNHEA	RCGGNAFRIK
51	IAAAERAGDV	RFFAQVEEIG	QDFFADAVDQ	ETALAVERSA	GECAEDVSDK
101	TARNGGIEED	GVVACRDAAA	AESAQSAAGG	GLTDGFGAVH	IRMAAGGIVP
151	VVALHAVFVG	GNDAAAGNAV	DALPVCQKTV	GVAVNVLVMA	GLHRRAGFVF
201	<u>DALILVQGG</u> L	FALFCQADGG	FRIQIPFVVK	VGVDVLRHQ	LGVGKSGATV
251	FGGVAGDVXX	GADGVAQGLF	GEIGGAGAAF	AFADVNGNVQ	RIVLLKLDLF
301	DFAQPHADAL	SQ*FAEIGFG	GGCARRFCQV	ERAAAEVEEF	SGSVVEQHRN
351	LS**CFAAF*				

```

a515      10      20      30
m515.pep      GKSGGCAFFAQVEEIGQDFSADAVDQETALA
               ::| | | | | | | | | | | | | | | |
a515      AEEIAFDNAVLNHEARCGGNAFRKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
               30      40      50      60      70      80

               40      50      60      70      80      90
m515.pep      VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
               ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VERSAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
               90      100      110      120      130      140

               100      110      120      130      140      150
m515.pep      GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRRAFGVFDALIL
               || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRRAFGVFDALIL
               150      160      170      180      190      200

               160      170      180      190      200      210
m515.pep      VQGGLFALFCQADGGXRIQIPFVKVGVADVFECHQTIGIGKSGATVFGGVAGDVGDFDGV
               || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VQGGLFALFCQADGGFRIQIPFVKVGVADVLRHQLGVGKSGATVFGGVAGDVXXGADGV
               210      220      230      240      250      260

               220      230      240      250      260      270
m515.pep      LQGGFGEVVGSTGAFAFADVNGNVQRLVLLLELDLXDQAOPHADALSQXFAEIGFGGGCAR
               ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      AQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLDFDAQPHADALSQXFAEIGFGGGCAR
               270      280      290      300      310      320

               280      290      300
m515.pep      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
               || | | | | | | | | | | | | | | | | | | | | | |
a515      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
               330      340      350      360

```

g515-1.seq

1 ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA


```

51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTGTA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCCGCCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGCGCGG GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTTGCCG
551 TAAACGTATT GGTAGTGTCG GGTTTGCACC GCCGCGCCTT CCGAGTTTTC
601 GATGCGGCTG TCCGTGTCCA ACGCTGCCTG TTCGCATTGT TTTGCCAAGC
651 CGACGCGCGG TCCGTATCC AAATCCCAT CTGTGTAAG GTCGGGGTG
701 CCATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGCGCGTG TGGCGGGCGA TGTCGGCGGC GCGCGGACG GTGTCGCGCA
801 GGGCTTGTT GGAGAAGTCG GCGGTGCCG GCGGCGCTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGATTTGTCC TGCTGGAAC CGATTTGTTC
901 GATTTCGCCC AAGCGCACGC TGACGCTTTC TCCGAGCGAT TCGCTGAAGT
951 CGGCTTCGGG GCGGGTCGCG CCCGCTGCTT TTGCCAAGTC GAGCGTGGG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAAT
1051 CTTTCTTGGT GGAGCGTTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEEIA FDNAVLNHEA RRGNTFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADEVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSAFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVVS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGADVLRHQ LGVGKSGATV
251 FGGVAGVDVG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RVLLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFQV ERAAAEVEEF GSGVVEQHNN
351 LSWWSVAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGGTTGT GCGCGCGGCC GCGGTGCCCC GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTGTA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGCGCGG GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGATGCGCGT TTTCTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTTGCCG
551 TAAACGTATT GGTAAATGCC GGTTTGCACC GCCGCGCCTT CCGAGTTTTC
601 GATGCGGCTA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGCGCGG TCCGTATCC AAATCCCAT CTGTGTAAG GTCGGGGTG
701 CCATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTCGCGGGTG TGGCGGGCGA TGTCGATGGC GGCTTTGACG GTGCTTGCA
801 GGGCTTTTTC GGAGAAGTCG GCAGTACTGG CCGGCGCTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTC TGCTGGAAC CGATTTGTTC
901 GATTTCGCCC AGCCGCACGC TGACGCTTTC TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEEIA FDNAVLNHEA RCGGNAPRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADEVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSAFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGLL FALFCQADGG FRIQIPFVVK VGADVLFHQ TGIGKSGATV
251 FGGVAGVDVG GFDGLVQGF GEVGTGAAG AFADVNGNVQ RVLLELDLF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

```

          10      20      30      40      50      60
g515-1.pep  MVQIQVVRAAGVARGLHSEFARAVTAEEIAFDNAVLNHEARRGNTFRIKIAAAERAGDV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m515-1      MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVLNHEARRCGGNAPRIKIAAAERAGDV
          10      20      30      40      50      60

```

770

	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSVFVGGNDAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
	190	200	210	220	230	240
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVKVGVDVLRHQ					
m515-1	GVAVNVLMAGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVKVGVDVFCHQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
g515-1.pep	LGVGKSGATVFGGVAGDVGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFVLLDLF					
m515-1	TGIGKSGATVFGGVAGDVGGFDGVLQGGFGEVGGSTGAFAFADVNGNVQRLVLLDLF					
	250	260	270	280	290	300
	310	320	330	340	350	360
g515-1.pep	DFAQAHADALSERFAEVFGGGRARCFQVERAAAEVEFGSGVVEQHNNLSWSVVAFX					
m515-1	DFAQPHADALSQX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATG GTTCAA TAAAGTTGT GCGCGCCGCC GCGCTGCCCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAAC TGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTGTAA TCACGAAGCG CGGTGCGGTG GCAACGCCCT CCGCATCAAA
151 ATAGCTGCTG CGGAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTGTA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCCGTAGA CCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGGCGGCGGC GGTTCGACCG
401 ATGGTTTTCG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCTGCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAACCGTA GGTGTTGCCG
551 TAAACGTATT GGTAAATGGCC GGTTCGACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTGA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGCGCGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GCGCGCGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTC TGTGAAACT CGATTGTTC
901 GATTTCGCCC AGCCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA GVARGLHSEF ARAVTAEEIA FDNVNLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADDEVSDK
101 TARNNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLMMA GLHRRAFGVF
201 DALILVQGGF FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF
301 DFAQPHADAL SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNNGGIEEDGVVACRDAAA					
	:					

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m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
	70 80 90 100 110 120
a515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
	130 140 150 160 170 180
a515-1.pep	GVAVNVLMAGLHRRRAFGVFDALILVQGGFLFCQADGGFRIQIPFVVKVGVDVLRHQ
m515-1	GVAVNVLMAGLHRRRAFGVFDALILVQGGFLFCQADGGFRIQIPFVVKVGVDVFCQ
	190 200 210 220 230 240
a515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKDLDF
m515-1	TGIGKSGATVFGGVAGDVGGGADGVLQGGFGEVGTGAFAFADVNGNVQRLVLLKDLDF
	250 260 270 280 290 300
a515-1.pep	DFAQPHADALSQX
m515-1	DFAQPHADALSQX
	310

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

g516.seq

```

1 atgttggtcc gtaaaacgac cgccgccgtt ttggcggcaa ccttgatact
51 gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacggt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgccca attggaaaag ggcagcctgg tgatgatggg
201 cgggaaatac tggttcgccg tcaatcccga agattcggcg aagctgacgg
251 gccttttgaa ggcggggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg cccgccacca agccctgccg gtcaaattcg aagcgcccgg
351 cagccagaat ttcagtaccg gaggtctttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcgggtcaa
451 ctcgacaatc ggaccattta cacgcgctgc gtatccgcca aaggcaaata
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaagtg
551 tgcccgcga tatttattat acggttactg aaaaacatac cgacaatcc
601 aagctgtttg gaaatatctt atatacggcc cccttgttga tattggatgc
651 ggcggccgcg gtgctgtgct tgcctatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

g516.pep

```

1 MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQITIRKRV DKDQIRAFGV
51 VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNIIYTP PLLILDAAA VLVLPALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

m516.seq

```

1 ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51 GAACGGCTGT ACGTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGC GC CTTCCGTTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
201 CGGAAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCCGCG AAGCTGACGG
251 GCATTTTGA GGCAGGGCTG GACAAACCC TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

```

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501 CTACGCCACA CCGCAAAAC TGAACGCCGA TTACCATTT GAGCAAAGTG
 551 TGCCTGCCGA TATTTATTAC ACGGTTACTG AAGAACATAC CGACAAATCC
 601 AAGCTGTTTG CAAATATCTT ATATACGCCC CCCTTTTGA TACTGGATGC
 651 GCGGGGCGCG GTACTGGCCT TGCCTGCGGC GGCTCTGGGT GCGGTCGTGG
 701 ATGCCGCCCG CAAATGA

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

m516.pep

1 MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV
 51 VAEDNAQLEK GSLVMMGGKY WVVNPEDSA KLTGILKAGL DKPFQIVEDT
 101 PSYARHQALP VKLESPGSON FSTEGCLLRY DTDKPADIAK LKQLGFQAVK
 151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEEHTDKS
 201 KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

m516/g516

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDQIRAFGVVAEDNAQLEK					
g516	MLFRKTTAAVLAATLILNGCTMMLRGMNPNVSQTITRKHVDKDQIRAFGVVAEDNAQLEK					
	10	20	30	40	50	60
m516.pep	70	80	90	100	110	120
	GSLVMMGGKYWVFNPEDSA KLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSON					
g516	GSLVMMGGKYWFAVNPEDSA KLTGILKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSON					
	70	80	90	100	110	120
m516.pep	130	140	150	160	170	180
	FSTEGCLLRYDTDKPADIAKLKQLGFQAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF					
g516	FSTGGLCLRYDTGRPDIAKLKQLEFKAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF					
	130	140	150	160	170	180
m516.pep	190	200	210	220	230	239
	EQSVPADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
g516	EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLLILDAAGAVLALPAAALGAVVDAARK					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

a516.seq

1 ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGTT
 51 GAACGGCTGT ACGGTAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA
 101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTTGCGTGTG
 151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
 201 CGGGAAATAC TGGTTCGTCG TCAATCCTGA AGATTCGGCG AAGCTGACGG
 251 GCATTTTGAA GGCCGGGTTG GACAAGCAGT TTCAAATGGT TGAGCCCAAC
 301 CCGCGCTTTG CCTACCAAGC CCTGCCGGTC AAATCGAAT CGCCCGCCAG
 351 CCAGAATTTC AGTACCGAAG GCCTTGCCT GCGCTACGAT ACCGACAGAC
 401 CTGCCGACAT CGCCAAGCTG AAACAGCTTG AGTTTGAAGC GGTGGAATC
 451 GACAATCGGA CCATTTACAC GCGCTGCGTC TCCGCCAAAG GCAAATACTA
 501 CGCCACACCG CAAAACCTGA ACGCCGATTA TCATTTGAG CAAAGTGTGC
 551 CTGCCGATAT TTATTACAG GTTACGAAAA AACATACCGA CAAATCCAAG
 601 TTGTTTGAAA ATATTGCATA TACGCCACC ACGTTGATAC TGGATCGCGT
 651 GGGCGCGGTG CTGGCCTTGC CTGTCGCGGC GTTGATTGCA GCCACGAATT
 701 CCTCAGACAA ATGA

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

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```

1  MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFVVPEDSA KLTGILKAGL DKQFQMVEPN
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIACL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVFADIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

```

      10      20      30      40      50      60
m516.ppep  MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDDKDQIRAFGVVAEDNAQLEK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a516       MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHVDDKDQIRAFGVVAEDNAQLEK
          10      20      30      40      50      60

      70      80      90     100     110     120
m516.ppep  GSLVMMGGKYWFVVPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a516       GSLVMMGGKYWFVVPEDSAKLTGILKAGLDKQFQMVEPNRFA-YQALPVKLESPASQN
          70      80      90     100     110

      130     140     150     160     170     180
m516.ppep  FSTEGLCLRYDTPDKPADIACLKQLGFEAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a516       FSTEGLCLRYDTPDRPADIACLKQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF
      120     130     140     150     160     170

      190     200     210     220     230     239
m516.ppep  EQSVFADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARKX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a516       EQSVFADIYYTVTKKHTDKSKLFENIAYTPTTLILDAVGAVLALPVAALIAATNSSDKX
      180     190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1  atgcatcggg ttccagacgg cattggagtg tcagtcgtgt tctgccgatt
51  cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 ccggtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcacg
151 tgcgtctttc aatccccgatt tgatgttttt gggcaggtcg atttggctgg
201 tgtcgccggg aatgacggct ttccgcgccg agccgatgcg ggtcaggaac
251 attttcattt gttcggggcg ggtgttttgc gcttcgtcga ggatgatgta
301 tgcgccgttg agcgtcctgc cgcgcatata ggcgagcggg gcgatttcaa
351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcaggtca
401 tagagggcat cataaagcgg acggaggtag gggtcgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

```

g517.ppep
1  MHRVSDGIGV SVVFCRFVGF DDFLHQMPD NVFAGEGMEI QSCHAVQFLT
51  CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TEVGVDFLQG
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1  ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51  CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGCTCTCG
101 CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACGTTGTGCA GTTCTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCTG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTGAGGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCGATTTCAG
351 TCAGGCCTTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```

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451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGEI QPFHVQFLT
51 RIFXSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ
151 VSGQEAQFLA GFDGWAH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
g517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGEGMEIQSCHAVQFLTCVFQSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
g517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAH					
	: : : :					
g517	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLTGFDGRPN					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTTT TGCACCAAAG GATGCCGGAC AACGCTTCG
101 CCGGTAAGG TGTGGAATA CAGCCCTTCC ACGCCGTGCA GTTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCCCGGCT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTGAGGAAC
251 ATTTTCATTG GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCGAGCGGG GCAATCTCAA
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTGGAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGEI QPFHAVQFLT
51 RIF*SRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGNLNQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ
151 VTGQRTQFLA GFDGRPH*

m517/a517 93.4% identity in 167 aa overlap

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
a517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGEIQPFHAVQFLTRIFXSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
a517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGNLNQTF					

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	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVIGIDFLGQVSGQEAQFLAGFDGWAHX					
a517	FNQLGDTVEAHQVIEGIIKRTKVIGIDFLGQVTGQKTQFLAGFDGRPHX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1  atgacgtttt cggcggcaaa gctcaacatt tcggcactga tgttggtgtc
51  ttcggcagga atgaccgttt tactttccgc ttttttactg ctccgaccgg
101 aaggcagcat cttattcaac catTTTTTca gcataaatat tctgaccgca
151 agagcggcat ctccacgggc aaccgtgttc agactgcatac aggcggtagc
201 attccacaag atgccgaaaa ccataagcaa aatgcgtaga aactacgccg
251 tccgaatcac gccgcctcct cgggcggcaa cgcttcatta taacagattg
301 ccccttaaaa aatcagaccc tgcttttgtg gcggagtctg aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1  MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RLHQAVRFHK MPKTISKMRN NYAVRITPPP RAATLHYNRL
101 PLKSDPAFV AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTGCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTTCA GCATAAATAT TCTGACCGCA
151 AGAGCGGCAT CTCCACAGGC AACCGTGTTC AGACGGCATC AGGCGCGGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCG TAGAACTAC GCCGTCCGAA
251 TCACGCCGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCCGC CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTTT TGTGGCAGAG TCTGAAATT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPOATVF RRHQARFARC RTINKRRRNY AVRITPPSXA ATRHYNRLPS
101 AAGLVRRERR RCAVILSNR KKSDPAFVAE SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR RAASPOATVF
g518      MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR RAASPRATVF
              10      20      30      40      50      60

              70      80      90      100     110
m518.pep  RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSN
g518      RLHQAVRFHKMPKTISKMRNRYAVRITPPRAATLHYNRLPL-----
              70      80      90      100

m518.pep  120      130
g518      GRKSDPAFVAESEI
              |||||
g518      --KKSDPAFVAESEI
              110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATCAAC CATTTTTCA GCATAAATAT TCTAACCCGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTTC AGACGGCATC AGGCGGTACG
201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAAATCAGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC .....
351 ... ..AAAAAAT CAGACCCTGC TTTGTGGCA GAGTCTGAAA
401 TTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAA SPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*
```

m518/a518 79.9% identity in 134 aa overlap

	10	20	30	40	50	60
m518.pep	MTFSAAKLNI SARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF					
a518	MTFSAAKLNI SARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF					
	10	20	30	40	50	60
	70	80	90	100	110	119
m518.pep	RRHQAVRFRKMPPTINKRRRN YAVRITPSSXAATRHYNRLPSAAGLVRRERRRCAVILSNG					
a518	RRHQAVRFRKMPPTINKRRRN YAVRITPSSXAATRHYNRLPS-----					
	70	80	90	100		
	120	130				
m518.pep	RKKSDFAFVAESEIX					
a518	-KKSDPAFVAESEIX					
		110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaat tttt tcattatctt gttggcagcc gtcgcccgtt tcggcttcaa
51  atcctttgtc gtcaccccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatttt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgcttc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcccg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctgaggctgc
651 ggtcaatgcg tccaatgccg agaaaatcgc ccgcatcaac cgcgccaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccgcct tcaaacccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaaag ttgccgaaat cgggaaccct
901 aattttcggc ggcataaaaa attttcgcca gaagcaaaaa cggccaaata
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
```


101 SNYIMAITQL AQTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESG RKIEQINLAS
 201 GQREAEIQQS EGEEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAEN
 251 RQIAAALQTO SGADAVNLKI AGQYVTAFAK LAKEDNTRIK PAKVAEIGNP
 301 NFRRHEKFSP EAKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

m519.seq (partial)
 1 ..TCGGTTATCG GCGTATGGA GTTGACAAA ACGTTTGAAG AACGCGACGA
 51 AATCAACAGT ACTGTTGTTG CCGCTTTGGA CGAGGCGGCC GGGgCTTgGG
 101 GTGTGAAGGT TTGCGTTAT GAGATTAAAG ACTTGGTTCC GCCGCAAGAA
 151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
 201 CCGTATCGCC GAATCCGAAG GTCGTAAAT CGAACAAATC AACCTTGCCA
 251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGCGCA GGCTCAGGCT
 301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
 351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
 401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
 451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
 501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTGCGGAC ATCGGCAGCC
 551 TGATTCTGCG CGGTATGAAA ATTATCGACA GCAGCAAAC CGCCAAaTAA

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

m519.pep (partial)
 1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
 51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLASGQREAE IQQSEGEAQA
 101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTGGADAV
 151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

m519/g519

m519.pep				10	20	30
				SVIGRMELDKTFEERDEINSTVVAALDEAA		
g519	YFQVTDPKLASYGSSNYIMAITQLAQTLRSVIGRMELDKTFEERDEINSTVVSALDEAA					
	90	100	110	120	130	140
m519.pep		40	50	60	70	80
		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE				
g519		GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLASGQREAE				
		150	160	170	180	190
m519.pep		100	110	120	130	140
		IQQSEGEAQAANASNAEKIARINRAKGEAESLRLVAEANAENAEAIRQIAAALQTGGADAV				
g519		IQQSEGEAQAANASNAEKIARINRAKGEAESLRLVAEANAENAEANRQIAAALQTQSGADAV				
		210	220	230	240	250
m519.pep		160	170	180	190	200
		NLKIAEQYVAFAFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK				
g519		NLKIAGQYVTAFAKLNKEDNTRIKPAKVAEIGNPNFRRHEKFSP EAKTAK				
		270	280	290	300	310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

a519.seq
 1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
 51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
 101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCTACCG CCATTCGCTG AAGAAATCC CTTTAGACGT

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201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTA'TCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGC'AACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGT'TATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCA'ACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTG'AAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCT'TCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTA'TCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGT'CAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGT'CAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTG'AAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGT'CAAATG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCT'GAAGATT GCGGAACAAT ACGTCGCGCG GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATT'TCTGCCG GTATGAAAT TATCGACAGC AGCAAACCG CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFGRKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQOS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTC GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

m519/a519 99.5% identity in 199 aa overlap

m519.pep
10 20 30
SVIGRMELDKTFEERDEINSTVVAALDEAA
|||||
a519 YFOVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
90 100 110 120 130 140

m519.pep
40 50 60 70 80 90
GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
|||||
a519 GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
150 160 170 180 190 200

m519.pep
100 110 120 130 140 150
IQQSEGEAQAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
|||||
a519 IQQSEGEAQAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
210 220 230 240 250 260

m519.pep
160 170 180 190 200
NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSTAKX
|||||
a519 NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSTAKX
270 280 290 300 310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCCTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCCCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGT'TATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAAGCGGAA AAACGCGCCC
551 GTATTGCGCA ATCCGAAGGC CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGT'CAGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGT'CAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGT'CAAATG CCGCCGCCCT TCAAACCCAA GGCGGGGCGG ATGCGGTCAA

```

801 TCCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANABAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
 101 GGCCTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
 151 ATCGACGCGG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
 201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTG
 301 AGCAACTAGA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGCG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
 401 TCAACAGTAC TGTGTGTGCG GCTTTGGACG AGGCGGCGGG GGCTTGGGGT
 451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAAGCGGAA AAACGCGCCC
 551 GTATCGCGCA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTCAAGCGG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
 651 GGTCAATGCG TCAATGCGG AGAAATCGC CCGCATCAAC CGCGCCAAAG
 701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCGG AAGCCAATGC CGAAGCCATC
 751 CGTCAAAATG CCGCGCCCTT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANABAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESBGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESBGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep						
m519-1						

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1   ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTCCGCG CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCCG AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTGAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCG CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTGTGTGCGG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCAA GCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTGCGCGG GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCGG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1   MEFFFIILLAA VVVFQKSFV VIPQEVHV VRLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGANG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESG RKIEQINLAS
201 GQREAEIQS EGEAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFFIILLAAVVVFQKSFVVIPQEVHVVERLGRFHRALTAGLNILIPPIDRVAYRHS
              |||||
m519-1      MEFFFIILLVAVVFQKSFVVIPQEVHVVERLGRFHRALTAGLNILIPPIDRVAYRHS
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              |||||

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m519-1      KRARIAESEGRKIEQINLASGQREABIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240
              250      260      270      280      290      300
a519-1.pep  LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAPNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAPNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300
              310
a519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in *E. coli* as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in *E. coli*. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1  atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctggtgcc gttaataatg ccggcgaatgg
101 atttaatcct gtttgccgcc aaaccttcgc gcacggcctt gatgattggg
151 ataccgcccg ctactgccgc ttcaaattgg acgatgacgt tttgtttttc
201 cgccagcggg aagatttcgt tgccgtatc ggcgagcagt ttttggttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttccttg
301 gcaatgcccg tgccgccgaa caattcgacc aagacatcga cgtcttttacg
351 cgcgaacagt tcgaacggat cttttgacaa gggcgggcga cgggcccatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa ataccgattt
451 cgcgccccaa gcggcgggaa atttcctctg cgttgtcccg caacacggca
501 gccgcaccgc cgccgaccgt acctaagcct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1  MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILIFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP PSMAFNATSL
101 AMVPPNNST KTSTSLRANS SNGSFDKGG RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1  ATGCTTGC GC TTCTTTCA GT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTTCG Gk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATC CT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCC G CTA CTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGG G AAGATTCTGT TGCCGTATTC GCGGAGCAGT TTTTGTGTTG
251 CGGTAACG AT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

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301 GCAATGCCGG TACCGCCGaa CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCAGACAGT TCGAACGGAT CTTTGACAAA GGCTGc.CGG ACGGGCAGGT
401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATT
451 CGCGCCCCAA GCGACGGGAA ATTTCTCCG CGTTGTCCCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:

```

m520.pep
  1 MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDILFAA KPSRRALMIG
 51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF
151 RAPSDGKFPP RCXATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng) from *N. gonorrhoeae*:

m520/g520

	10	20	30	40	50	60
m520.pep	MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNW					
g520	MPALLSIRANALPFSRISERMKLLVPLIMPAMDILFAAKPSRTALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
g520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTKTSTSLRANS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
g520	SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFPLRCPATRQPHRRRPYLSLDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRLLKCKY					
g520	CLLASLCLLVSRLLKCKY					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1463>:

```

a520.seq
  1 ATGCCTGCGC TCTTTTCAGT ACATCGG.CA AACGCGCTGC CTTTTTCGCG
 51 CATTTTCGAG AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTAAGTCCGC TTCAAATTGG ACGATGACGT TTGTTTTTC
201 CGCCAGCGGG AAGATTTTCGT TGCCGTATTC GGCGAGCAGT TTTTGTGTTG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG
301 GCAATGCCGG TACCGCCGAA CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCAGACAGT TCGAACGGAT CTTTGACAAA GGCTG.CGG ACGGGCAGGT
401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATT
451 CGCGCCCCAA GCGACGGGAA ATTTCTCCG CGTTGTCCCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:

```

a520.pep
  1 MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDILFAA KPSRRALMIG
 51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF

```

1 51 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRKCKYX					
a520	CLLASLCLLVSRKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTCGTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTtCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTGGC GGGCTTTTTC
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTC CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCGTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSLRATSS
101 NGSILTKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTCGTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACCGTGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTC GGGCTTTTTC
351 TTTCACTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTC CTCTGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS

```

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101 NGSLLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
 151 TVPKPKRPMF TGFIVSPCKP TEM*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNWTMTCFSASGKISLPYSASSF					
m520-1	MKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNWTMTCFSASGKISLPYSASSF					
	10	20	30	40	50	60
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSLRATSSNGSLTKAADGQIWRAFSSLK					
m520-1	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
	70	80	90	100	110	120
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPKRREISSALSNTAAAPPTVPKPKRPMFTGFIVSPCKPTEMX					
m520-1	SHTAEIRISRPKRREISSALSNTAAVPPPTVPKPKRPMFTGFIVSPCKPTEMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq

1 ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
 51 TGCCGCCCAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
 101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
 151 ATTTTCGTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
 201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC
 251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTCACGTGC GACCAGTTCG
 301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTC GGGCTTTTC
 351 TTCACTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
 401 GGGAAATTC CTCCGCGTTG TCCGCAACA CGGCAGCCGT ACCGCCGCCG
 451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
 501 TTGTAAGCCG ACTGAAATGT AA

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep

1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTCFSASGK
 51 ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS
 101 NGSLLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
 151 TVPKPKRPMF TGFIVSPCKP TEM*

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNWTMTCFSASGKISLPYSASSF					
m520-1	MKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNWTMTCFSASGKISLPYSASSF					
	10	20	30	40	50	60
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
m520-1	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
	70	80	90	100	110	120
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPKRREISSALSNTAAVPPPTVPKPKRPMFTGFIVSPCKPTEMX					
m520-1	SHTAEIRISRPKRREISSALSNTAAVPPPTVPKPKRPMFTGFIVSPCKPTEMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq

1 ATGAAATCAA AACTCCCTT AATCCTAATC AACCTTCCC TGATTTCAGG
 51 CCCATTGGGT GCGAATGCGG CCAAATCTA TACCTGCACA ATCAACGGAG
 101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTG


```

151  CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCTGC CCCAACTCC
201  CGAACCGGCA CCATCACCCT CAAACGGCGG ACAGGCTGTC AAATATAAG
251  CCCCAGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCTCAA
301  CAAGCACCTG TAAATAACAG CAGACGCTCC ATTCTcgaag caGaattaag
351  cAatgaacgc aaagccctGa ctGaAGCCCA AAAAATGTTA TCACAagcac
401  gtCtGGCAAA AGGCGgcaAC AtcaaCCatc aaaAaatcaa cgcattgtaa
451  AGCAATGTTt tggacAGACA GCAAAATaTC Caagcactgc aaaGagAATt
501  GGGACGTATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1472; ORF 521.ng>:

g521n .pep

```

1  MKSKLPLILI NLSLISSPLG ANAAKIYCT INGETVYTTK PSKSCHSTD
51  PPIGNYSER YILPQTPEPA PPSNNGQAV KYKAPVKTVS KPAKSNTPPO
101 QAPVNSRRS ILEAELSNER KALTEAQKML SQARLAKGN INHQKINAL*
151 SNVLDROQNI QALQRELGRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1473>:

m521 .seq

```

1  ATGAAATCAA AACTCCTCTT AATCCTAATC AACTTTTCCC TGATTCAAG
51  CCCATTGGGT GCGAATGCGG CCAAAATCTA sACTGCACA ATCAACGGAG
101 AAACCGTTTA CACCAsCAAG CCGTCCAAAA GCTGCCACTC AACCGATTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAACGCC
201 CGAACCGGTA TCATCACCCT CAAACGGCGG ACwGGTTGTC AAATATAAG
251 CCCCAGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CACGTCTGGC AAAGGGCGGC AACATCAACC ATCAAGAAAT AAATGCATTA
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATTCAAGCCC TGCAAAGGGA
501 ACTGGGGCGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1474; ORF 521>:

m521 .pep

```

1  MKSKLLLLILI NLSLISSPLG ANAAKIXCT INGETVYTXK PSKSCHSTD
51  PPIGNYSER YIPPQTPEPV SSPNNGGXV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNSRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLDROQN IQALQRELGR M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from *N. gonorrhoeae*:

m521/g521

	10	20	30	40	50	60
m521 .pep	MKSKLLLLILINFLISSPLGANAAKIXCTINGETVYTXKPSKSCHSTDLPPIGNYSER					
	: : : : : : :					
g521	MKSKLPLILINLSLISSPLGANAAKIYCTINGETVYTTKPSKSCHSTDLPPIGNYSER					
	10	20	30	40	50	60
m521 .pep	70	80	90	100	110	120
	YIPPQTPEPVSSPSNNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNSRRSILETELSNE					
	: : : : : : :					
g521	YILPQTPEPAPSPNNGQAVKYKAPVKTVSKPAKSNTPP-QQAPVNSRRSILEAELSNE					
	70	80	90	100	110	
m521 .pep	130	140	150	160	170	
	RKALVEAQKMLSQARLAKGNNINHQEINALQSNVLDROQNIQALQRELGRMX					
	: : : : : : :					
g521	RKALTEAQKMLSQARLAKGNNINHQNALXSNVLDROQNIQALQRELGRMX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1475>:

a521 .seq

```

1  ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTCAAG

```

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```

51 CCCATTGGGT GCGAATGCGG CCAAATCTA CACCTGCACA ATCAACGGAG
1 01 AAACCGTTTA CACCACCAAG CCGTCCAAA GCTGCCTCTC AACCGATTG
1 51 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAACATC
2 01 CGAACCGACA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
2 51 CCCCAGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
3 01 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AACAGAATT
3 51 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CAAAAAATG TTATCACAAG
4 01 CACGTCTGGC AAAAGGCGGC AACATCAACC ATCAAGAAAT CAACGCATTG
4 51 CAAAGCAATG TATTGGACAG GCAGCAAAT ATCCAAGCAC TGCAAAGAGA
5 01 ATTGGGACGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1 MKSKLPLILI NFSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCLSTDL
51 PPIGNYSSE YIPPQTSEPT PSPSNGGQAV KYKAPVKTVS KPAKSNTPPP
1 01 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
1 51 QSVLDRQON IQALQRELGR M*

```

m521/a521 94.2% identity in 171 aa overlap

	10	20	30	40	50	60
m521.pep	MKSKLLILINFLISSPLGANAAXIXTCTINGETVYTKPSKSCHSTDLPPIGNYSSE					
a521	MKSKLPLILINFLISSPLGANAAXIYTCTINGETVYTTKPSKSCLSTDLPPIGNYSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVYKAPVKTVSKPAKSXTPPPQQAPSNNRRSILETELSNE					
	: :					
a521	YIPPQTSEPTSPSNGGQAVKYKAPVKTVSKPAKSNTPPPQQAPSNNRRSILETELSNE					
	70	80	90	100	110	120
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
a521	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1 atgactgagc cgaaacacga aacgccgacg gaagagcagg ttgccgcgcg
51 caaaaaagca aaagccaaaa tccgcaccat ccgcatttgg gcgtgggtca
101 ttttgcggtt gctcgcttca accgccctgc tctcccaatg cgcgatgtcc
151 aaaccgcagg caaaacagaa aattgtcgag tcttgcattga aaaatattcc
201 gtttgctgaa aaatggcaga acgatttgaa agcgcgcggc ttggatgcgg
251 acaatacccc tctcgccgtc gactactgca aatgtatgtg ggagcagcct
301 ttggacggat tgagcgagaa acagatcagc tccttcggca aactcgggtc
351 acaagaacag cttgacctgc tcggcgccgc aaacgcgttt gaaactcgag
401 acaacaatg tgcgcggat ttgaaagccg attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1 MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAM
51 KPQAKQKIVE SCMKNIPFAE KWQNDLKARG LDADNTRLAV DYCKCMWEQP
101 LDGLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1 ATGACTGAGC CGAAACACGA AATGCTGACG AAAGAGCAGG TTGCCGCGCG
51 CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTGCG GCGTGGGTCA
101 TTTTGGCGTT GCTCGCTTTA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
151 AAACCGCAGG CAAAACAGAA AATTGTCTGAG TCTTGCGTGA AGAATATTCC
201 GTTTGCCGAA AAATGGCAAA ACGATTGCGG GGCCCCGCGT TTAGATTCAA
251 ACAATACCCG CCTCGCCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT

```

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301 TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG
 401 ACAAGCAGTG TGTGCGGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMSKPQAKQKIVE
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKMWEQP
 101 LDRLSEKQIR SFGKLGAQEQ LDLLGGANAF EARDKQCVAD LKSE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng)

from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKMWEQPLDRLSEKQIRSFGLGAQEQ					
	: : :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKMWEQPLDGLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLLGGANAFEARDKQCVADLKSEX					
	: :					
g522	LDLLGGANAFETRDKQCVADLKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCG
 51 CAAAAAAGCA AAAGCCAAA TCCGCACCAT CCGCATTTGG GCATGGGTCA
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
 151 AAACCGCAGG CAAAACAGAA AATGTGCGAG TCTTGCGTGA AGAATATTCC
 201 GTTTGCCGAA AAATGGCAA ACGATTGCG GGGCCGCGGT TTAGATTCAA
 251 ACAATACCG CTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT
 301 TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG
 401 ACAAGCAGTG TGTGCGGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMSKPQAKQKIVE
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKMWEQP
 101 LDRLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKSE*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKMWEQPLDRLSEKQIRSFGLGAQEQ					
	: :					
a522	SCVKNIPFAEKWQNDLRARGLDSDNNTRLTVDYCKMWEQPLDRLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120

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```

                130      140
m522.pep      LDLLGGANAFEARDKQCVADLKSEX
                |||||:|||||
a522          LDLLGGANAFETRDKQCVADLKSEX
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1483>:

```

g523.seq
1   atgactgtat ggtttgttgc cgctgttgcc gtcttaatca tcgaattatt
51  gacgggaacg gtttatcttt tggttgtcag cgcggtcttg gcgggttcgg
101 gcattgccta cgggctgact ggcagcacgc ctgccgccgt cttgaccgcc
151 gCactgcttt ccgcgctggg catttggttc gtacatgcc aaaccgccgt
201 gggaaaagtt gaaacggatt catatcagga tttggatacc ggaaaatatg
251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt tttttatcgc
301 ggtacgcact ggcaggcgca aaatacgggg caggaagtgt ttgaaccggg
351 aacgcgcgcc ctcatcgctc gcaaagaagg taaccttctt atcatcgcaa
401 acccttaa

```

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>:

```

g523.pep
1   MTVWFVAAVA VLIIELLTGT VYLLVVSAA LAGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKAEILRYT GGNRYEVFVR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1485>:

```

m523.seq (partial)
1   ..GCCGTCCTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51  nAGCGCGGCT TTGGCGGGTT CGGGCATTGC TTACGGGCTG ACCGGCAGTA
101 CGCCTGCCGC CGTCTTGACC GncGCTCTGC TTCCGCGCT GGGTATTnG
151 TTCGTACACG CCAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTTGGAT GCCGACAAT ATGTCGAAAT CCTCCGACAC ACAGGCGGCA
251 ACCGTTACGA AGTTTTtTAT CGCGGTACGc ACTGGCAGGC TCAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACCTCG GCCCTCATG TCCGAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>:

```

m523.pep (partial)
1   ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDLD AGQYVEILRH TGGNRYEVFY RGTHWQAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF523 shows 91.3% identity over a 126 aa overlap with a predicted ORF (ORF 523.ng)

from *N. gonorrhoeae*:

m523/g523

```

                10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLTXALLSALGIXF
                |||||:|||||:|||||:|||||:|||||
g523          MTVWFVAAVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLTAALLSALGIWF
                10      20      30      40      50      60

                60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDL DAGQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
                |||||:|||||:|||||:|||||:|||||:|||||:|||||
g523          VHAKTAVGKVETDSYQDLDTGKYAEILRYTGGNRYEVFYRGTHWQAQNTGQEVFEPGTRA
                70      80      90      100     110     120

                120
m523.pep      LIVRKEGNLLIITHP
                |||||:|||||

```

g523 LIVRKEGNLLIIANPX
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

a523.seq
1 ATGACTGTAT GGTTCGTTGC CGCTGTTGCC GTCTTAATCA TCGAATTATT
51 GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTTGGTTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401 AACCTTAA

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

a523.pep
1 MTWVFVAAVA VLIIELLTGT VYLLVSAAL AGSGIAYGLT GSTPAAVLTA
51 ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GQYAEILRHA GGNRYEVFYR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*

m523/a523 94.4% identity in 126 aa overlap

	10	20	30	40	50
m523.pep	AVLIIELLTGTVYLLVSAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF				
a523	MTWVFVAAVAVLIIELLTGTVYLLVSAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523.pep	VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
a523	VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
	70	80	90	100	110
	120				
m523.pep	LIVRKEGNLLIITHPX				
a523	LIVRKEGNLLIIAKPX				
	130				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

g525.seq
1 atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca
51 agcggcggtt gccgaaatgg ttcaaatacga aggcggcagc taccgcccgc
101 tttatctgaa aaaagatacc ggcctgatta aagtcaaacc gttcaaactg
151 gataaatatc ccggtaccaa tgccgagttt gccgaatttg tcaacagcca
201 ccccaaatgg caaaaaggca ggatcggttc caaacaggca gaaccgctt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggcgaattga aacagccggt taccaatatt tcctgggttg ccgccaacgc
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcttccgcc acgcagaaaa aacggctcaa acgaaccggg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc
501 tgcacgatgt cggcaagca ccgccgaac tactgggggtg tttatgatat
551 gcacgggctg a

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

g525.pep
1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQKRLPTID EWEFAGLASA TQKKRLKRTR
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

790

m525.seq

```

1 ATGAAGTATG TCCGGTTATT TTWCCTCGGC GCGGCACTCG cCrrCACTCA
51 ArCGGCGGCT GcCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCrC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGc GCCGAAGgCG
301 GgCGAATTAA AACAACCGGT AACCAATGTT TCCTGGWTTG CCGCCAACGC
351 CTAtTGC GCCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA A.CGGCTCAA ACGAACCCGG
451 CTACAACCGC ACTATTCTCG ATTGGTATGC CGACGGCGGA CGGAAAGGCC
501 TGCACGATGT CGGCA.AAGG CCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:

m525.pep

```

1 MKYVRLFXLG AALAXTQXAA AEMVQIEGGS YRPLYLKKDT GLIKVPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVTNV SWXAANAYCA AQGKRLPTID EWEFAGLASA TQXRLKRTR
151 LQPHYSRLVC RRRTERPARC RXKAARTTGA FMICTG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng)

from *N. gonorrhoeae*:

m525/g525

	10	20	30	40	50	60
m525.pep	MKYVRLFXLG AALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVPFKLDKYPVTNAEF					
	:					
g525	MKYVRLFFLG TALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVPFKLDKYPVTNAEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m525.pep	AEFVNSHPQWQKGRIGSKQAEPAAYLKHWMKNGSRSYAPKAGELKQPVTNVSWXAANAYCA					
g525	AEFVNSHPQWQKGRIGSKQAEPAAYLKHWMKNGSRSYAPKAGELKQPVTNISWFAANAYCA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m525.pep	AQGKRLPTID EWEFAGLASATQKXRLKRTRLQPHYSRLVCRRRTERPARCRXKAARTTGA					
g525	AQGKRLPTID EWEFAGLASATQKXRLKRTRLQPHYSRLVCRRRTERPARCRQSTARTTGV					
	130	140	150	160	170	180
	FMICTGX					
m525.pep	FMICTGX					
g525	FMICTGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1493>:

a525.seq

```

1 ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGGATTTAA AACAACCGGT AACCAATGTT TCCTGGTTTC CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAG.AAA AACGGCTCAA ACGAACCCGG
451 CTACAACCGC ACTATTCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC
501 TGCACGATGT CGGCAAAG.G TCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
1  MKFTRLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKQPVTNV SWFAANAYCA AOGKRLPTID EWEFAGLASA TQXKRLKRTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

      10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
          ||::||: | ||| | ||||| ||||| ||||| ||||| ||||| |||||
a525      MKFTRLFLCAALAGTQAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
          10      20      30      40      50      60

      70      80      90      100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNVSWXAANAYCA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
          70      80      90      100     110     120

      130     140     150     160     170     180
m525.pep  AOGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCRRTTERPARCRXKAARTTGA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AOGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCRQXVARTTGA
          130     140     150     160     170     180

m525.pep  FMICTGX
          ||||
a525      FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
1  ATGAAGTACG TCCGGTTATT TTTCCTCGGC ACGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGGAATGTA AACAGCCGGT TACCAATATT TCCTGTTTGG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCCGACT TGCTTCCGCC ACGCAGAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAGACC GCCCGAATA CTGGGGTGT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTCG AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAATATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAACT TGGGCTTCCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
1  MKYVRLFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AOGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKDRPNYGV YDMHGLIEW TEDFNSLLS
201 SGNANAQMF C SGASVGASD S NYAAFLRYG IRTSLQSKYV LHNLFRCAS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
1  ATGAAGTATG TCCGGTTATT TTTCCTCGGC GCGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```

```

151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCC CAATGG CAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTCCGCC ACGCAGAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGGCC GCCGAACTA CTGGGCGT TATGATATGC
551 ACGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```

1 MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKGRPNYWG YDMHGLIEWE TEDFNSSLSS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/g525-1 97.6% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL DKYPVTNAEF					
g525-1	MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL DKYPVTNAEF					
	10	20	30	40	50	60
m525-1.pep	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKAGELKQPVTV SWFAANAYCA					
g525-1	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKAGELKQPVTV SWFAANAYCA					
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKAGELKQPVTV SWFAANAYCA					
g525-1	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKAGELKQPVTV SWFAANAYCA					
	70	80	90	100	110	120
m525-1.pep	AQGKRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYADGGKRLHDV GKGRPNYWG					
g525-1	AQGKRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYADGGKRLHDV GKGRPNYWG					
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYADGGKRLHDV GKGRPNYWG					
g525-1	AQGKRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYADGGKRLHDV GKGRPNYWG					
	130	140	150	160	170	180
m525-1.pep	YDMHGLIEWE TEDFNSSLSS SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV					
g525-1	YDMHGLIEWE TEDFNSSLSS SGNANAQMFC SGASVGSADS SNYAAFLRYG IRTSLQSKYV					
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWE TEDFNSSLSS SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV					
g525-1	YDMHGLIEWE TEDFNSSLSS SGNANAQMFC SGASVGSADS SNYAAFLRYG IRTSLQSKYV					
	190	200	210	220	230	240
m525-1.pep	LHNLGFRCTSRX					
g525-1	LHNLGFRCA SRX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

m525-1.seq

```

1 ATGAAGTTA CCCGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCGCG
101 TTTATCTGAA AAAAGATACC GGCTTGATTA AAGTCAAACC GTTCAAAC TG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCC CAATGG CAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTCCGCC ACGCAGAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GATGGCGACC GGAAAGACCT
501 GCACGATGTC GGCAAAGGTC GCCGAACTA CTGGGCGT TATGATATGC
551 ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCG TTGCACAAGC
751 CGATAA

```


This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1 MKF*TRLLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51 DKY PVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDL KQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNR TILDWYA DGRKDLHDV GKGRPNYWGV YDMHGLIEWE TEDFNSSLLS
201 SGN ANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/a525-1 97.2% identity in 251 aa overlap

```

              10      20      30      40      50      60
m525-1.pep  MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
a525-1      MKFTRLLFLCAALAGTQAAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
              10      20      30      40      50      60

              70      80      90      100     110     120
m525-1.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNVSWFAANAYCA
a525-1      AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
              70      80      90      100     110     120

              130     140     150     160     170     180
m525-1.pep  AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWGV
a525-1      AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGDRKDLHDVGKGRPNYWGV
              130     140     150     160     170     180

              190     200     210     220     230     240
m525-1.pep  YDMHGLIEWETEDFNSSLLSSGNANAMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV
a525-1      YDMHGLIEWETEDFNSSLLSSGNANAMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV
              190     200     210     220     230     240

              250
m525-1.pep  LHNLGFRCTSRX
a525-1      LHNLGFRCTSRX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1 atgggttttac cagtctcctt ttttcagcct gtccagttgg cggcgggtcgc
51 gcttggtcgg tctgccgtcg ggatgggcgg aagtgatgcg gctgaattgg
101 tcgagctggt tgcactcttc cctcaatgct gccgttttcg cgtcttcttc
151 atacagaagc cgcgccctcg gtgccgggcg gcgttggtgg ttcaaacctt
201 taaccttgat tttatgggga agggaattga gcgtcaggtc gataatateg
251 ccgatgtcta tggttttact gtttttgact ttcgagccgt ttacttgaac
301 cctacccagt tcgatatgct tttgcgcaag ggaacggggtc ttgaaaaaac
351 gtgccgccca aagccatttg tccagccgca tggcggaaga atcgtgcttg
401 tctttcatac gattttggtt gaaataattg aatttgtttc gagtttagca
451 taa

```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1 MVLVPSFFQP VOLAAVALGR SAVGMGGSDA AELVELFALF PQCCRFRVFF
51 IQKPRLLGCRA ALVVQTFNLD FMKGIERQV DNIADVYGFT VDFRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1 ATGGT TTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTGCG
51 GCTTG GTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAG CTGTT TGCCTCTTTC CCTCAATGTT GCCGTTWTCG CGTCTCTTTC
151 ATACAG AAGC CGCGCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT

```

794

```

2 01 TAACCKTGAT TTTATAGGGA AGGG.AATtk AgCkTCaGty GrTwATaTCG
2 51 CsGATGTmTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC
3 01 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
3 51 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
4 01 TCTTTCATAC GATTTGTTT GAAATAATTG AATTGTTTC GAGTTAGCA
4 51 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

```

m527.pep
1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVL
51 IQKPRXGCRA ALVVQTFNLD FIGKXNXASV XXIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVLFIQKPRXGCRA					
g527	MVLPSVFFQP VQLAAVALGR SAVGMGGSDA AELVELFALF PQCCRFRVFFIQKPRLGCR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m527.pep	ALVVQTFNLD FIGKXNXASV XXIADVYGFT VFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
g527	ALVVQTFNLD FMGKIERQVDNIADVYGFT VFDLRAVYLNPTQFDMLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLA					
g527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLA					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

```

a527.seq
1 ATGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTGCG
51 GCTTGGTCCG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TCGGCTCTTC CCTCAATGTT GCCGTTTTCG CGTCTCTTTC
151 ATACAGAAGC CGCGCTCCG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
251 CCGATGTCTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTGTTT GAAATAATTG AATTGTTTC GAGTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

```

a527.pep
1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVL
51 IQKPRLGCR ALVVQTFNLD FIGKIERQV DNIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

m527/a527 93.3% identity in 150 aa overlap

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVLFIQKPRXGCRA					
a527	MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLFIQKPRLGCR					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m527.p ep	ALVVQTFNKFDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
a527	ALVVQTFNLDFIGKGIERQVDNIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.p ep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaattc  gggttaataaa  atatacggca  acggctgcgt  tgtttgcatt
51  tacggttgca  ggctgccggc  tggcgggggtg  gtatgagtgt  ttgtccttgt
101 cggctggtg  taagccgaga  aaacctgccg  ccatcgattt  ttgggatatt
151 ggcggcgaga  gtccgctgtc  tttagaggac  tacgagatac  cgctttcaga
201 cggcaatcgt  tccgtcaggg  caaacgaata  tgaatccgag  caaaaatctt
251 acttttatag  gaaaataggg  aagtttgaag  cctgcgggtt  ggattggcgt
301 acgcgtgacg  gcaaaccttt  ggttgagagg  ttcaaacagg  aaggtttcga
351 ctgtttgga  aagcaggggt  tgcggcgcaa  cggcctgtcc  gagcgcgtcc
401 gatggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA  TAALFAFTVA  GCRLAGWYEC  LSLSGWCKPR  KPAAIDFWDI
51  GGESPLSLED  YEIPLSDGNS  SVRANEYESA  QKSYFYRKIG  KFEACGLDWR
101 TRDGKPLVER  FKQEGFDCLE  KQGLRRNGLS  ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAAATTC  GGGCAATAAA  ATATACGGCA  ATGGCTGCGT  TGCTTGCAAT
51  TACGGTTGCA  GGCTGCCGGC  TGGCGGGGTG  GTATGAGTGT  TCGTCCCTCA
101 CCGGCTGGTG  TAAGCCGAGA  AAACCGGCTG  CCATCGATT  TTGGGATATT
151 GCGGCGGAGA  GTCCGCCGTC  TTTAGGGGAC  TACGAGATAC  CGCTTTCAGA
201 CGGCAATAGT  TCCGTCAGGG  CAAACGAATA  TGAATCCGCA  CAACAATCTT
251 ACTTTTACAG  GAAAATAGGG  AAGTTTGAAG  C.TGCGGGCT  GGATTGGCGT
301 ACGCGTGACG  GCAAACCTTT  GATTGAGACG  TTCAAACAGG  GAGGATTTGA
351 CTGCTTGGA  AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA  MAALLAFTVA  GCRLAGWYEC  SSLTGWCKPR  KPAAIDFWDI
51  GGESPPSLGD  YEIPLSDGNS  SVRANEYESA  QKSYFYRKIG  KFEACGLDWR
101 TRDGKPLIET  FKQGGFDCLE  K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

m528/g528

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
g528	MEIRVIKYTATAALFAFTVAGCRLAGWYECLESLSGWCKPRKPAAIDFWDIGGESPLSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
g528	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLVERFKQEGFDCLE					
	70	80	90	100	110	120

m528.pep K
 |
 g528 KQGLRRNGLSERVRW

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1511>:

a528.seq
 1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
 51 TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
 1 01 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATT TTGGGATATT
 1 51 GGCGGCGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
 2 01 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
 2 51 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
 3 01 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
 3 51 TTGTTTGAAA AAGCAGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
 4 01 GATGGTAA

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

a528.pep
 1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
 51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
 1 01 TRDGKPLIET FKQEGFDCLK KQGLRRNGLS ERVRW*

m528/a528 95.0% identity in 121 aa overlap

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
a528	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLK					
a528	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLK					
	70	80	90	100	110	120

m528.pep K
 |
 a528 KQGLRRNGLSERVRW
 130

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1513>:

g528-1.seq
 1 ATGGAAATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCATT
 51 TACGGTTGCA GGCTGCCGGC TGGCGGGTG GTATGAGTGT TCGTCCCTGT
 101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATT TTGGGATATT
 151 GGCGGCGAGA GTCGCTGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
 201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAAATCTT
 251 ACTTTTATAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
 301 ACGCGTGACG GCAAACCTTT GGTGAGAGG TTCAAACAGG AAGGTTTCCA
 351 CTGTTTGAA AAGCAGGGT TCGGCGCAA CGGCCTGTCC GAGCGCGTCC
 401 GATGGTAA

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>:

g528-1.pep
 1 MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
 51 GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
 101 TRDGKPLVER FKQEGFDCLK KQGLRRNGLS ERVRW*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1515>:

m528-1.seq
 1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT

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```

51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GGC GGC GAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGAA AAGCAGGGGT TCGCGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAIDFWDI
51  GGESPPSLGD YEIPLSDGNS VRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLK KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

	10	20	30	40	50	60
g528-1.pep	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAIDFWDIGGESPLSLED					
	: : : : : : : : : : :					
m528-1	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAIDFWDIGGESPPSLGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g528-1.pep	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLK					
	: : : : : : : : : : :					
m528-1	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLK					
	70	80	90	100	110	120
	130					
g528-1.pep	KQGLRRNGLSERVRWX					
	:					
m528-1	KQGLRRNGLSERVRWX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1  ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GGC GGC GAGA GTCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGCGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAIDFWDI
51  GGESPPSLED YEIPLSDGNS VRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLK KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

	10	20	30	40	50	60
a528-1.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAIDFWDIGGESPPSLED					
	: : : : : : : : : : :					
m528-1	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAIDFWDIGGESPPSLGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a528-1.pep	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLK					
	: : : : : : : : : : :					
m528-1	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLK					
	70	80	90	100	110	120
	130					
a528-1.pep	KQGLRRNGLSERVRWX					
	:					
m528-1	KQGLRRNGLSERVRWX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

```
g529.seq (partial)
1 atgacccata tcaaacccgt cattgccgcg ctgcactca tcgggcttgc
51 cgctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101 ggctgcaccg cctgatcaaa ctggaagtcc cgctgattt gaacaacccc
151 gaccaaggca acctctaccg cctgcctgcc gggtcgggag ccgtccgcgc
201 cggggatttg gaaaaacgcc gcacaccgc cgtccaacag ccagcggatg
251 ccggaagtat tgaaaagcgt caaaggcgtc cgcttcgagc ggcgacggca
301 gccaacgcct ggcttgtcgt tgacggcaaa tccccgcgc aaatctccgc
351 cgctttctg.
```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

```
g529.pep (partial)
1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101 ANAWLVVDGK SPAEISAAF..
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

```
m529.seq
1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTGCGACCG CCTGATCAAA CTGAAGTCC CACCTGATT GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGCGAGC
301 CAACGCTGGC TCGTTGTGCG CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
451 CCCCAAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501 CTACTCCACC GCGGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGTTGGC
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GGCGCACCGT GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGTCAA AACACCGAAC GCCACGCCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAATTACC GAACAAAAAC CCGGCCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTGCGCA ACGGCTCGCG CATCGTCCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGCG AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

```
m529.pep
1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PDAEVLKSV KGVRLERDGS
101 QRWLVDGKS PAEIWPLLKA FWQENGFDIK SEEPAIGQME TEWAENRAKI
151 PQDSLRLRFD KVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGKDKDTTV WQSPSPDPNL EAAFLTRFMQ YLGVDGQQA NASAKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRTVLAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPGLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

```

10      20      30      40      50      60
g529.pep  MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
```

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```

m529      |||||
           MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
           10      20      30      40      50      60

           70      80      90      100     110     120
g529.pep   GSGAVRAGDLEKRRTPAVQQPADAGSIEKRQRRLRAATAANAWLVVDGKSPAEISAAFX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m529      GSGAVRASDLEKRRTPAVQQPADAIEVLKSVKGVRLER-DGSQRWLVDGKSPAEIWPLLK
           70      80      90      100     110

m529      AFWQENGFDIKSEEPaIGOMETEWAENRAKIPQDSLRLRLFDKVLGGIYSTGERDKFIVR
           120     130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1523>:

```

a529.seq
1   ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51  CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTCGCACCG CCTGATCAAA CTCGAAGTCC CACCTGATT TTAACAACCC
151 GACCAAGGCA ACCTCTACCG CCTGCCGCGC GGTTCCGGCG CCGTCCGCGC
201 CAGCGATTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTCTG CCGCAAGTCT CATGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG TGCCAAATC
451 CCCCAGACA GCTTGCGCCG CCTATTGAC ACAGTCGGT TGGCGGCAT
501 CTACTCCACC GCGGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCGTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGGGCG
701 TTGACGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GGCGCACCGC GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAC CCGGCTTGT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCCGAG CCTGTGCGCA ACGGCTCGCG CATCGTCTG
1051 CTAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAACCT CATTCCGAAC TGCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1524; ORF 529.a>:

```

a529.pep
1   MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51  DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PDAEVLKSV KGVRLERDGS
101 QRWLVDGKS HAEIWPLLKA FWQENGFDIK SEEPaIGOME TEWAENRAKI
151 PQDSLRLRLFD TVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGKDKDTTV WQSPSPDPNL EAAFLTRFMQ YLGVDDGQAE NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRALAL DRIGLTVVGQ NTERHAFIVQ
301 KAPNESNAVT EQKPLFKRL LGKGKAEPKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELK*

```

m529/a529 99.2% identity in 375 aa overlap

```

           10      20      30      40      50      60
m529.pep   MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a529      MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
           10      20      30      40      50      60

           70      80      90      100     110     120
m529.pep   GSGAVRASDLEKRRTPAVQQPADAIEVLKSVKGVRLERDGSQRWLVDGKSPAEIWPLLKA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a529      GSGAVRASDLEKRRTPAVQQPADAIEVLKSVKGVRLERDGSQRWLVDGKSHAEIWPLLKA
           70      80      90      100     110     120

           130     140     150     160     170     180

```

800

```

m529.pep  FWQENGFDIKSEEPaIGOMETEWAENRAKIPQDSLRLRLFDKVLGGIYSTGERDKFIVRI
a529      FWQENGFDIKSEEPaIGOMETEWAENRAKIPQDSLRLRLFDTVLGGIYSTGERDKFIVRI
           130      140      150      160      170      180

           190      200      210      220      230      240
m529.pep  EQGKNGVSDIFFAHKAMKEVYGGKDKDITVWQPSPSDPNLEAAFLTRFMQYLGVGQQQAE
a529      EQGKNGVSDIFFAHKAMKEVYGGKDKDITVWQPSPSDPNLEAAFLTRFMQYLGVGQQQAE
           190      200      210      220      230      240

           250      260      270      280      290      300
m529.pep  NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTVLALDRIGLTVVGQNTERHAFLVQ
a529      NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTALALDRIGLTVVGQNTERHAFLVQ
           250      260      270      280      290      300

           310      320      330      340      350      360
m529.pep  KAPNESNAVTEQKPGLFKRLLGKGKAEKPAEQPELIVYAEPVANGSRIVLLNKDGSAYAG
a529      KAPNESNAVTEQKPGLFKRLLGKGKAEKPAEQPELIVYAEPVANGSRIVLLNKDGSAYAG
           310      320      330      340      350      360

           370
m529.pep  KDASALLGKLHSELRX
a529      KDASALLGKLHSELRX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1  atgagtgcga ggcgggcaat gacgggtttg atatgggtca tcgtgtcatc
51 ctgtgtgatg gatattaaag tgtttgcgat gttatgccgt ccgaacggtt
101 cagacggcat ggctatatatt aaagtgtgcc tgaggctttc agggcggcgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgcacg
201 tgcggtccgc atccgcccaa ggcggatacc gccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgtcgtaaat cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1  MSASAAMTGL IWVIVSSCVM DIKVFVMLCR PNGSDGMAIF KVVLRLSGRR
51  GLLPVRLPSA ERAAGARAVR IRPRRIPPIS VRRDWVRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1  WTGAGTGCGA GCGCGGCAAT GACGGGTyTG ATATGGGTCA TCGTGTATC
51  sTGTGTGATG GATATTAAAG TGtyTGTTC GwTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTkTTGC WTGTCCGTTT yCCGTCAGCG GAACGAGCGG CAGGCGGACG
201 TCGGGTTCGC ATCTGCCCAg GCGGATACC GCCATTTCG GTGCGGCGGG
251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT CGGTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1  XSASAAMTGL IWVIVSSCVM DIKVXVAXCR PNGSDGMXIF KVVLRLSGRR
51  GLLXVRFPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRTW CRKSESVGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

m530/g530

```

m530.pep  XSASAAMTGLIWVIVSSCVM DIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA 60
          |||

```


g530	MSASAAMTGLIWVIVSSCVMDIKVFVMLCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA	60
	10 20 30 40 50 60	
m530 . pep	ERAAGGRAVRICPGRIPPISVRRGWVRTWCRKSESVGR	99
	: : : :	
g530	ERAAGARAVRIRPRRIPPISVRDWRVRTWCRKSESAGR	99

```
a530.seq
1   ATGAGTGCGA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTATC
51  CTGTGTGATG GATATTAAAG TGTTTGTTGC GTTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTTTTGC CTGTCGCCTT TCCGTACGCG GAACAGCGCG CAGGCGGACG
201 TGCGGTTCGC ATCTCGCCAC GCCGATACCC GCCCATTCG GTGCGCGGCG
251 GCTGGGTTCC CAGAACATGG TGTCTAAAT CGGAATCAGC CGGTCTTTGA
```

a530.pep
1 MSASAAMTGL IWVIVSSCVM DIKFVVALCR PNGSDGMAIF KVLRLSGRR
51 GLLPVRLPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESAGR*

```

              10      20      30      40      50      60
m530 . pep  XSASAAMTGLIWVIVSSCVM DIKVXVAXCRPN GSDGMXIFKVVLRLSGRRGLLXVRFPSA
             |||||
a530        MSASAAMTGLIWVIVSSCVM DIKV FVALCRPN GSDGMAIFKVVLRLSGRRGLLPVRLPSA
              10      20      30      40      50      60

              70      80      90     100
m530 . pep  ERAAGGRAVRI CPGRIPPISVRRGWVRRTWCRKSESVGRX
             |||||
a530        ERAAGGRAVRI CPGRIPPISVRRGWVRRTWCRKSE SAGR X
              70      80      90     100

```

```
g531.seq
  1  ATGACCGCCC TACTCGTCAT CCTCGCCCTC GCCCTGATAG CGGTCGGCAC
51  GGCAGGCATC GTCTATCCCG CCCTGCCCGG CTTGGCATTG ATGTTTGCCG
101 GAACATGGCT GCTTGCCCTAT GCCGGCGGCT ATCAAATCTA CGGCGCAGGC
151 ATCTTGTGGA CGGTCGGACT CATCAGCCTT GGCGGCATAC TGGCGGACTA
201 TATGGCAGGC ATGTTGGGGG TAAAATACAC TGGGGCAGGC AAATCGCCG
251 TCCGAGGTGC ATTGGCCCGC AGCATCATCG GCATATTTTT CTCCCTTCCC
301 GGACTAATAC TCGGCCCTTT TATCGGCGCG CGGCAGGGC AACTGATCGA
351 TCGGCGCAAT ATGCTTCAGG CAGGTAAGC GGGCTTGGGT ACGCTGTTGG
401 GGCTTGTCGT CGGCACGGCG TTCAAATCG GCTGCGCCGT ATCCATCTTG
451 TTTATCCTGT TGGTGAAATA CATCGCATAC CTGTTTTAA
```

g531.pep

1	<u>MTALLVILAL</u>	<u>ALIAVGTAGI</u>	<u>VYPALPGLAL</u>	<u>MFAGTWLLAY</u>	<u>AGGYQIYGAG</u>
51	<u>ILWTVGLISL</u>	<u>GGILADYMag</u>	<u>MLGVKYTGAG</u>	<u>KLAVRGALAG</u>	<u>SIIGIFFSLP</u>
101	<u>GLILGPFPIA</u>	<u>AGELIDRRN</u>	<u>MLQAGKAGLG</u>	<u>TLLGLVVGTA</u>	<u>FKIGCAVSIL</u>
151	<u>FILLVKYIAY</u>	<u>LF</u>			

```
m531.seq
  1  ATGACCGTAC TGACCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
 51  GGCGGGCATC GTTTaCCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGCCG
101  GAACATGGCT GCTTGCCCTAT GCCGGCGGCT ACCAAATCTA CGGCGCGGGC
151  GTTTTGTTGA CGGTCGGACT CATCAGCCTT GCCGGCATA TGGCGGACTA
201  TTGCGCAGGC ATATGGGGGA CAAAATATAC CGGAGCGGGC AAGCTCGCCG
251  TTCGCGCGCG ATTGGCCGGC AGCATCATCG GCATATTTTT CTCCTTCCC
301  GGACTAATAC TCGGTCCCTT TATCGGCGCG CGCGCAGGCG AACTGATCGA
```


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```

a531      |||||||
          AGILADYVAGIWGKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFFIGAAAGELIERRN
          70      80      90      100     110     120

          130      140      150      160
m531. pep  MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          |||||||
a531      MLQAGKAGLGTLLGLIVGTAFAKIGCAVSILFILLVKYIAYLFX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaaa acaggcggat tcgectgatt tgggtgtacgg
51  tttggaagac aggccgccgt tcgtaatgc gctcttgagc gcggttaccc
101 atcttttggc gattttcgtg ccgatgatta cggccgcgct gattgtgggc
151 ggccgcgctgg aattgccggt ggagatgacg gcgtatctgg tgcgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcaggtaaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSMAMVA SGVGTYLQVN RFGSVGSGML SIQRYRHDCA
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTCTG GCACCTATTG GCAGGTCAAC CGCTTCGGGC
251 CGGTGCGGTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTCTGT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTT
401 TGGTGTGTTT CTCGCGGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGGCATT ACCGATTTCT GCGGCGGCTT CCGCGCGAAG CCGGACGGCA
551 CGTTGCGGTC GATGAAAAAC TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCCG CTGTGCGCA TGAGCGGCAT
651 TGCGGTCGGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTTAAATACG GTTTTGCTTT CGACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCCTG
901 CGCGGCGGCG TGTTCGCTGA CCGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTTCGCTG CCGCTGACGA CGTTTGCGCA AAACAACGGC GTGATTCAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTGGT CCGCGGTTTA CGACGATTC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTCCGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCG CCGCGAAGCG
1201 TCGATTGCGG CAACGTCGGT CCGTTTGGGC TTGGGTGTCTG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSMAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVF GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```

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201 VLVFNCKMNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLFPV
 251 FKYGFAFDWH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEYTKRL
 301 RGGLVADGLV SVIATAGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
 351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRRREA
 401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
 451 EAAVKFDTDH LEH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF532 shows 91.4% identity over a 93 aa overlap with a predicted ORF (ORF 532.ng) from *N. gonorrhoeae*:

g532/m532

	10	20	30	40	50	60
g532.pep	MAETMKKQADSPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	: :					
m532	MSGQLGKGADAPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	
g532.pep	AYLVSMAMVASGVGTYLQVNRFGSVGSGMLS IQRYRHDCARRGDERGRFEX					
m532	AYLVSMAMVASGVGTYLQVNRFGVPVSGMLS IQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

a532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAGGAT AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTGCGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT CTCGTTCTGT
301 ACCGTCATGA TTGCGCTCGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT TTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGTGTGGT GGTGATGCTG ATCGGCTTGA GTTTGGTACA
501 CGTCGGTATT ACCGATTTCC GCGGCGGCTT CCGCGCAAAG GCGGACGGCA
551 CGTTGCGGCTC GATGGA AAAAC TTGGGGCTGG CATCGCTGGT GCTGCTGATT
601 GTGCTGGTGT TCAATTGCAT GAAAAACCCG CTGCTGCGGA TGAGCGGCAT
651 TGCGGTCGGT CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC GGCAGTCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTTAAATATG GTTTTGCTTT TGA CTGGCAC GCATTTATTG TGGCGGGTGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTG ACGGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGCGG AGGAATACAC CAAACGCTTG
901 CGCGGCGGCG TGTGGCGGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTTCGCTG CCGCTGACGA CGTTTGACAA AAACAACGGC GTGATTACAG
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGA CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTCCGG TTGATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGCCACG GCATCCGCAG GCGCGAAGCG
1201 GTAATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTGCG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAACTCTT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1542; ORF 532.a>:

a532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSMAMVA SGVGTYLQVN RFGVPVSGML SIQSVNFSFV

```

```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
251 FKYGFAFDWH AFIVAGAI FL SVFEAVGDL TATAMVSDQP IEIEEEYTKRL
301 RGGVLADGLV SVIATAGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA
401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

m532/a532 100.0% identity in 463 aa overlap

	10	20	30	40	50	60
m532.pep	MSGQLGKGADAPDLVYGLDRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
a532	MSGQLGKGADAPDLVYGLDRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m532.pep	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
a532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m532.pep	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK					
a532	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m532.pep	ADGTFGSMENLGLASLVLLIVLVFNCMKNP LLRMSGIAVGLIAGYIVALFLGKVDFSALQ					
a532	ADGTFGSMENLGLASLVLLIVLVFNCMKNP LLRMSGIAVGLIAGYIVALFLGKVDFSALQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m532.pep	NLPLVTLVPVFKYGFADWHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL					
a532	NLPLVTLVPVFKYGFADWHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m532.pep	RGGVLADGLVSVIATAGSLPLTTFAQNNGVIQMTGVASRHVGKYIAVILVLLGLFPVVG					
a532	RGGVLADGLVSVIATAGSLPLTTFAQNNGVIQMTGVASRHVGKYIAVILVLLGLFPVVG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m532.pep	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF					
a532	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF					
	370	380	390	400	410	420
	430	440	450	460		
m532.pep	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX					
a532	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

g535.seq

```

1  atgccctttc ccggttttcag acaantat ttt gcttngtct tgcacggtt
51  ttttgccgta ggtcggattc tcgaatccga catttccaac agcgggtttt
101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatttaca tcgcttccaa ttgcgaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagttga tggtcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttgcggc tgtttgaagt

```

806

```

3 51 catcgatgat tttgtcccgt tgtacggtgg tttggcgcgt gttgccgtag
4 01 ctgtcgaagg cgggtttttt gacggacagg tagtgcaata cttctggcgg
4 51 gatttcttcg acgaagcggg atgcatgccc gaattgggtt tgtccgtgca
5 01 gcatgcggtt gtgtgccatg gtgatgtaga ggcgtttgag ggcgcgggtg
5 51 atggcgacgt acatgaggcg gcgttcttct tcgaggccgc cgcgctcggc
6 01 aaggctcatt tcgctgggga aacgcccctc ttccataccg gtgaggaaga
6 51 cggcggtgaa ttccaagcct ttggcggcgt ggacggtcat cagttggacg
7 01 gctttttcgc ctgcccctgc ttggttttcg ccggattcga gggcggcgtt
7 51 gctcaagaag gcgaggatgg ggaaggcggg atcgtctga

```

This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:

g535.pep

```

1 MPFPVFRQXF AXSLLRFFAV GRILESDISN SGFSETINAS NVFFVGYEYP
51 ACISNLHRFQ FRKLGIQFFH ALFAEVDGQS GGFAFVCGID NHAGAEFGVT
1 01 DVLSDAEACV GLRLFEVIDD FVPLYGGLAR VAVAVEGGFF DQVQVQYFWR
1 51 DFFDEAGCDA ELGLSVQHAL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
2 01 KAHFAGETPL FHTGEEDGVE FQAFGGVDGH QLDGFFACPC LVFAGFEGGV
2 51 AQEGEDGEGG IV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1545>:

m535.seq

```

1 aTGCCCTTtC CCGTTTTTCAG ACGGCCTTTT GCTTTGTCTT TACTtACGTT
51 TTTTGCCGTA AGTCAGATTC TTGTATCCGA CATTTCACAC AGCGGTGTTT
1 01 CGGAAACAAT AGACGCGTCA AATGTTTTTG TCGGATACGA ATATCCGACC
1 51 TACATTTCAA ATTTACATCT CTTCCAATTT CGCAAACCTG GTGTCCAAC
2 01 CTTTCACGCC CTGTTTGCCG AAATTGATGG TCAGTCGGGC GGATTGCGCT
2 51 TTATCTGCGG CATCGATAAT CACGCCGGTG CCGAATTGG CGTGGCGGAC
3 01 GTTTTGTCCG ATACGGAAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
3 51 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GCGCGGTGTT GCCGTAAC
4 01 TCGTAGGCAG GCTTTTTGAC GGACAGGTAG TGCAATACTT CGGGTGGGAT
4 51 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCAGCA
5 01 TGCGTTGTTG CGCCATGGTG ATGTAGAGGC GTTTGCGGGC GCGGGTGATG
5 51 GCGACGTACA TGAGGCGGCG TTCTTCTTCG AGGCCGCCGC GTTCGGCAAG
6 01 GCTCATTTTC CTGGGGAAGC GGCCTTCTTC CATGCCGGTG AGGAAGACGG
6 51 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGGTCATGAG TTGGACGGCC
7 01 TTTTCGCCTG CGCCTGCCTG GTTTTCACCG GATTGAGGG CGGCATTGCT
7 51 TAGGAAGGCG AGAATGGGGA AGGCGGGGTC GTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:

m535.pep

```

1 MPFPVFRPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
51 YISNLHLFQF RKLGVQLFHA LFAEIDQSG GFAPICGIDN HAGAEEFGVAD
1 01 VLSDETTCVG LGLFVVVDDF IFGCGGLARV AVTVVGLRFD GQVQYFQWD
1 51 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFEAAAFGK
2 01 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
2 51 XEGENGEGGV V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

m535/g535

```

          10      20      30      40      50      59
m535.pep  MPFPVFRPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ
          |||||: || ||| ||||: || ||||| ||||: ||||| |||||: ||||| ||
g535      MPFPVFRQXFAXSLLRFFAVGRILESDISNSGFSETINASNFFVGYEYPACISNLHRFQ
          10      20      30      40      50      60

          60      70      80      90     100     110     119
m535.pep  FRKLGVLQFHALFAEIDQSGGFAPICGIDNHAGAEFGVADVLSDETTCVGLGLFVVDD
          |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: ||
g535      FRKLGIQFFHALFAEVDGQSGGFAPVCGIDNHAGAEFGVTDVLSDAEACVGLRLFEVIDD
          70      80      90     100     110     120

```

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	120	130	140	150	160	170	179
m535.pep	FI FGCGGLARVAVTVVGR LFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFA						
	: : :						
g535	FVPLYGGLARVAVAVEGGFFDGQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHLDGLFACAC						
	: : : :						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVVEFQAFGGVDGHQLDGGFFACPC						
	190	200	210	220	230	240	
	240	250	260				
m535.pep	LVFTGFEGGIA XE GENGEGGVV						
	: :						
g535	LVFAGFEGGVAQEGEDGEGGIV						
	250	260					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1547>:

a535.seq (partial)

1	TT	CAGACGGC	CTTTTGCCTT	GTCCTTGCTA	CAGTTTTTTG	CCATAGGTCG
51	GAT	TCTCGAA	TCCGACATTT	CCAACAGCGG	TTTTTCGGAA	ACGATAGACG
101	CGT	CAAATAT	TTTTGTCGGA	TACGAGTATC	CAGCCTGCAT	TTCAAATTTA
151	CAT	CGCTTCC	AATTTTCGAA	ACTTGGTGTC	CAACTCTTTC	ACGCCCTGTT
201	TGCC	GAAATT	GATGGTCAGT	CGGGCGGATT	CGCCTTTATC	TGCGGCATCG
251	ATAAT	CACGC	CGGTGCCGAA	TTTGCGTGG	CGGACGTTTT	GTCCGATACG
301	GAAAC	CTGCG	TAGGTTTGGG	GCTGTTTGTG	GTCGTCGATG	ATTTTGTCTT
351	TGGG	CGCGGC	GTTTGGCGC	GTGTGCCAT	AGCGGTCGTA	GGCGGGTTTT
401	TTGAC	GGACA	GGTAGTGCAA	TACTTCGGGC	GGGATTTCTT	CGACGAAGCG
451	GGAGAC	GATG	CCGAATTGGG	TTTGTCGTG	CAGCATGCGT	TGTTGCGCCA
501	TGGT	GATGTA	GAGGCGTTTG	CGGGCGCGGG	TGATGCGGAC	GTACATCAGG
551	CGGCG	TTCTT	CTTCGAGGCC	GCCGCGTTTC	GCAAGGCTCA	TTTCGCTGGG
601	GAAGC	GGCCT	TCTTCCATGC	CGGTGAGGAA	TACGGCGTTA	AATTCCAAGC
651	CTTTG	CGCGC	GTGCACGGTC	ATGAGTTGTA	CGGCTTTTTT	GCCCGCGCCT
701	GCTT	GGTTTT	CGCCGGATTC	GAGAGCAGCA	TTGCTTAGGA	AAGCGAGGAT
751	GGGA	AAGCGC	GGGTCGTCTG	A		

This corresponds to the amino acid sequence <SEQ ID 1548; ORF 535.a>:

a535.pep (partial)

1	FRR	PFALSLL	OFFAIGRILE	SDISNSGFSE	TIDASNIFVG	YEYPACISNL
51	HRF	QFRKLG	V	QLFHALFAEI	DGQSGGFAFI	CGIDNHAGAE
101	ETC	VGLGLFV	VVDDVFVGRG	GLARVAIAV	GGFFDGQVVQ	YFGRDFFDEA
151	GDD	ELGLSV	QHALLRHGDV	EAFAGAGDGD	VHQAAFFFEA	AAFGKAHFAG
201	EAA	FFHAGEE	YGVKFQAFGG	VHGHELYGFF	ARACLVFAGF	ESSIA*ESED
251	GEG	GVV*				

m535/a535 88.7% identity in 256 aa overlap

	10	20	30	40	50	60
m535.pep	MPFPVFRFPFALSLLTFFAVSQILVSDISNSGVSETIDASNVFVGVEYPTYISNLHLFQF					
a535	FRRPFALSLLQFFAIGRILESDISNSGFSETIDASNIFVGVEYPTACISNLHREFQF					
	10	20	30	40	50	
	70	80	90	100	110	120
m535.pep	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVDDF					
a535	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVDDF					
	60	70	80	90	100	110
	130	140	150	160	170	180
m535.pep	IFGCGGLARVAVTVVGR LFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	: : :					
a535	VFGRGGLARVAIAVVGFFDGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	120	130	140	150	160	170

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	190	200	210	220	230	240
m535.pep	AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACACL					
a535	AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKFQAFGGVHGHELYGFFARACL					
	180	190	200	210	220	230
	250	260				
m535.pep	VFTGFEGGIXAEGENEGGVVX					
a535	VFAGFESSIAXESEDGEGGVVX					
	240	250				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

g537.seq

```

1  atgaaatccc tttttatttg gctgcttcta ttgggctcgg cggcaggcgt
51  tttctaccat acccaaaacc aatccctgcc cgcgggcgaa cttgtctatc
101 cgtccgcacc gcaaatcagg gacggcgcg atgcgctgca ctacctcaac
151 cgcattccgca caaaaatcgg tttgcacgcg ctggcacacg cgcgggtttt
201 ggaaaattcc gcccgcaggc acgcacgcta tctcacgctc aatcccgaag
251 acggacacgg cgaacacccat cccgacaatc cgcactacac cgcacaaaag
301 ctgaccgaac gcacacgcct tgccgggtat ctctacaacg gcgtgcatga
351 aaacatcagc acggaagagg aagccgccga atcgtccgac agcgacatcc
401 gcacgcagca acgccaagtg gacgctttga tgagcgcaat ctaccaccgc
451 ctttcgctgc ttgaccgcca taccgacgaa gcagggtcgg catttgctgc
501 cgaaaacggc aaaaccgtcc tcgtattcaa tcagggcaac ggcagcttcg
551 agcgcgcctg tgcaaaagga aggcggcagc cgaagcagg acggaaatat
601 taccgcaacg cttgccacaa cgggtgcggc gtttatgctg acgaagccat
651 gcccgtaacg gaattgcttt ataccgccta tccggttggc ggcggcgcg
701 tgctttattt ttacggggaa cgtcccgacc cgtgcccga atatgaaatc
751 acaggcaatc ctgccagcat tgatttttcc gaggcggcag gcaaaattgc
801 gatgaaaagt ttcaagctgt atcagggtaa aaacgaaatc cgccccgtca
851 ggggttttaac cgcgggcaac gaccctaacg gcaggctgac cgcgcaccaa
901 ttgcgccttt tccgcgtcaa acccttgga taccggcacg tttatacggc
951 ggtattcgac tatgtccgca acggacggca cgcgcaggcg aaatggcagt
1001 ttagaaccgg aaaaccgat tacccttatt ttgaggtaaa cggcggcgag
1051 acacttgagg ttgaaaaagg cgaaaaatat ttcattccat ggcgcggacg
1101 ctggtgtctg gaagcgtgta cccgttatat ctaccggcgg cagttcggca
1151 acagcctgtc catactccgg caggaagcgg gcggcattgt cttcagcgtc
1201 agcggaatgg cgggaagcgg catcaggctt actccggaag acagcccgga
1251 acgcgggtga accctttatt tgcaggattg a

```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

g537.pep

```

1  MKSLFIWLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
51  RIRTOIGLHA LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LINGVHENIS TEEEAESSD SDIRTQORQV DALMSAIYHR
151 LSLDDRHTDE AGAAFVRENG KTVLVFNQGN GSFERACAKG RROPEAGRKY
201 YRNACHNGAA VYADEAMPVT ELLYTAYPVG GGALPYFYGE RPDFVPEYEI
251 TGNPASIDFS EAAGKIAMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAHQ
301 FALFPLKPLE YGTLTYAVFD YVRNGRHAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRR QFGNSLSILR HEAGGIVFSV
401 SGMAGSRIRL TPEDSPERGV TLYLQD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

m537.seq (partial)

```

1  ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCCG CGGCAGGCGT
51  TTTTACCAT ACCCAAmCC AATCCCTGCC CGCGGGCGAA CTGTCTATC
101 CTTCCGCACC GCAAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGAG CCCAAATCGG TTGACACAAG CTGGCACACG CGCCGGTTTT
201 GGAAACTCC GCCCGCAGGC ACGCAAGCTA CTCACGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG

```


3 01 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 3 51 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 4 01 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 4 51 CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

m537.pep (partial)
 1 MKSLFIRLLL LGSAAGVFYH TOXQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LINGVHENIS TEEEAESSD SDIRTQORQV DGLMSAIYHR
 151 LSLDRHTDE SGAA...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

m537/g537

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAGVFYHTOXQSLPAGELVYPSAPQIR DGGDALHYLN RIRAQIGLHK					
g537	MKSLFIWLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIR DGGDALHYLN RIRIQIGLHA					
	10	20	30	40	50	60
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHH PDNPHYTAQKLTERTRLAGY LINGVHENIS					
g537	LAHAPVLENSARRHARYLTLPEDGHGEHH PDNPHYTAQKLTERTRLAGY LINGVHENIS					
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHH PDNPHYTAQKLTERTRLAGY LINGVHENIS					
g537	LAHAPVLENSARRHARYLTLPEDGHGEHH PDNPHYTAQKLTERTRLAGY LINGVHENIS					
	70	80	90	100	110	120
m537.pep	TEEEAESSDSDIRTQORQVDGLMSAIYHRLSLDRHTDESGAA					
g537	TEEEAESSDSDIRTQORQVDALMSAIYHRLSLDRHTDEAGAA FVRENGKTVLVFNQGN					
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQORQVDGLMSAIYHRLSLDRHTDESGAA					
g537	TEEEAESSDSDIRTQORQVDALMSAIYHRLSLDRHTDEAGAA FVRENGKTVLVFNQGN					
	130	140	150	160	170	180
g537	GSFERACAKGRRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

a537.seq

1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT
 51 TTCTATCAT ACCCAAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
 101 CGTCCGCACC GCAAATCAGG GACGGCGCGC ATGCGCTGCA CTACCTCAAC
 151 CGCATCCGCG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGGTTTT
 201 GGAAATTCG GCCCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG
 251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
 301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGCGG
 501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG
 551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
 601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT
 651 GCCCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC
 701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
 751 ACGGGCAATC CTGCCAGCAT TGATTTTTCG GAGGCGGCAG GCAAAATTAC
 801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AACGAAATC CGCCCCGTCA
 851 GGGTTTTAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
 901 TTCGCGCTTT TCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC
 951 GGTATTCGAC TATGTCCGCA ACGGACGCGC CGCGCAGGCG AAATGGCAGT
 1001 TTAGAACCCG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGGCGGCGAG
 1051 ACACTTGCGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GCGCGGACG
 1101 CTGGTGTGTA GAAGCGTGA CCCGTATATC CTACCGGCAG CGACCCGGCA

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1 151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTCAGCGTT
 1 201 GACGGAATGG CGGGCAGCCG CATCAGCGTT GCACCGGAAG GAGAAACGGA
 1 251 ACGAGGCGTA ACCCTTTATT TACAGATTG A

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

a537.pep
 1 MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLGY LYNVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDRHTDE AGAAFVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY
 201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDFVPEYEI
 251 TGNPASIDFS EAAGKITMKS FKLYQGKNEI RFVRVLTAGN DPNRRLTAYQ
 301 FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE
 351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RPGSRLSISR HKAGGIVFSV
 401 DGMAGSRITL APEGETERGV TLYLQD*

m537/a537 98.2% identity in 164 aa overlap

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAGVFYHTQNQSLPAGE LVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
a537	MKSLFIRLLL LGSAAGVFYHTQNQSLPAGE LVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASLYTLNPEDGHGEHHPDNPHYTAQK LTERTRLGALYNVHENIS					
a537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQK LTERTRLGALYNVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
a537	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDEAGAAFVRENGKTVLVFNQGN					
	130	140	150	160	170	180
a537	GRFERHCAQGRNQPEAGRKYRNACHNGAVVYTDEAMPAQ ELLYTAYPVG NGALPYFHGE					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

g538.seq
 1 atgtcaggta gaacaggacg gaacagtgcc actcaggcgc aaccgga acg
 51 cgtcatgctg gtggcgctaa tgttgataa agatgatacg ggcagca atg
 101 ccgcccgtct gaacgggttt cagacggcat tggcggaagc cgtcgag ctg
 151 gtcaaaagcgg cggcgggcga ttccgtacgc gtggagactg ccaaaccg cga
 201 ccgcccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagc tgt
 251 cggagcagcgt tgccgcagac ggcattgatt tggcgtatt caaccac gaa
 301 cttactcca cgcaggaacg caatttgga aaaatcctcc aatgccg cgt
 351 attggacaga gtggggctga ttctggcgat ttctgcccgc cgcggccgca
 401 cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttg gcg
 451 ggacgcttga tacgcgggta cggacatttg caaagccagc gcggcggtat
 501 cggcatgaaa gggccgggcg aaaccaaact ggaaaccgac cgccgat taa
 551 ccgcccacat gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaa aaa
 601 cagcgcgccc tgcgcgcaa gtcccgcgag tcgggcagaa tcaaacg tt
 651 tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaacc ggc
 701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctc gac
 751 acgacggcgc ggcggctgta catcagtcgc gcatgcagca ttatcct gac
 801 gataccgtc ggattcgta cgcgctgcc gcacaaactg atttccg cct
 851 tttccgccac cttggaagaa accgtgcaag ccgatgtgct gctgcac gtc
 901 gtcgatgctg ccgcccggaa cagcgggcag cagattgaag acgtggaaa aa
 951 cgtactgcaa gaaatccatg cccacgatat tccgtgcatc aaggtgtaca
 1001 acaaaaccga cctgtgcgg tctgaagaac aaaacacggg catatgg cgc
 1051 gacgctgcgg gaaaaattgc cgccgtccgc atttccgttg ctgaaaa ttc

This corresponds to the amino acid sequence <SEQ ID 1556; ORF 538.ng>:

g538.pep

```

1  MSGRTGRNSA TQAQPERVML VGVMLDKDDT GSNAARLNGF QATALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLTVFNHE
101 LTPTQERNLE KILQCRVLDL VGLILAI FAR RARTQEGRLQ VELAQLSHLA
151 GRLLIRGYGHL QSQRGGIGMK GPGETKLETD RRLTAHRINA LKKQLANLKK
201 QRALRRKSRE SGRIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
251 TTARRLYISP ACSIIILTDV GFVSDLPKHL ISAFSATLEE TVQADVLLHV
301 VDAAARNSGQ QIEDVENVLQ EIHADIPCI KVYNKTDLLP SEEQNTGIWR
351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

m538.seq

```

1  ATGACAGGCA GAACAGGCGG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTGGACAA AGATGGTACG GGCAGTAGTG
101 CCGCCCCTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCCGCTGTG TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CAGAAGCAGT TGCCGAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTCACGCCCA CGCAGGAACG CAACCTTGAA AAAGAACTsA AATGCCCGGT
351 ATTGGACAGG GTAGGGCTGA TTCTGGCGAT TTTCGCTCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CGCAATTGAG CCATTGCGG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCGGCGG AAACCAAACCT GGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGATAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TGCGCGCGAA GTCnCGCGAA TCGGCGACAA TCAAAACGTT
651 TCGCTGGTTC GGCTATACAA ATGTCGGAAA ATCCAGCCTG TTCAACCGGC
701 TGACAAAGTC GGGCATATAT GCAAAGGACA AGCTTAGTCC CGAATGCAGC
751 ATTATCCTGA CCGATACCGT CGGATTCGTn AGCGATCTGC CGCacAACT
801 GATTTCCGCC TTTTCgCC.A CGCTGGAAGA AACCGCGCAA GCCGATGTGC
851 TGCTGCACGT CGTCGATGCC GCCGCTCCGA ACAGCGGACA GCAGATTGAA
901 GACGTGGAAG ACGTACTGCA AGAAATCCAT GCCGCGGATA TTCCGTGCAT
951 cAAGGTGTAC AACAAAACCG ACCTGCTGCC GTCTGAAGAA CAAAACACGG
1001 GCATATGGCG CGACGCTGCG GGAAAAATTG CCGCCGTCCG CATTTCCGTT
1051 GCTGAAAATA CCGGTATAGA CGCACTGCGC GAAGCcATTG CCGAGTCTTG
1101 TGCCGCCGCA CCAAACACAG ACGAAACCGA AATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

m538.pep

```

1  MTGRTGGNGS TQAQPERVML VGVMLDKDGT GSSAARLNGF QATALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLTVFNHE
101 LTPTQERNLE KELKCRVLDL VGLILAI FAR RARTQEGRLQ VELAQLSHLA
151 GRLLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LIKQLANLKK
201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDKLSPECS
251 IILTDTVGFV SDLPKHLISA FSXTLEETAQ ADVLLHVDA AAPNSGQQIE
301 DVENVLQEIH AGDIPCIKVY NKTDLLPSEE QNTGIWRDAA GKIAAVRISV
351 AENTGIDALR BAIAESCAAA PNTDETEMP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

m538/g538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQATALAEAVELVKAAGGDSVR					
	: ::					
g538	MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQATALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLTVFNHELTPQERNLEKELKCRVLDL					
g538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLTVFNHELTPQERNLEKILQCRVLDL					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
g538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGTYNVGKSSLFNRLTKSGIY					
g538	RRLTAHRINALKKQLANLKKQALRRKSRESGRIKTFALVGTYNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILTDTVGFVSDLPKLI SAFSXTLEETAQADVLLHV					
g538	AKDQLFATLDTTARRLYISPACSIILTDTVGFVSDLPKLI SAFSATLEETVQADVLLHV					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
g538	VDAAARNSGQQIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAESCAAAPNTDETEMPX					
g538	ISVAENTGIDALREAIAEYCAAAPNTDETEMPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1   ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGTCT GAACGGTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCCA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTGGAA AAAATCCTCC AATGCCGCGT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTTCGCCCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTGGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAAC TGGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TGCGCCGCAA GTCCCGCGAA TCGGGCACAA TCAAAACGTT
651 TGCGCTGGTC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGCG
701 TGACCAAGTC GGGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GCGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCGTCA GCGATCTGCC GCACAAACTG ATTCCGCCT
851 TTTCCGCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGAAAAA
951 CGTACTGCAA GAAATCCATG CCGGCGATAT TCCGTGCATC AAGGTGTACA
1001 ACAAACCGA CCTGCTGCCG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCCGTCGCG ATTTCCGTTG CTGAAATAC
1101 CGGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1   MTGRTGRNGS TQAQPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLVVFNHE
101 LTPTQERNLE KILQCRVLDL VGLILAIFAR RARTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

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201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
 251 TTARRLYISP ECSIILTDV GFVSDLPKLI ISAFSATLEE TAQADVLLHV
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538 . pep	MTGRTGGNGSTQAQPERVMLVGVM LDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
a538	MTGRTGRNGSTQAQPERVMLVGVM LDKDGTGSSATRLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538 . pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKELKCRV LDR					
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKILQCRV LDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m538 . pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
a538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538 . pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
a538	RRLIAHRINALKKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538 . pep	AKDKL-----SPECSIILTDVGFVSDLPKLI SAFSXTLEETAQADVLLHV					
a538	AKDQLFATLDTTARRLYISPECSIILTDVGFVSDLPKLI SAFSATLEETAQADVLLHV					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538 . pep	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
a538	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538 . pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
a538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539 . seq

1 atggaggatc tgcaggaaat cgggttcgat gtcgccgccg taaaggtagg
 51 tcggcagcgc gaacatcatc gtctgcatca taccagtcg ggcaacggca
 101 aggcggacga tgtattgttt gcgttctttt tggttggcgg cttcgatttt
 151 ttgcgcgtca tagggtgcgg cgggttagcc tgtctgccgg attttcaaca
 201 gaatgtcggg gaggcggatt ttgccgtcgt cccagacgac gcggcagcgg
 251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaag
 301 ctgctgttcg atcagccaga cgcaggcggc gcaggtaatg ccgctgagca
 351 tcagcactgc ttcgtgcgtg ccattatggg tttccacaaa gtcggatttg
 401 acttcgggca ggtcgtagc gcggatttgg tcgaggattt cttggggcgg
 451 cagttcgggt tttttcgcgt cggcggtagc tcgtttgtaa taactgcccc
 501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
 551 gtttcgcggt cttcgccttc gtagcggacg gtcagatgca gggtttcggg
 601 aacgtccagc ccgcagtgga aacagggttt tttcatggca tttcgggttc

g539.pap

1	MEDLQEIGFD	VAAVKVGRQR	EHRLHHTQS	GNGKADDVLF	AFFLVGGFDF
51	<u>LRVIGCGGVA</u>	CLPDFQONVG	EADFAVVPDD	AAAVRAVIEV	DADDAVCAQK
101	LLFDQPDAGG	AGNAAEHQHC	FVRAIMGFHK	VGLDFGQVVQ	ADLVEDFLGR
151	QFGFFRVGGA	SFVITAQAGI	DDALCDCLTA	DAAGFAVFAP	VADGQMQVFG
201	NVQPAVETGF	FHGISVSSVF	GAAQYQSAMA	SRSASIPVFS	ATEMRTAAIF
251	PAASRHMPVF	CSSDGRSRVL	LYTLMHGISW	AWISCTSFST	SSICCLPFRA
301	AASTTCSSTS	ACTVSSKVAE	KAELISLGRS	LTNPTVSVRI	MLHAGLMYSR
351	WAVSVRVAKS	WSFAYMPDLV	SRLNRLDLPT	LV*	

m539.seq (partial)

1	ATGGAGGATT	TGCAGGAAAT	CGGGTTCGAT	GTCGCCGCCG	TAAAGGTAGG
51	TCGGCAGCGC	GAACATCATC	GTCTGCATCA	TCCCCAGCCC	GGCAACGGCG
101	AGGCGGACGA	TGTATTGTTT	GC GTTCTTTT	TGGTTGGCGG	CTTCGATTTT
151	TTGCCGCGTC	TAGGGTGC GG	CGGTGTAGCC	TATCTGCCTG	ATTTTCAACA
201	GAATGTCCGA	AAGGCGGATT	TGCGCGTCGT	CCGACAGCac	GCGGCaGcGg
251	TGCTGTGCTG	AATTGAGGTG	GATGCCGACG	ATGCCGCTCG	TACCGCAAAAG
301	CTGCTGTTCG	ATCAGCCAGA	CGCAGGCGGC	GCAGGTGATG	CCGCCGAGCA
351	TTAAAACCGC	CTCGCGCGTG	CCGCCGTGGG	TTTCCACAAA	GTCGGACTGG
401	ACTTCGGGCA	GGTCGTACAG	GCGGATTTGG	TCGAGGATTT	CTTGGGGCGG
451	CAgCTCGGTT	TTTTGCGCGT	CGGCGGTGCG	TTGTTTGTA	TAACTGCCCA
501	AGCCCCGCGT	AATAATGCTT	TGTGCGACCG	CCTGACAGCC	GGCGCaCaGg
551	GTTTTCGCGT	CTTCGTTTTT	GTAACGGACA	GTCAGGTGGA	GGTGTTCGGG
601	AACATCCAGA	CCGCGAGTGA	AACAGGTTTT	TTTCAATGCA	TTTCGGTTTT
651	GCTCTGTTTT	GGTGC GCGG	CACAAGACTC	GGCAATgGCT	TCGCGCAGTG
701	CGTCTATACC	GGTATTTTCA	GCAACGGAAA	TGCGGACGGC	GGCAATTTTT
751	CCCGCAGCGT	CGCGCCATAT	GCCCGTGT TT	TGTTCTTCAG	ACGGCAGCAG
801	GTCGGTTTTG	TTGTACACCT	TgATGCACGG	AATATCGCCG	GCATGGATTT
851	CTTGCAGTAC	GTTTTCCACG	TCTTCAATCT	GCTGTCCCGT	GTTCCGGAGCG
901	GCGGCATCGA	CGGATGTCAG	CAGCACAATCG	GCTTCCGCGG	TTTCTTCCAG
951	CGTGGCG. AA	AAGGCGGAAA	TcAGTTTgTG	CGCGACATCG	CtnACGAATC
1001	CGACGGTATC	GGTCAGGATA	ATGCTGCATT	CGGGAC...	

m539.pep (partial)

1	MEDLQEIGFD	VAAVKVGRQR	EHHRLHHQPQ	GNGEADDVLF	AFFLVGGFDF
51	<u>LRVIGCGGVA</u>	YLPDFQQNVG	KADFAVVPDD	AAAVRAVIEV	DADDAVCTQK
101	LLFDQPDAGG	AGDAAEH*NR	LARAAVGFHK	VGLDFGQVVQ	ADLVEDFLGR
151	QLGFLRVGGA	LFVITAQARV	NNALCDRLTA	GAQGFVAVFV	VTDSQVEVFG
201	NIQTAVETGF	FHGISVSSVF	GAAAQDSAMA	SRSAISPFVS	ATEMRTAAIF
251	PAASRHMPVF	CSSDGRSRVL	LYTLMHGISP	AWISCTFVST	SSICCPALFGA
301	AASTTCSSTS	ACAVSSSVAX	KAEISLCGRS	LTNPNTSVRI	MLHSG...

Homology with a predicted ORF from *N. gonorrhoeae*

***N. gonorrhoeae*:**

m539/q539

	10	20	30	40	50	60
m539.pap	MEDLQEI	GFDVAAVKVGRQREH	HLHHPQPGNGEADDV	LAFFL	VGGFD	FLRVIGCGGVA
g539	MEDLQEI	GFDVAAVKVGRQREH	HLHTQSGNGKADDV	LAFFL	VGGFD	FLRVIGCGGVA

815

	10	20	30	40	50	60
m539 . pep	70	80	90	100	110	120
	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
	70	80	90	100	110	120
m539 . pep	130	140	150	160	170	180
	LARAAVGFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	FVRAIMGFHKVGLDFGQVVQADLVEDFLGRQFGFRVGGASFVITAQAGIDDALCDCLTA					
	130	140	150	160	170	180
m539 . pep	190	200	210	220	230	240
	GAQGFVAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS					
g539	DAAGFAVFAFVADGQMVFQVFNQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
m539 . pep	250	260	270	280	290	300
	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSTFTSSICCPFLGA					
g539	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISWAWISCSTFTSSICCPFLRA					
	250	260	270	280	290	300
m539 . pep	310	320	330	340		
	AASTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	AASTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGIMYSRRVVSRAVKS					
	310	320	330	340	350	360
g539	WSFAYMEDLVSRNLRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539 . seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTTCGATTTT
151 TTGCGCGTCA TAGGCTGCGG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TCGGTGCTGT AATTGAGTTC GATGCGGACG ATGCCGTCTG TACGCCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAACCCGC CTCGCGCGTG CCGCCGTGGG TTTCACAAA GTCCGACTGG
401 ACTTCGGGCA GGTCGTACAG GCGGATTGG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTTGCCTGT CCGCGGTGCG TTGTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GGCGCAGCAG
551 GTTTCGCGGT CTTCTGTTTC GTAACGGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTTT TTTCATGGCA TTTCGGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TCGCGACGGC GGCAATTTTT
751 CCGCGAGCGT CGCGCATAT GCGCGTGTTC TGTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCCTGG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CCGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTGAGGATA ATGCTGCATT CCGGACTGAT GTACAGCCGC
1051 CGCGCCGTCG TGTCGAGTGT GGCGAAAAGC TGGTCTTTTC CATATATGCC
1101 CGACTTGGTC AGCCGGTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539 . pep
1  MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGGDF

```

816

```

51  LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAVRAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVO ADLVEDFLGR
151 QLGLRVGGA LFVITAQARV NNALCDCLTT GAAGFAVEVF VTDGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
301 AASTCSSTS ACAVSSSVAE KAEISLCGRS LTNPTVSVRI MLHSGLMYSR
351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

m539/a539 97.1% identity in 345 aa overlap

```

m539.pep      10      20      30      40      50      60
MEDLQEIGFDVA AVKVGQR EHHRLHHPQPGNGEADDVLFAFFLVGGFDL RVIGCGGVA
|||||
a539          10      20      30      40      50      60
MEDLQEIGFDVA AVKVGQR EHHRLHHPQPGNGEADDVLFAFFLVGGFDL RVIGCGGVA

m539.pep      70      80      90      100     110     120
YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR
|||||
a539          70      80      90      100     110     120
YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR

m539.pep      130     140     150     160     170     180
LARAAGVFHKVGLDFGQVVOADLVEDFLGRQLGLRVGGALFVITAQARVNNALCDRLTA
|||||
a539          130     140     150     160     170     180
LARAAGVFHKVGLDFGQVVOADLVEDFLGRQLGLRVGGALFVITAQARVNNALCDCLTT

m539.pep      190     200     210     220     230     240
GAQGFAVVFVTD SQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS
|||
a539          190     200     210     220     230     240
GAAGFAVVFVTDGQMVFVFGNVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS

m539.pep      250     260     270     280     290     300
ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA
|||||
a539          250     260     270     280     290     300
ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA

m539.pep      310     320     330     340
AASTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG
|||||
a539          310     320     330     340     350     360
AASTCSSTSACAVSSSVAEKAEISLCGRSLTNPTVSVRIMLHSGLMYSRRRAVVSSVAKS

a539          370     380
WSFAYMPDLVSRLNRLDLPTLVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

g540.seq

```

1  atgccgccct cccgacgcgg caacgggggtg tttatcaaa acggcaaact
51  tgccaatgcg gtttccgctt gccgattgcc aaaccggcaa acctttcccg
101  tgccggtgcc gaaccgatg ccgtctgaac cttcagacgg catcgggtgt
151  ttatttgtcc actcggacgg gtgcaggttc gtattgtgtc gattcgctgc
201  cgtaatacag cagcccgagt ttgacgggga tgcgtccctg cgatttgcg
251  tggcggttgg aatcgcgcaa ggaatacgcg cagccgcagt attcctgctg
301  gtagaagttt tcgctgttgc tgatttcaat catacgcgcg ccgccgcgc
351  ctttgcgcca gttgaagtc caataggcca catcatcgta aggcgcggcg
401  gcacggtgtc cgcagtcgtt gatttgcgcc atattttcc agcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1568; ORF 540.ng>:

g540.pep

```

1  MPPSRRGNGV FYQNGKLANA VSACRLPNRQ TFPVVPNPM PSEPSDGIGC

```


818

m540/a540 92.8% identity in 111 aa overlap

						10	20	30
m540 . pep						PNMPMPSEPSDGIGCLFVHPDGGRFVLCRFV		
a540	GNGVFYQNGKLANAVSDCRLENRQTFVPMMPMPSEPSDGIGCLFVHPDGGRFVLCRFV							
	10 20 30 40 50 60							
		40	50	60	70	80	90	
m540 . pep	AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHARAAAAFAPVEIPIH							
a540	AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHTRAAAAFAPVEIPIH							
	70 80 90 100 110 120							
		100	110					
m540 . pep	HIIVRRGGAVSAVVDLRHIFPAX							
a540	HIIVRRGGAAAVVNLVHVFP							
	130 140							

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

g542 . seq
 1 atgccgaaat ggtcgcgcac acggcgttgc agcgtccttt cgctgatgtt
 51 cagcgcggct gtcagccggt tgacttggtg tgcgccgcgc tcgaacgcgg
 101 cattcagggt gcggtgaag tcttcagacg gcatagcgtc tgcttccgcc
 151 gtttgccccc cgcgcggctc gatgccgtct gaaaccgtgt cccacaaatc
 201 cgacagcagc cgcaacacgt ccgcctcgcg gcgcaatgtt tcgccccaat
 251 gccccttttg gacggtttgc aggcaggatg ccgccaagcc gcgcaggttt
 301 gggggcaaat cccatatact gaccggttcg cggttaa

This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:

g542 . pep
 1 MPKWSRIRRC SVLSLMFSAA VSRLTWCAPP SNAAFVRLK SSDGIASASA
 51 VCPAAGSMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTVC RQDAAKPRRF
 101 GGKSHILTGS R*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

m542 . seq
 1 ATGCCGAAAT GGTGCGCAT ACGGCGTTGC AGCGTCCTTT CACTGATGTT
 51 CAGCGCGTCT GTCAGCCGGT TGACTTGGTG TGCGCCGTCG GCAAACGCGG
 101 CATTAGGGT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
 151 GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
 201 CGACAGCAGC CGCAACACGT CCGCCTCGCG .CGCAATGTT TCGCCCCAAT
 251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC
 301 GGGGGCAAT CCCATATCCT GACCGGTTTC CGGTAA

This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:

m542 . pep
 1 MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVRLK SSDGIASASA
 51 VCPAAGPMPS ETVSHKSDSS RNTSASRAMF RPNAFLGRNV SPKCPFGTAF
 101 RQDAAKPRRF GGKSHILTGS R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

m542/g542

						10	20	30	40	50	60
m542 . pep						MPKWSRIRRC	SVLSLMFSAS	VSRLTWCAPS	ANAAFRVRLK	SSDGIASAS	AVCPAAGPMPS
g542						MPKWSRIRRC	SVLSLMFSAA	VSRLTWCAPP	SNAAFVRLK	SSDGIASAS	AVCPAAGSMPS
						10 20 30 40 50 60					
		70	80	90	100	110					
m542 . pep		ETVSHKSDSS	RNTSASXRN	VSPKCPFGT	AFRQDAAK	PRRF	GGKSHILT	GSRX			

g542 ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

```
a542.seq
1  ATGCCGAAAT  GGTGCGCAT  ACGGCGTTGC  AGCGTCTTT  CGTGATGTT
51  CAGCGTGCT  GCGGCGCGT  TGACTTGATG  TGCGCCGCCG  GCAAACCGCG
101  CATTCAAGAT  GCCGCTGAAG  TCTTCAGACG  GCATAGCGTC  TGCTTCGCG
151  GTTTGCCCG  CCGCCGCCCG  GATGCCGTCT  GAAACCGTGT  CCCACAAGTC
201  CGACAGCAGC  CGCAACAGCT  CCGCCTCGCG  GCGCAATGTT  TCGCCCAAAT
251  GCCCCTTTGG  GACGGCTTTC  AGGCAGGATG  CGGCCAAGCC  GCGCAGGTT
301  GGGGCGCAAT  CCCATATCCT  GACCGTTTCG  CGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

a542.pep

1	MPKWSRIRRC	SVLSLMFSVS	ASRLT*CAPP	ANAAFRMLRK	SSDGIASASA
51	VCPAAGPMPS	ETVSHKSDSS	RNTSASRRNV	SPKCPFGTAF	RQDAAKPRRF
101	GGKSHILTGS	R*			

m542/a542 94.6% identity in 111 aa overlap

	10	20	30	40	50	60
m542 . pep	MPKWSRIRRC	SVLSLMFSA	SVSRLTWC	APSANAAFR	VRLKSSDGI	ASASAVCPA
a542	MPKWSRIRRC	SVLSLMFSA	SVSRLTXC	APPANAAF	FRMLKSSDGI	ASASAVCPA
	10	20	30	40	50	60
	70	80	90	100	110	
m542 . pep	ETVSHKSDS	SRNTSASX	RNVSPKCP	FGTAFRQD	AAKPRRF	GKGSHILTS
a542	ETVSHKSDS	SRNTSASX	RNVSPKCP	FGTAFRQD	AAKPRRF	GKGSHILTS
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

```

g543.seq
1 atggtttgtc ggttatttgc cgcggtttt ggctttcaac tcggcaatca
51 gcccgtcgat gcctttggct ttgatgattt cgccgaattg gttgcggtac
101 acggtaacca ggctcgtgcg ttcgatggcg acgttgtagg tacggtattt
151 gccgcgcgtt tggtaggtgg taaagtcatt atgacgggcg ttttgaccgg
201 ggatcgccac ttccgcaagg acagcagatt ccttgccgcc cttattgacg
251 atgggattgt ctttgacggt gacggtcgcg tttttgaatt tcagcatcgt
301 gccggaatag gtgcggatca gcagggtttg aaattctttg gccaacgcgt
351 gtttttgcgc gtccgacgcg gtacgccaa ggttgccgac cgccaatgcg
401 gtcatacgtt ggaatcgaa atagggaacc gcataggctt cggcttttgg
451 gcgtgcagaa gccgcgtcgc cgcttttaga catggtcaaa acctgtgttg
501 cgttttgagg gatttgtccc actcgctcgg cggggaggcg aaatgcatgt
551 ccgatgctca aaataccgat gcccaatgcg ctgatgaagg aggatttttt
601 cacgatgtct ttctgaaaa tggatgtgta tgtttattct gcggcttttt
651 ccgcattgcc gccctcagcg tttttctcgg cgaagctggt catgaattta
701 ccgatcaggt tttccagaa cattgcagaa ctggttacgg agatggtgtc
751 gccgcgcaga aggttttcgc tatcgccgcg ctgctgcagc ccgatgtact
801 gttcgcccaa aagtcgcgaa gtcaggattt gcgcggaaac gtcactgtcg
851 aactgatact tgccgtccaa atcaaggcgc acctcgcct gataggattt
901 cgggtcaagc ccgatagcgc cgacgcgcc gaccaatacg cctgcggatt
951 tgacgggggc attgaccttc aaaccgcga tgtcgccgaa atcggcataa
1001 accgctgaag ttttgtccga accgcgcaac gccgcgcgcg ccgccacgcg
1051 gaggcagata aaggcaaccg ccgcgcgcgc gatcaagacg aacagtcgca
1101 cccaaaatcc caatatgttc tttttcata a

```

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

g543.pap
1 MVCRLEAAVF GFQLGNQPV D AFGFDDFAEL VAVHGNOARA FDGDVVGTVF

m543.seq

1	ATGTTTGTGC	GGTTATTTCG	CGCCGTTTTT	GGCTTTCAAC	TCGGCAATCA
51	GTCCGTCCAC	GCCTTTTCGT	TTGATAATTT	CGCCGAATTG	GTTGCGGTAC
101	ACGGTAACCA	GGCTCGCGCC	TTCCGATGGC	ACGTTGTAGG	TACGGTATTT
151	ACCGCCGCTT	TGGTAGGTGC	TGAAGTCCAT	GTTGACGGGT	TTTTGCCCGT
201	GTACGCGAC	TTCCGCGCGG	ACGATGATTT	CTTTGCCGCC	TTTTATTGACG
251	ATGGGATGTT	CTTTGACGTT	GACGTTGGCG	TTTTTTAATT	TCAGCATCGT
301	GCCGGAATAG	GTGCGGATCA	GCAGGGTTTG	AAATTCCTTG	GCCAACGCTT
351	GTTTTTTCGC	GTCGGACGCG	GTGCCCAAG	GGTTGCCGAC	CGCCAATGCG
401	GTCATACGTT	GGAAATCGAA	ATAGGGAATC	GCATAGGCTT	CGGCTTTTTG
451	GCGAGCGGTG	TGGCATATCG	CGTTTTTTAA	GATGCTCAAT	ACTTGTAGTG
501	CGTTTTTGAC	GATTTGGCTT	ACCGGTCGCG	CAGGGGCGCG	AAATGCCATG
551	CCGATGCTCA	AAATACCGAT	GCCCAATGCG	CTGATGAGGG	AGGATTTTTT
601	CATGATTAAG	TGTCTTAGTT	TGAATATGAT	GGCATAAGTT	TATTCGGCGG
651	CTTTTTCCGC	ATTGCCGCGC	TCGGCATTTT	TCTCGGCAAA	ACTCGTCATG
701	AATTTGCCGA	TAAGGTTTTT	CAGAACCATT	GCAGAATCTG	TTACGGAGAT
751	GGTGTCGCCG	GCAGCAAGGT	TTTCCGTGTC	GCCGCCCTGC	TGCACGCCGA
801	TGTACTGCTC	GCCCAAAAGT	CCCGAAGTCA	GGATTTCGCG	GGAAACGTCG
851	CTGCTGAACT	GATACTTGCC	GTCCAAATCG	AGGCGCACCC	TCGCTTGATA
901	GGATTTCCGG	TCAAGTCCGA	TAGCGCCGAC	GCGCCCGACC	AATACGCCTG
951	CGGATTGTAC	GGGGGCATTG	ACCTTCAAAC	CGCCGATGTC	GCCGAAATCG
1001	GCATAAACGG	CGTAAGTTTT	GTCCGAACCG	CCGACATGCG	CACCGCCGGC
1051	CACGCGGAAA	CGAGAAAAGG	CAACCCGCGC	CGGCCCAATC	AGGACGAACA
1101	GTCCGACCCA	AAATTCCAAT	ATGTTCTTCT	TCATTAA	

m543 . pep

1	MVCRLFAAVF	GFQLGNQSVH	AFRFDNFael	VAVHGnQARA	FDGDVVGTVF
51	TAALVGGEVH	VDGFLPGYAD	FGADDDFFAA	FIDDGIVFDV	DVGVFxfQHR
101	AGIGADQQGL	KFFGQRLFLR	VGRGAPRVAD	RQCGHTLEIE	IGNRIGFGFL
151	ASGVGIAVFX	DAQYLSGVLt	DLAYRVGRGG	KCHADAQNTD	AQCADEGGFF
201	HDXVSXFEYD	GIRLFGGFFR	IAAQGISFLGK	TRHEFADKVF	QNHCRtGYGD
251	GVAGSKVFRV	AALLQPDVLL	AAKSRSQDLR	GNVAELILa	VQIEAHPRLI
301	GFRVKSDSAD	APDQYACGFD	GGIDRLQTA DV	AEIGINGVSF	VRTAERRTAG
351	HAESEKGNRR	RANQDEQSDP	KFQYVLLH*		

from *N. gonorrhoeae*:

m543/g543

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRFDNF	AELVAVHGNQARAFDGDVVGTVFTAALVGGEVH				
		:		:	:	
g543	MVCRLFAAVFGFQLGNQPVD	AFGFDDFAELVAVHGNQARAFDGDVVGTVFAAALVG	GKVH			
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGYADFGADDDFFAA	FIDDGIVFDVDVGVF	XFQHRAGIGADQQGLKFFGQRLFLR			
	:	: :				
g543	IDGLLTGDADFGTDDD	FLAALIDDGIVFDVDGRVFEFQHRAGIGADQQGLKFFGQRLFLR				
	70	80	90	100	110	120
	130	140	150	160	170	180

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```

m543 . pep      VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
g543            VGRGTPRVADRQCGHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLGCVLADLSHCVGRGG
                  130      140      150      160      170      180

                  190      200      210      220      230      239
m543 . pep      KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIA AVGIFLGKTRHEFADKV
g543            KCHADAQNTDAQCADEGGFFHDXV---FPENGCVCLFCGFFRIAALSVFLGEAGHEFTDQV
                  190      200      210      220      230

                240      250      260      270      280      290      299
m543 . pep      FQNHCRRTGYGDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAAELILAVQIEAHPRL
g543            FQNHCRRTGYGDGVAGSKVFRIAALLQPDVLFQAQKRSQDLRGNVTAEILILAVQIKAHPRLL
                240      250      260      270      280      290

                300      310      320      330      340      350      359
m543 . pep      IGFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEKGNR
g543            IGFRVKPDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRAARHAESEKGNR
                300      310      320      330      340      350

                360      370      379
m543 . pep      RRANQDEQSDPKFQYVLLHX
g543            RRADQDEQSDPKFQYVLFHX
                360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543 . seq
1   ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTTAAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATCTTTG GCCAACGCTT
351 GTTTTTGCGC GTCGGACGCG GTGCGCCAAG GGTGCGGAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 CGGGGCGGTG TTGGCATCAC CGCTTTTAA GATGCTCAAT ACTGAGTGG
501 CGTTTTGACG GATTTGTTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCCGC ATTGCCGCGG TCGGCATTTT TCTCGGCAA ACTCGTCATG
701 AATTGCCGA TAAGGTTTTC CAGAACCAT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTTCGCG GGAAACGTCG
851 CTGCTGAAT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTCGGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGAACGCGC CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAG CAACCGCCG CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATTCCAAT ATGTTCTTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543 . pep
1   MAYGLLAAVX SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGVTF
51  TAALVGGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQQGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVGITAF* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFRR IAAVGIFLGK TRHEFADKVF QNHCRRTGYGD
251 GVAGSKVFRV AALLQPDVLL AQKRSQDLR GNVAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQTADV AEIGINGVSF VRTAERRTAG

```

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
a543	MAYGLLAAVXSLQLXNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGYADFGADDDFFAAFIDDGIVDFVDVGVVFXFQHRAGIGADQQGLKFFGQRLFLR					
a543	VDGFLPGXADFGADDDFFAAFIDDXIVDFVDVGVVFXFQHRAGIGADQQGLKFFGQRLFLR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m543.pep	VGRGAPRVADRQCCHTLEIEIGNRIGFGFLASGVGIAXDAQYLSGVLTDLAYRVGRGG					
a543	VGRGAPRVADRQCCHTLEIEIGNRIGFGFLAGGVGITAXDAQYLSGVLTDLVYRVGRGG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m543.pep	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIIRLFGGFFRIAAVGIIFLGKTRHEFADKVF					
a543	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIIRLFGGFFRIAAVGIIFLGKTRHEFADKVF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m543.pep	QNHCRITGYGDGVAGSKVFRVAALLQPDVLLAQKSRSDLRGNVAELI LAVQIEAHPRLI					
a543	QNHCRITGYGDGVAGSKVFRVAALLQPDVLLAQKSRSDLRGNVAELI LAVQIEAHPRLI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m543.pep	GFRVKSDSADAPDQYACGFDGGIDLQTAADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
a543	GFRVKSDSADAPDQYACGFDGGIDLQTAADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
	310	320	330	340	350	360
	370	379				
m543.pep	RANQDEQSDPKFQYVLLHX					
a543	RANQDEQSDPKFQYVLFHX					
	370					

g544.seq

This corresponds to the amino acid sequence <SEQ ID 1586; ORF 544.ng>:

g544.pap

1 KKKILTAAAV ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGV
51 TLINFWFPSC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG

151 KLYQEIDTAL AQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1587>:

m544.seq

```

1  ATGAWAAAAA TACTCACC GC CCGTCGTC GCACTGATCG GCATCCTCCT
51  TGCCATCGTC CTCmTCCCCG ACAGCAAAAC CGCGCCCGCC TTCTCCmTGC
101 CCGACCTGCA CGGAAAAACC GTTTCCAACG CCGACCTGCA AGGCAAAGTA
151 ACCCTGATTA ATTTTGGTT TCCCTCCTGT CCGGGTTGTG TGAGCGAwAT
201 GCCCAAAATC ATTA AACCG CAAATGACTA TAAAAwCAAA AACTTCCAAG
251 TACTTGCCGT CGCCAGCCC ATCGATCCGA TAGAAAGCGT CCGCCAATAT
301 GTCAAAGACT ACGGTTTGCC GTTTACCGTC ATGTATGATG CGGACAAAGC
351 TGTCGGACAG GCGTTCGGCA CACAGGTTTA TCCGACTTCC GTCCTTATCG
401 GCAAATAAGG CGAAATCTTC AAAACCTACG TCGGCGAACC CGATTTCGGC
451 AAACCTTACC AAGAAATCGA TACGCGCGTG GCGCAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1588; ORF 544>:

m544.pep

```

1  MXKILTAADV ALIGILLAIV LXPDSKTAPA FSXPD LHGKT VSNADLQGV
51  TLINFWFPSC PGCVSXMPKI IKTANDYKXK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGK*GEIF KTYVGEPDFG
151 KLYQEIDTRV AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 544 shows 90.7% identity over a 162 aa overlap with a predicted ORF (ORF 544.ng) from *N. gonorrhoeae*:

m544/g544

	10	20	30	40	50	60
m544.pep	MXKILTAADVVALIGILLAIVLXPDSKTAPAFSXPD LHGKT VSNADLQGVTLINFWFPSC					
	: : : : :					
g544	MKKILTAADVVALIGILLATVLPDSKTAPAFSLPD LHGKT VSNADLQGVTLINFWFPSC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVSXMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTV MYDADKAVGQ					
	: : : : :					
g544	PGCVSEMPKVTKTANDYKKNDFQVLAVAQPIDPIESVRQYVKDYGLPFTVIYDADKAVGQ					
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
	: : : :					
g544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1589>:

a544.seq

```

1  ATGAAAAAAA TACTCACC GC CCGTCGTC GCACTGATCG GCATCCTCCT
51  TGCCATCGTC CTCATCCCCG ACAGCAAAAC CGCGCCCGCT TTCTCCCTGT
101 CCGANCTGCA CGGAAAAANC GTTTNCAACG CCGACCTGCA AGGCNAAGTT
151 ANCCTGATTA ANTTTGGTT TCCCTCCTGT CCGGGTTGTG TGAGCGAAAT
201 GNCCANAATC ATTA AACCG CAAATGACTA TAAAAACAAA AACTTCCAAG
251 TCCTTGCCGT CGCCAGCCC ATCGATCCGA TAGAAAGCGT CCGCCAATAT
301 GTCAAAGACT ACGGTTTGCC GTTTACCGTC ATGTATGATG CGGACAAAGC
351 TGTCGGACAG GCGTTCGGCA CACAGGTTTA TCCGACTTCC GTCCTTATCG
401 GCAAAAAAAG CGAAATCCTC AAAACTTATG TCGGCGAACC CGATTTCGGC
451 AAACCTTACC AAGAAATCGA TACCGCGCTG GCACAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1590; ORF 544.a>:

a544.pep

```

1  MKKILTAADV ALIGILLAIV LIPDSKTAPA FLSXLHGKX VKNADLQGVX
51  XLIXFWFPSC PGCVMEXXI IKTANDYKXK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG

```

	10	20	30	40	50	60
m544.pep	MXKILTA	AAVVALIGILL	AIVLXPDSKT	APAFSXPD	LHGKTVSNAD	LQGVTLINFWFPSC
a544	MKKILTA	AAVVALIGILL	AIVLIPDSKT	APAFSLSLX	LHGKXVXNAD	LQGVXLIXFWFPSC
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVS	XMPKIIKT	ANDYKXKN	FQVLAVAQ	PIDPIESV	RQYVKDYGLPFTVMYDADKAVGQ
a544	PGCVSEM	XXIIKT	ANDYKKN	FQVLAVAQ	PIDPIESV	RQYVKDYGLPFTVMYDADKAVGQ
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQ	VYPTSV	LIGKKGEI	FKTYVGE	PDFGKLYQE	IDTRVAQX
a544	AFGTQ	VYPTSV	LIGKKGEI	LKTYVGE	PDFGKLYQE	IDTALAQX
	130	140	150	160		

g547.seq

This corresponds to the amino acid sequence <SEQ ID 1592; ORF 547.ng>:

g547.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547.seq

This corresponds to the amino acid sequence <SEQ ID 1594; ORF 547>:

m547.pcp

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

825

	10	20	30	40	50	60
m547 . pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547 . pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547 . pep	ELLTILVKNLSPNGKKRFVFCCK					
g547	ELLTILVKNLSPNGKKRFVFCCK					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```
a547 . seq
1  ATGTCGTAG ATAACGATT TAATAAACG GTAGCGAGTT TTGCCCAAAT
51  CGTCGAACT TTCGACGTAT TCTTCTTTAG GAACAATTGC ACCTTTTTTA
101 CGCAGATGAA ACAGCGGTGC GGTGGGTCT GTCGTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG CTTGAGATT CCGAACCGCT CCTTTAAAGA
201 CCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG
251 CCGAAGTCGA GATAGATGCT CATTACTTCC CCTTACTCAG AAAATATTTA
301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTT.TGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT T
```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```
a547 . pep
1  MFVDNGFNKT VASFAQIVET FDVFFFRNNC TFFTQMKQRC GWVCSLVYLV
51  DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEIDA HYFPLLRLKYL
101 KFIMLHIFTN IKVFXCVCVK ELLTILV
```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547 . pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547 . pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547 . pep	ELLTILVKNLSPNGKKRFVFCCK					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```
g548 . seq
1  atgttttccg taccgcgttc ctttttgccg ggcgttttcg tacttgccgc
51  gcttgccgcc tgcaaaccctc aagacaacag tgcggcgcaa gccgcttctt
101 caagtgcata cgcgcggctt gcggaataat cggcaaagcc gcaaacgcgc
151 ggtacggata tgcgtaagga agacatcggc ggcgatttca cactgaccga
201 cggcgaagga aagcctttca gcctgagcga tttgaaaggc aaggtcgtga
251 ttctgtcttt cggctttaag cactgtcccg atgtctgccc gacagggcct
```

```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtgggtg ttgctcagca tcgatccgga acgcgacacg cctgaaatca
401 tcgggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acgggcgggc aaaacctgcc ggtcatcaag cagcaatacc gcgtgggttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccggtgc gtatcttatc gataaaaacg gtgaggttgc cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

g548.pep

```

1 MFSVPRSFPLGVFLAALAA CKPQDNSAAQ AASSASAPA AENAAKPQTR
51 GTDMRKEDIG GDFTLTDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSIDLKQL GQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGGQNLPIK QYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1 ATGTTTTCCG TACCGCGTTC CTTTTTGCCG GCGTTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGCGCGCAA GTGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAATG CGGCAAAGCA AnACACGCGC
151 GGTACGGATA TGCCTAAGGA AGACATCGGC GCGGATTCA CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCGAG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTCAATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAATATTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTCTCTCG
601 CTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1 MFSVPRSFPLGVFLAALAA CKPQDNSAAQ VASSASASA AENAAKQXTR
51 GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSIDLKQL GQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIXLTA
151 TGGQNLPIK QYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFPLPGVFLAALAAACKPQDNSAAQVASSASASAAENAAKQXTRGTDMRKEDIG					
g548	MFSVPRSFPLPGVFLAALAAACKPQDNSAAQAASSASAPAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSIDLKQLGGQAKDVKVV					
g548	GDFTLTDGEGKPFSLSDLKGKVVILSFGFTHCPDVCPTGLLTYSIDLKQLGGQAKDVKVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTPETIIGKYAKQFNPDFIXLTATGGQNLPIKQYRVVSAKVNQKDDSENYL					
g548	FVSIDPERDTPETIIGKYAKQFNPDFIGLTATGGQNLPIKQYRVVSAKINQKDDSENYL					
	130	140	150	160	170	180

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	190	200	210
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
g548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
	190	200	210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

a548.seq

```

1  ATGTTTTCCG TACCGCGTTC CTTTTTGCCG GCGTTTTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GCGGATTTCG CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCG GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AACTATTGTC GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

a548.pep

```

1  MFSVPRSFPLGVFVLAALAA CKPDNSAAQ VASSSASASA AENAAKPQTR
51  GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIK QYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTL*

```

m548/a548 97.7% identity in 217 aa overlap

	10	20	30	40	50	60
m548.pep	MFSVPRSFPLGVFVLAALAAACKPDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG					
a548	MFSVPRSFPLGVFVLAALAAACKPDNSAAQVASSSASASAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKV					
a548	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTP EIIGKYAKQFNPDFIXLTATGGQNLPIKQYRVVSAKVNQXDDSENYL					
a548	FVSIDPERDTP EIIGKYAKQFNPDFIGLTATGDQNLPIKQYRVVSAKVNQKDDSENYL					
	130	140	150	160	170	180
	190	200	210			
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
a548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

g550.seq

```

1  atgataacgg acagggttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttgccag cgtaagcttc

```

828

```

151 caaatctgca atcggacggg ttgccacgcc gctttccatc gctgctttgg
201 cggcagccgt agcgacgcga ggcagcaggc gggaatcgaa cggagtagga
251 atcaggtatt ccgcgcgaa ttcgaatttc ttaccgtaag cggcaaccac
301 ttcttcggtt acttcttcca tcgccaaatc tgccaaagca tacacgcagg
351 cgcgtttcat ttcttcgttg atggtggttg cgcgcacatc caacgcgccc
401 cgggaagatga acgggaagca caatacgttg ttcacttggt tcgggaagtc
451 ggagcggccg gtaccgataa ccacgtccgg acgggtttct ttcgccagcg
501 gcggcaggat ttccggattc gggttggcca tggcgaacac gatgggtttt
551 tcgttcacatg tggtcaacat ttcaggcgtc agcaggtttg cgccggagag
601 gcccaagaag atgtctttgc ctttaaccgc atcggcaagt acgcgccggc
651 cgttgtcttc aacggcgtag aatttttttg attcgtccat gcggtctttg
701 tcttcgcggg tttggtaaat cacgcctttg gaggttgaaa cggttacgtt
751 ttcacgtttc aagcccaaat ccagcagttg gttcaggcag gcaatcgagg
801 cggcacctgc gccggagcac accaaagtgc cttcttcgat tttacggcgg
851 gtataacgca gggcgttcaa tacggcgggc gcggtaatga tggccgtgcc
901 gtgctggtca tcatgaaata cggggatttt gcagcgtttg cgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1604; ORF 550.ng>:

g550.pep

```

1 MITDRFHLFH FPVSFIYQSD NKMPPENSSD GILTTNGLQL PFAQLGSVSF
51 QICNRTGCHA AFHRCFGSR SDARQQAGIE RSRNQVFRAE FEFLT VSGNH
101 FFGYFFHRQI QSIHAGAFH FFVDGGCADI QRAPEDEREA QYVHLVREV
151 GAAGTDNHVR TGFFRQRRQD FRIRVGHGEH DGFFVHRVQH FRRQVCAGE
201 AQEDVFAFNR IGKYAPAVVF NGVEFFGFVH AVFVFAGLVN HAFGVANGYV
251 FTFQAQIQQL VQAGNRGGTC AGAHQSRFFD FTAGITQGVQ YGGGGNDGRA
301 VLVIMKYGDF AFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

m550.seq (partial)

```

1 ..GACGGCATCG GCAAGCACGC GCTGGCCGTT GTCTTCAATG GCGTAGAACT
51 GTTTGGACTC GTCCATACGG TCTTTGTCTT CGCGGGTTTG GTAAATCAGC
101 CCTTTGGAGT CGCAAACGGT CACGTTTTCG CGTTTCAAGC CCAAATCCAG
151 CAATTGGWTC AAGCAGGCAA TCGCGGCCGC ACCTGCGCCG GAACACACCA
201 AAGTCGCTTC TTCGATTTTA CGGCCGGTAA AACGCAKGGC GTTCAATACG
251 GCGGCGGCGG TAATGATGGC CGTGCCGTGC TGGTCGTCGT GGAATACGGG
301 GATTTGCAG CGTTTGCCTA A

```

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

m550.pep (partial)

```

1 ..DGIGKHALAV VFNGVELFGL VHTVFVFAGL VNHAFGVANG HVFAFQAQIQ
51 QLXQAGNRGR TCAGTHQSRF FDFTAGKTXG VQYGGGGNDG RAVLVVVEYG
101 DFAAFA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

m550/g550

				10	20	30
m550.pep				DGIGKHALAVVFNGVELFGLVHTVFVFAGLVN		
				: : : : : : :		
g550	DGFFVHRVQHFRROQVCAGEAQEDVFAFNRI	IGKYAPAVVFNGVEFFGFVHAVFVFAGLVN				
	190	200	210	220	230	240
	40	50	60	70	80	90
m550.pep	HAFGVANGHVFAFQAQIQQLXQAGNRGR	TCAGTHQSRFFDFTAGKTXGVQYGGGGNDGRA				
	: : : : : :	: : : : : :				
g550	HAFGVANGYVFTFQAQIQQLVQAGNRGGT	CAGAHQSRFFDFTAGITQGVQYGGGGNDGRA				
	250	260	270	280	290	300
	100					
m550.pep	VLVVVEYGDFAAFAX					
	: : : : :					
g550	VLVIMKYGDFAAFAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1 CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51 TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAG ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGCACAATA CATTGTTTAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTTCGC
451 CAGCGGCGGC AGGATTTCGG GATTGCGGTT GGCCATAGCG AACACGATGG
501 GTTTTTCGTT CATGGTGTTT AGTATTTCAG GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCCTTG ACGGCATCGG CAAGCACGCG
601 CTGGCCGTTG TCTTCAATGG CGTAGAACTG TTTGGAATCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTTCG GTTTCAAGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGGCGGT AATGATGGCC
851 GTGCCGTGCT GGTCGTCGTG GAATACGGGG ATTTGCAGC GTTTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1 LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51 FGSSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQRTAE DEREAYIVH LVREVGAAGT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNGVEL FGLVHTVFVF AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYSGSG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```
m550.pep
10 20 30
DGIGKHALAVVFNGVELFGLVHTVVFVAGL
|||||
a550 EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVVFVAGL
170 180 190 200 210 220

40 50 60 70 80 90
VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDG
|||||
a550 VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYSGGGNDG
230 240 250 260 270 280

100
RAVLVVVEYGDFAAFAX
|||||
a550 RAVLVVVEYGDFAAFAX
290 300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1 atgaagctga aaaccttggt attgcccttc gccgcactgg cattgtgtgc
51 caacgcattt gccgccccgc ccggcgacgc gtcgttgga cgttggtgcg
101 atacgcagaa tttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcgttat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgccgtga aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcggtca gtccgtcgtt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaat tagcggatc ttggactgca
```

830

451 ttgtcagga aaatcgcgcg acatcatctg cccgagttta cggagagatt
 501 acggcgcatc atctcgcgcg gtatagtga ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep

1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
 101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
 151 LSGKIARHHL PEFTEELRRI ICGGIVD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)

1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
 51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
 101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
 151 AATGCCGAT TTAACCGTA TGCGGACAAA GCCCTTGCCG AAATGCCGGA
 201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
 251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
 301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TGACCGGCAT
 351 GATTGCCTTT TACGTTTCGC CTGTGCGTCA GTCCGTCGTT GCCAAAAATC
 401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAG TAGCGGTATC TTGGACTGCA
 451 TTGTGAGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
 501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAAG
 551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)

1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
 101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
 151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
g552	MKLKTLLLPFAALALCANAFAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
m552.pep	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
g552	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
g552	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
m552.pep	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
g552	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIARHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
g552	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIARHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq

1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
 51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
 101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
 151 AATGCCGAT TTAACCGTA TGCGGACAAA GCCCTTGCCG AAATGCCGGA

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```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552 . pep
1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RFLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

	10	20	30	40	50	60
m552 . pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK					
a552	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m552 . pep	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
a552	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m552 . pep	YGSPVQSVVAKNPRLIKKSMEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
a552	YGSPVQSVVAKNPRLIKKSMEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
	130	140	150	160	170	180
	190					
m552 . pep	CKQAGQVGKRHQKX					
a552	CKQAGQVGKRHQKX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1 . seq
1 TTGAATATTA AACTGAAAC CTGTATTG CCCTTCGCCA CGCTGGCATT
51 GTGCACCAAT GCTTTTGCCG CCCGCGCCAG CGACGCGTGT TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAT CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCCG
301 AATACTTTAT TGAAGATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1 . pep
1 LNIKLKTL L PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVKDL ITPEVKQAVR
101 NTLKNAREI YTQEEIDGMI AFYGSVQGS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1 . seq

```

1  TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCCGCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCACTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1  LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEFN RYRENVLKDL ITPEVQAVR
101 NTLKKNAREI YTQEEIDGMI AFYGSFVGQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
m552-1	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
	10	20	30	40	50	60
a552-1.pep	DKALAEMPEAKKDQAAEFN RYRENVLKDL ITPEVQAVRNTLLKKNAREI YTQEEIDGMI					
m552-1	DKALAEMPEAKKDQAAEFN RYRENVLKDL ITPEVQAVRNTLLKKNAREI YTQEEIDGMI					
	70	80	90	100	110	120
a552-1.pep	AFYGSFVGQS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPEFTEELR RIICGGKNPD					
m552-1	AFYGSFVGQS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPEFTEELR RIICGGKNPD					
	130	140	150	160	170	180
a552-1.pep	AGCKQAGQVG KRRHQKX					
m552-1	AGCKQAGQVG KRRHQKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1  atggattatc tgcaaacct gtctttgggc ttgacaaaa agctgcccg
51  tatactgcaa acagaagtag cggagtgtgg cttggcatgt ctageggctg
101 tggccggatt ttatggtttc tatacggatt tgcgcgcact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatt gggctgacgg gacgggcgtt gaggtggat ttagacgaat
251 tgggcagttt gcgcctgccc tgtattctac attgggattt gaatcatttt
301 gtgggtgctg aatcggtatc ttcggacggg gctgccgtca tggatccggc
351 ttcgggacga cgaaagtca agacggagga aatatcgcg aagtttacgg
401 gaattgcttt ggaactgtgg ccaaacacgc gtctcgaggc aggggaagaa
451 aagcaggaaa tccgcatcct acccatgttg cgcgggattt ctgggctggg
501 gcggacattg tttcagcttt tggctttggc agcagcaatg gaagtgttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgcttgcg
601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctcccgaat caggcaaagt catgataaat gggcacgaca
701 tttacagctt accgccacct tttattccgc aatttgagtg cgatgggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaaccggt ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

833

```

1 MDYLQNLSLG LTKKLPVILQ TEVAECGLAC LAAVAGFYGF YTDLRALRSK
51 YCLSLKGENL ADIVRFADDM GLTGRALRLD LDELGSLRLP CILHWDNLNHF
101 VVLESVSSDG AAVMDPASGR RKVKTEEISR KFTGIALELW PNTRFEAGEE
151 KQEIRILPML RGISGLGRTL FOLLALAAAM EVFAFLQNVF FKIGRGESLA
201 LIGRSGCGKS TLLDILSGNL PPESGKVMIN GHDIYSLPPP FIPQFECDGQ
251 GRTMFYSGLN LNR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1621>:

```

m553.seq (partial)
1 ATGGATTATT TATCAAGACT GTCCTTTGGA TTTAACAAAA AGCTACCTGT
51 CATTCTGCAA ACAGAAGTTG CTGAATGTGG TTTAGCATGC CTGACATCCA
101 TCTTGTCTTA TTATGGCTTT CACACTGATT TAAGAACGTT ACGCCAAAAA
151 TACACCCTGT CATTAAAGGG CGCAAATCTT GCAGACATCA TGAGATTGG
201 CAATGAAATG AATTTAACGC CACGAGCTTT GCGTTTAGAG TTAGATGAGC
251 TGTCAAATTT ACAACTACCC TGCATTCTCC ATTGGAACCT AAACCATTTT
301 GTTGTACTTT GTTCCATTTT CAAAGACAGT ATCGTCATTA TGGACCCTGC
351 TGTCCGTATG CGAAAAATCA AAATGGACGA AGTTTCACAA AAATTCACAG
401 GGATTGCCCT AGAATTATTC CCCAATACCC ATTTTGAAGA GAAAAAGAA
451 ACAAAGAAAA TCAAATATT ATCTCTATTA AGGGGGGG T CAGGCTTAAA
501 ACGCTCTTTA ATTCAAATGC TTATATTAGC TATTCTTTG GAAGTCTTTG
551 CATTG...

```

This corresponds to the amino acid sequence <SEQ ID 1622; ORF 553>:

```

m553.pep (partial)
1 MDYLSRLSFG FNKKLPVILQ TEVAECGLAC LTSILSYGYF HTDLRTLROK
51 YTLSLKGANL ADIMRFGNEM NLTPRALRLD LDELNLQLP CILHWNLNHF
101 VVLCISIKDS IVIMDPAVGM RKIKMDEVSO KFTGIALELF PNTHFEKKE
151 TKKIKILSLL RGXSGLKRSI IQMLILALSL EVFAL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from *N. gonorrhoeae*:

m553/g553

	10	20	30	40	50	60
g553.pep	MDYLQNLSLGLTKKLPVILQTEVAECGLACLA	AAVAGFYGFYTDLRALRSKYCLSLKGENL				
	: : ::			::: :	: :	
m553	MDYLSRLSFGFNKKLPVILQTEVAECGLACL	TLSILSYGYFHTDLRTLROKYTL	SLKGANL			
	10	20	30	40	50	60
	70	80	90	100	110	120
g553.pep	ADIVRFADDMGLTGRALRLDLDELGSLRLP	CILHWDNLNHFVVLESVSSDGA	AVMDPASGR			
	: :	: :	: :	: :	: :	
m553	ADIMRFGNEMNLTPRALRLDLDELNLQLP	CILHWNLNHFVVLCISIKDSIVIMDPAVGM				
	70	80	90	100	110	120
	130	140	150	160	170	180
g553.pep	RKVKTEEISRKFTGIALELWPNTRFEAGEEK	KQEIRILPMLRGISGLGRTLFOLLALAAAM				
	: :		:	:	:	:
m553	RKIKMDEVSOQKFTGIALELFPNTHFEKKET	KKIKILSLLRGXSGLKRSIIQMLILALSL				
	130	140	150	160	170	180
	190	200	210	220	230	240
g553.pep	EVFAFLQNVFVKIGRGESLALIGRSGCGKST	LLDILSGNLPPESGKVMINGHDIYSLPPP				
	:					
m553	EVFAL					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1623>:

```

a553.seq
1 ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAGAAAA AGCTGCCTGT
51 TATCCTGCAA ACAGAAATAT CAGAATGCGG CTTGCCATGT CTGGCGGCTG
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCCACT GCGTTCAAAA
151 TAC

```

This corresponds to the amino acid sequence <SEQ ID 1624; ORF 553.a>:

```
a553.pep
  1  MPHQLNLSLG LKKKLPVILQ TEISECGLAC LAAVAGFHGF HTNLRALRSK
 51  Y
```

m553/a553 62.7% identity in 51 aa overlap

	10	20	30	40	50	60
m553.pep	MDYLSRLSFGFNKKLPVILQTEVAECGLACLT	SILSYYGFTDLRTL	RQKYTSLKGANL			
	: : : : : : : : : :	: : : : : : : : :	: : : : : : : : :			
a553	MPHQLNLSLG LKKKLPVILQTEISECGLAC	LAAGVAGFHGFHTNLRALRSKY				
	10	20	30	40	50	
	70	80	90	100	110	120
m553.pep	ADIMRFGNEMNLTPRALRLEDELSNLQLPCILHWNLNHFVVLCSISKDSIVIMDPAVGM					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

```
g554.seq..
  1  atgacagcac ataaaatcct gcccgctcctt cttcccatca tcttaggcgt
 51  ttctcacgca acggctgcat cgcccgcgcc caacagaccg acggtacacg
101  ccgccccac gctccaaaca cccgaaaccc tcacggcggc acacatcggt
151  atcgaccttc aaagcaggca gactttatcc gccaaaaaca ccaatacccc
201  tgtcgaaacg gcggcactaa cccaactgat gaccgcataat ttggttttca
251  aaaacatgaa atcgggaaat atccaatctg aagaaaactt aaaaataccc
301  gaatccgcat gggcttcaga aggaagcaga atgtttgtac gtcccgcgca
351  tacggtcagc accgacaaac tcttaaaagg catgattgcc ctatgcgcaa
401  acgatgccgc cctaaccctt gccgaccggc tgggcaacgg ctcgattgaa
451  aattttgtgc aacaaatgaa caaagaagcc cgacgcttgg gcatgaagaa
501  caccgtattc aaaaaccgca caggcttggg tagagaagga caggtttcca
551  ccgccaaga cctctccctg ctgtctgaag cattgatgcg cgactttccg
601  gaatattacc cgctgttttc catcaaactg ttcaagtttg aaaaataga
651  acaaaacaac cgcaatatcc ttttatatag ggacaacaat gtaaacggcc
701  tgaaagccgg gcacacagaa agcggcggtt acaaccttgc cgtgtcatac
751  tcgggcaacg gcaggcacat ccttgatcac acactagggt cggaatcggc
801  ggaaaccgca gcatcggaca acagcaagct gctgaaccgg gcattgcagg
851  ccttcgatac gcccataata tatccgaaag gcaaaaccgt tgcccaaatc
901  caaatttcgg gaggcagcaa aaaaaccgtc cgcgagggtt tcctcaaaga
951  agcctacatc actctgccac ataaagaagc gaaaatggca gaacagattt
1001  tggaaacccat acagccgatt cccgccccgg taaaaaaagg gcagatttta
1051  ggaaaatcga aatcaggca aaacggacat accattgccg aaaaagaaat
1101  cgtcgcaactg gaaaacgtag aaaaaagaag ccggtggcaa aggccttgga
1151  cgcgtctgac agggcagtaa
```

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

```
g554.pep..
  1  MTAHKILPVL LPIILGVSHA TAASPAPNRP TVHAAPTLOT PETLTAAHIV
 51  IDLQSRQTLA AKNTNTPVEP AALQQLMTAY LVFKNMKSGN IQSEENLKIP
101  ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LCANDAALTL ADRLNGSIE
151  NFVQOMNKEA RRLGMKNTVF KNPTGLGREG QVSTAKDLSL LSEALMRDFP
201  EYYPLFSIKS FKFENIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251  SGNRHLVI TLGSESAETR ASDNSKLLNR ALQAFDTPKI YPKGKTVAQI
301  QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKQIL
351  GIKIRQNGH TIAEKEIVAL ENVEKRSRWQ RLWTRLTGQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

```
m554.seq..
  1  ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
 51  TTCTCACGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGTACACG
101  CCGCCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151  ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
201  TGTTGAACCG GCGGCACTAA CCAACTGAT GACCGCATAT CTGGTTTTC
251  AAAACATGAA ATCGGGCAAT ATCCAATCTG AAGAAACTT AAAAATACCC
```

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```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCGG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCTATC
751 TCCGGCAACG GCAGGCACAT CCTTGTCTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACCTG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
101 ESAWASEGSR MFVRPGDTSV TDKLLKGMIA LSANDAALT LAGRLNGSIE
151 NFWQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHLILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKT V RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKI KIRONGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

m554.pep	10	20	30	40	50	60
	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSKQILS					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSRQTL					
	10	20	30	40	50	60
m554.pep	70	80	90	100	110	120
	AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTSV					
g554	AKNTNTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTSV					
	70	80	90	100	110	120
m554.pep	130	140	150	160	170	180
	TDKLLKGMIALSANDAALTLAGRLNGSIEFVQQMNKEARRLGMKNTVFKNPTGLSREG					
g554	TDKLLKGMIALCANDAALTADRLNGSIEFVQQMNKEARRLGMKNTVFKNPTGLGREG					
	130	140	150	160	170	180
m554.pep	190	200	210	220	230	240
	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFENIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
m554.pep	250	260	270	280	290	300
	SGGYNLAVSYSGNRHLIVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					

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```

g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNRLAQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300

           310      320      330      340      350      360
m554 .pep  QISGGSKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKQILGKIKIRONGY
           |||||
g554      QISGGSKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKQILGKIKIRONGH
           310      320      330      340      350      360

           370      380      390
m554 .pep  TIAEKEIVALENVKRSRWQRLWACLGTGX
           |||||
g554      TIAEKEIVALENVKRSRWQRLWTRLTGQX
           370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```

a554.seq
1  ATGACAGCAC ATAAATCCT GCCCGTCCTG CTTCCATCA TCTTAGGCGT
51  TTCTACGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGCACACG
101 CCGCCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
201 TGTCGAACCG GCGGCACTAA CCCAAGTAT GACCGCATAT CTGGTTTTCA
251 AAAACATGAA ATCGGGAAAT ATCCGATCTG AAGAAACTT AAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTGTAC GTCCCGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT GCCGGCCGCG TGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCAG CTGTCTGAAG CATTGATGCG CGACTTCCG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTC AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCCG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCAATC
751 TCCGGCAACG GCAGGCACAT CCTGTGCATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAAGTGG GCATTGCAAG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCAGC TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```

a554.pep
1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQMTAY LVFKNMKSNG IRSEENLKIP
101 ESAWASEGSR MFVRPGDVS TDKLLKGMIA LSANDAALTL AGRLGNLSIE
151 NFVQQMKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPLFSIKS FKFNIEQNN RNILLYRDNV VNLKAGHTE SGGYNLAVSY
251 SGNGRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKQIL
351 GKIKIRONGY TIAEKEIVAL ENVKRSRWQ RLWACLGTQ*

```

m554/a554 99.2% identity in 389 aa overlap

```

           10      20      30      40      50      60
m554.pep  MTAHKILPVL LSIILGVSHATAASPAPNRPVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           |||||
a554      MTAHKILPVL LSIILGVSHATAASPAPNRPVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           10      20      30      40      50      60

           70      80      90      100     110     120
m554.pep  AKNINTPVEPAALTQMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDVS
           |||||
a554      AKNINTPVEPAALTQMTAYLVFKNMKSNGIRSEENLKIPESAWASEGSRMFVRPGDVS

```

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	70	80	90	100	110	120
m554.pep	130	140	150	160	170	180
a554	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQOMNKEARRLGMKNTVFKNPTGLSREG					
	130	140	150	160	170	180
m554.pep	190	200	210	220	230	240
a554	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNLKAGHTE					
	190	200	210	220	230	240
m554.pep	250	260	270	280	290	300
a554	SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300
m554.pep	310	320	330	340	350	360
a554	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRONGY					
	310	320	330	340	350	360
m554.pep	370	380	390			
a554	TIAEKEIVALENVKKRSRWQRLWACL TGQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51  cgccgtttta agcctcatta tcgtattgat tgcgattcc  tggccgcttg
101 ccatcctgct tgccgcccgc atcgtcgccg ccgctgcggg cggctttggt
151 tggacatccc gccgacagca acgccagttt atcgaacgtc tgaaaaaatt
201 cgacatcgat ccgaaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcggacaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cacgctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaattgc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKRPRTR QEINQMAAKQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAAC T GCGCTTGGGC GGCCTGATT TACTGACCAC
51  CGCCGTTTTA AGCCTCATT TCGTATTGAT TGTGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTGCTG CCGCTGCGGG CGGTTTTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTGCGCAA AATGTTTCGGT GGACGAGGCG CACGCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

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101 LSQKCSVDEA HAMFKRPTR QEINQMAAQ SRGQKRPHR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKT KLRLG LILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
g556	MDNKT KLRLG LILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKRPTR					
g556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKRPTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAQSRGQKRPHRX					
g556	QEINQMAAQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACCAA	ACT	GCGCTTGGGC	GGCCTGATTT	TACTGACCAC
51	CGCCGTTT	AGCCTCATTA	TCGTATTGAT	TGTCGATTCC	TGGCCGCTTG	
101	CCATCCTGCT	TGCCGCCGTC	ATCGTCGCCG	CCGCTGCGGG	CGGCTTTGTT	
151	TGGACATCCC	GCCGACAGCA	ACGCCAGTTT	ATCGAACGTC	TGAAAAAATT	
201	CGACATCGAT	CCCGAAAAAG	GCAGAATCAA	CGAGGCAAAC	CTGCGCCGTA	
251	TGTACCACAG	CGGCGGACAA	CACCAAAAAG	ATGCGATTAC	CCTGATCTGC	
301	CTGTCGCAA	AATGTTCTGGT	GGACGAGGCG	CACGCTATGT	TCAAAAAACG	
351	CCCGACACGT	CAGGAAATCA	ATCAAATGGC	GGCAAAACAG	TCGCGCGGTC	
401	AGAAACGTCC	GCACCGTTAA				

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKT KLRLG	GLILLTTAVL	SLIIVLIVDS	WPLAILLAAV	IVAAAAGGFV
51	WTSRRQQRQF	IERLKKFDID	PEKGRINEAN	LRRMYHSGGQ	HQKDAITLIC
101	LSQKCSVDEA	HAMFKRPTR	QEINQMAAQ	SRGQKRPHR*	

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKT KLRLG LILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
a556	MDNKT KLRLG LILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKRPTR					
a556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKRPTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAQSRGQKRPHRX					
a556	QEINQMAAQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pep..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq. .

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

m557.pap.

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1641>:

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a557.seq
 1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
 51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
 101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG
 151 CTGTATCAGG CTTCCGGTAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
 201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC
 251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
 301 GTATTGAAAC GCGGCGAGCC GGTCGCAGAA CCGATGACCG TGTCCTGCCG
 351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
 401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
 451 CGCCGCCTGA CCTTCTGAA GGCGGAATGA

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

a557.pep
 1 MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
 51 LYQASGRVDD AAGAQMTLRI DSVSQNKETY TVTRA AVINE YLLILTVEAQ
 101 VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
 151 RRLTFLKAE*

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA AV LMLGACGFHLKGADGISPPLTYRSWHIEGGQALRFPLETA	LYQASGRVDD				
a557	MNKLFLTA AV LMLGACGFHLKGADGISPPLTYRSWHIEGGQALQFPLETA	LYQASGRVDD				
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTL RIDS V SQNKETY TVTRA AVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
a557	AAGAQMTL RIDS V SQNKETY TVTRA AVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEILGKQEEEAALWAE MRQDAAEQIVRRLTFLKAE X					
a557	AYADNEILGKQEEEAALWAE MRQDAAEQIVRRLTFLKAE X					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

g558.seq..
 1 ATGGATGCTT GTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
 101 TGCCCTTATA TACTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG
 201 ATTCTATCGC TATAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
 251 AGTCCATTTC CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
 301 CTTTCAGACG GCATTGTTTA G

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

g558.pep..
 1 MDACFFVIPA QAGIRRFIV FKRSGRILAG AGMPLYTFS ELYMLQQGTA
 51 HQAPHCVLPE RGCPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSENQSP
 101 LSDGIV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

m558.seq..
 1 ATGAATGCTT GTTTTTCGT CATTCCCA CA CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA
 101 TGCCCTTATA TACTTCTCC GAGCTTTATA TGTTTCAACA GGGGACGGCA
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG
 201 ATTCTATCGC CATAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
 251 AGTCCATTTC CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
 301 CTTTCAGACG GCATTGTTTA G

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

m558/g558

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

m558/a558 70.2% identity in 141 aa overlap

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1649>:

g560.seq
1 atgctcatca tccgcaacct gatttactgg ctgatactct gttccagcct

g560.pep..

```

1  MLIIRNLIYW LILCSSLIFL PPFMLLASPF RDGAHKMARV WVGILNWSLK
51 HIVGLKYRII GAEHIPDRPS VICAKHQSGV ETALAQEIFP PQVYVAKREL
101 FKIPFPWGWL KLVKTTGIDR NNRREANEQL IKOGLARKNE GYWTITFPEG
151 TRLAPGKGRK YKLKGIGARM MFEMDINEFVA LNSGEFWEKN SWFLYPGEIT
201 VLIICPTIPHA SGSEAEIMEK CEHLIETQOP LLSGAGPFAA EMPSET*

```

m560.seq

seq	1	ATGCTCATCA	TCCGCAACCT	GATTTACTGG	CTGATACTCT	GTTCCACCCT
51		GATTTTCTCT	TTTCCCTTTA	TGCTGCTGCG	CTCGCCTTTC	CGGGACGGGG
101		CGCACAGAT	GGCGCGGGTC	TGGGTCCGGC	TTCTCAACTG	GTCGCTCAAA
151		CACATCGTCG	GGCTCAAATA	CCGCATCATC	GGCGCGGAAA	ACATCCCGGA
201		CCGCCCCGCC	GTGATCTGCG	CCAAACACCA	AAGCGGCTGG	GAACAACGCTCG
251		CCCTTCAGGA	CATTTTTCGG	CCGCAGGTTT	ACGTTGCCAA	ACGCGAGTTG
301		TTCAAAATCC	CCTTTTTCGG	CTGGGGCTTG	AAACTGTTCA	AAACCATAGG
351		CATAGACCGC	AACAACCGCC	GCGAAGCCAA	CGAGCAGCTC	ATAAAACAGG
401		GGTTGGTGCG	CAAAAACGAA	AGCTATTGGA	TTACCATTTT	CCCCGAAGCG
451		ACGCGCCTTG	CGCCCGGAAA	GGCGTCGAAA	TACAAACTCG	CGCGGCGCGC
501		CATGGCGAAA	ATGTTTGAGA	TGGACATCGT	CCCCGTCGCC	CTCAACAGCG
551		GCGAATTTTG	GCCGAAAAAC	TCTTTTCTGA	AATATCCGGG	GGAAATCACC
601		GTCGTATCT	GTCCGACCAT	CCCGCACGCA	AGCGGCAGCG	AAGCCGAATT
651		GATGGA AAAA	TGCGAACATC	TCATCGAAAC	GCAACAACCG	CTTATTTCGG
701		GCGCGAGCCC	GTTTGGCGCC	AAAATGCCGT	CTGAAACCGC	ATGA

m560.pep

1	MLIIRNLIYW	LILCSTLIFL	FFFMLLASPF	RDGAHKMARV	VWGILNWSLK
51	HIVGLKYRII	GAENIPDRPA	VICAKHQSGW	ETLALQDIFP	PQVYVAKREL
101	FKIPFFGWGL	KLKVTTIGDR	NNRREANEQL	IKQGLVRKNE	GYWITYPFEG
151	TRLAPGKRKG	YKLGGMARMA	MFEMDIIVPA	LNSGDFWPKN	SLKTYPGEIT
201	VVICPTIPHA	YKSEAELMEK	CEHLIETQOP	LISGAGPFPA	KMPSETA*

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 560 shows 97.2% identity over a 246 aa overlap with a predicted ORF (ORF 560.ng) from *N. gonorrhoeae*:

m560/g560

	10	20	30	40	50	60
m560.pep	MLIIIRNLIYWLILCSTLIFLFPFMLLASPRDGAHKMARVWVGILNWSLKHIVGLKYRII					
	:					
g560	MLIIIRNLIYWLILCSSLIFLFPFMLLASPRDGAHKMARVWVGILNWSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	: : :					
q560	GAEHIPDRPSVICAKHQSGWETLALQEIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					

843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
g560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```
a560.seq
1  ATGCTCATCA TCCGCAACCT GATTACTGG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCCTTC CGAGACGGGG
101 CGCACAAAGAT GGCGCGGGTC TGGGTCAAAA TCCTCAACCT CTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCGGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCGG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAATCC CCTTTTTCGG CTGGGGCTTG AACTGGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAAAACAGG
401 GGTGGCGCG CAAAACGAA GGCTATTGGA TTACCATTTT CCCCAGAGGC
451 ACACGCCTTG CGCCCGGAAA ACGCGGCAA TACAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCGCGTCGCC CTCACAGCG
551 GCGAATTTT GCGGAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGGAAA TCGAACACC TCATCGAAAC GCAGCAGCG CTCATTTCCG
701 GCGCAGGCC GTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA
```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```
a560.pep
1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK
51  HIVGLKYRII GAENIPDRPA VICAQHSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKR GK YKLGARMAM MFEMDIVPVA LNSGEFWPKN SLKYPGEIT
201 VVICPTIPHA SGSEAELEMGK CEHLIETQQP LISGAGPFAA KMPSETA*
```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK HIVGLKYRII					
a560	MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK HIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPA VICAQHSGW ETLALQDIFP PQVYVAKREL FKIPFFGWGL KLVKTIGIDR					
a560	GAENIPDRPA VICAQHSGW ETLALQDIFP PQVYVAKREL FKIPFFGWGL KLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					

844

	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
a560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMGKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
a560	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

m561.seq.

```

1  ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GCGGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAA ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCGTGCGC AAATTGACAA TCAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCT
301 TCGGACACCC CTCTTGCTTA TGATTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCCTCCA GTCCTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGCAGGCA
451 TTGGAATATG CCAACGAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTGCTC TGTACTGATG CTGTTTTGGC
551 ACCAGATTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTCGGGC GTTGTTTCAA TCAAATGGGC GGCAGGTTGA
701 AAATTTTATA TGATGATTTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAC AAAATCAAAA CCTGACCCTG CTGTACCAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCGTAGGA GCAGATTCCG GCAGAGTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTT CATTTCATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTG GGGAGTACC ATGAGGAAAT CTTCCTCATT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGG CATTTCTCTT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGCGGT
1101 ATCGCTTGCC GCGCAAAAC AGGAGGAAGA AAAACGCCTG CTTGCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAA CCGCTTTTGC
1251 CGAAAACAAA CGGGAGGAAG CCGCAGAAA CATCAGCTTT ATCAAAACAG
1301 GCGTGCAGGA ATGTTATGAA GATGTCCGCG AACTGCTGCT CAACTCCGT
1351 ACCAAAATCA GCAATAAAGA ATTTCCCGAA GCCGTTGCCG ACCTATTCGC
1401 CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAAACG
1451 GTTCGTTTCT GCGCCTCAG GAAGCGCAGC TCCAAATGAT TTTTATCCTG
1501 CAGGAAAGCC TGTCCAACAT CCGCAAACAC GCGGCGGCCA CCCATGTAAA
1551 ATTCACCTT TCCGAACACG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTCGACACG GAGAAAATAG GAGAACCAC GGGCAGCCAT
1651 GTCGGAAGTC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

m561.pep

```

1  MILPARFSDG ISLSRLRLKL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFELSLKRIA QSDAIHFLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRFFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
251 LEKQNQNLTLYQTTDLHQ SYIPQQAEEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGRLLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEERL LAVLQERNLI AQGLHDSIAQ
401 ALTFILNLQV MLETAFAENK REEAAENISF IKTGVEQECYE DVRELLNFR
451 TKISNKEFPE AVADLFARFT QQTGITVETA WENGSELPPO EAQLQMIFFL

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501 QESLSNIRKH ARATHVKFTL SEHGGRFTMT IQDNGQGFD T EKIGEPTGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQGGTTVS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALS	VVLTL	LLSLRL	ENAA	SVEE	EAGNLRMQAY
g561	MILPTRFSDGIPLSLRLKLLTGLWVGLAALS	VVLTL	LLSLR	ENAA	SVEE	EAGNLRMQAY
	10	20	30	40	50	60
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAE	FEKSLKRIA	QSDAIHPL	PSDTP	LAYDLIQ	SMLIIDWQA
g561	RLAYMAGEGSPRAQIDNQIAE	FEKSLKRIS	QSDAIHPL	SDNPLAY	DLIQ	SMLIIDWQA
	70	80	90	100	110	120
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYR	FAGNIELF	LQALENA	NEKNTW	WLRRFQ	WAIMLMTLVSSVLM
g561	NILPPLQAYRRPTQIELYR	FAGNIELF	LQALENA	GEKNTW	WLRRFQ	WVIMLMTLVSSVLM
	130	140	150	160	170	180
	190	200	210	220	230	240
m561.pep	LFWHQIWI	RPLQALRE	GAERIGR	RCFDIP	VP	EGGTPEFKQVGR
g561	LFWHQIWI	RPLQALRE	GAERIGR	HFQDIP	VP	EDVRENSNRSGGVSTKWRSGX
	190	200	210	220	230	
	250	260	270	280	290	300
m561.pep	EGQVAEQ	TRSLEKQ	NQNLTL	LLYQTT	RDHLQ	SYIPQQA

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

```

1  ATGATACTGC CAGCCCCTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GGCGGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAA ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAA TGCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCGTGC GC AAATTGACAA TCAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCTC
301 TCGGACACCC CTCTTGCTTA TGATTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCGCTCCA GTCCTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGCAGGCA
451 TTGGAAAATG CCAACGAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTCTG TGTACTGATG CTGTTTGGG
551 ACCAGATTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTCGGG GTTGTTCCTA TCAATGGGC GGCAGGTTGA
701 AAATTTTATA TGATGATTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCCTG CTGTACCAA CTACACGGGA
801 TCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTT CATTCATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTG GGAAGTACC ATGAGGAAAT CTTCCCATC GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACG CATTTCTCTT
1051 GATGAAGACG ACCGCATCCT GCTTCAACA CTAGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GGCGCAAAAC AGGAGGAAGA AAAACGCCTG CTGTCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAA CCGCCTTTGC
1251 CGAAAACAAA CGGGAGGAAG CCGCAGAAAA CATCGGCTTC ATCAAAACAG
1301 CCGTGCAGGA ATGTTATGAA GATGTCGCG AACTGCTGCT CAACTCCGT
1351 ACCAAAATCA GTAATAAAGA ATTTCCCGAA GCCGTGCGG ACCTATTCTC

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1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGGCCA CCCATATCAA
1551 ATTCAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAAGACA
1601 ACCGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAG TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
1  MILPARFSDG ISLSLRKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMILIOWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
251 LEKQONLTL LYQTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGRLLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQVQ MLETAFENK REEAAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFFE AVADLFSRFT QQTGTTVETA WENGTHLPQT DEQLQMIFIL
501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQFDT ENIGEPGSGH
551 VGLHIMQERA KRIHAVLEIR SQAQQTTSV LTVASEESLK *

```

m561/a561 96.9% identity in 590 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSLRKLLTGLWVGLAALS SVVLTLLLSLRLENAASVIEEAGNLRMQAY					
a561	MILPARFSDGISLSLRKLLTGLWVGLAALS SVVLTLLLSLRLENAASVIEEAGNLRMQAY					
	10	20	30	40	50	60
m561.pep	70	80	90	100	110	120
a561	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMILIOWQA					
a561	RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMILIOWQA					
	70	80	90	100	110	120
m561.pep	130	140	150	160	170	180
a561	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM					
a561	HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM					
	130	140	150	160	170	180
m561.pep	190	200	210	220	230	240
a561	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLLKILYDDL					
a561	LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLLKILYDDL					
	190	200	210	220	230	240
m561.pep	250	260	270	280	290	300
a561	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQONLTLTYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG					
a561	EGQVAEQTRSLEKQONLTLTYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG					
	250	260	270	280	290	300
m561.pep	310	320	330	340	350	360
a561	310	320	330	340	350	360
m561.pep	GSDVYVSIHHADCCTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT					
a561	GSDVYVSIHHADCCTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT					
	310	320	330	340	350	360
m561.pep	370	380	390	400	410	420
a561	370	380	390	400	410	420
m561.pep	LGRQLGVSLAGAKQEEKRLAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK					
a561	LGRQLGVSLAGAKQEEKRLAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK					

847

	370	380	390	400	410	420
	430	440	450	460	470	480
m561. pep	REEAAENISFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFARFTQQTGITVETA					
a561	REEAAENIGFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFSRFTQQTGTTVETA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m561. pep	WENGSLFPPEAQLQMIFILQESLSNIRKHARATHVKFTLSEHGGRFTMTIQDNGQGFD					
a561	WENGTHLPTQDEQLQMIFILQESLSNIRKHAHATHIKFRLKQDGSFTMTIQDNGQGFD					
	490	500	510	520	530	540
	550	560	570	580	590	
m561. pep	EKIGEPTGSHVGLHIMQERAKRIHAVLEIRSQAQGGTTVSLTVASEESLKX					
a561	ENIGEPSGSHVGLHIMQERAKRIHAVLEIRSQAQGGTTVSLTVASEESLKX					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562. seq..

```

1  atggcaagcc cgtcgagtct gcctttcaat tcgggcaaga ccaaaccgac
51  ggcttttgcc ggcgcggttt tggtcggaat catgttttcc acgccgctgc
101 gggcgcgccg caggtctttg tggcgcacgt cggtaacggt ttggtcgttg
151 gtcagtgcgt ggatggtggt cattgcgcct ttgacgatgc cgacgctttc
201 gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaacgct
251 tggaacgac ggtcatgtcg gcggtcagga cgctgtcgtt caccgcgtac
301 acgacggtt catcgacatc gtcgcgcgcc ggtgcggaat tgaggacttt
351 tttcgcgccg ctttcgaggt ggattttggc tttttctttg ctggtgaacg
401 cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451 tcggcagggg tgccgggtcga gaagaagggg attttgtcgc cgttgacgat
501 gaggttgccg ccgtcgtggg atacgtcggc ttcaaagcgt ccgtgtacgg
551 tgtcgaattt ggtcagatgg gcgttggttt caaggctgcc gctggcggtg
601 acggcgacga tttggagttg gtcttga

```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562. pep

```

1  MASPSSLPFN SGKTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMP TSLNLT LATGERQLVV QEALTTVMS AVRTLSTFPY
101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSM TSTPSSFHGS
151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRPLAL
201 TATIWSWS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562. seq

```

1  ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC
51  GGCTTTTGCC GCGCCGGTTT TGGTCGGAAT CATGTTTTC ACGCCGCTGC
101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGTTGTT CATCGCGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAACGCT
251 TGGAACGAC GGTGATGTCG GCGGTCAGGA CGCTGTCGTT CACGCCGTAC
301 ACGACGGTTG CATCGACATC GTCGCGGCC GGTGCGGAAA TGAGGACTTT
351 TTTCGCGCCG CTTTCGAGGT GGATTTTGGC TTTTCTTTG CTGGTGAACG
401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TGCGGGTCCA GAAGAAGGGG ATTTGTGCGC CGTTGACGAT
501 GAGGTTGCCG CCGTCGTGGG ATACGTGCGC TTCAAAGCGT CCGTGCACGG
551 TGTGGAATTG GGTGAGATGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA GTTGGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562. pep

```

1  MASPSSLPFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMP TSLNLT LATGERQLVV QEALTTVMS AVRTLSTFPY

```

848

1 01 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
 1 51 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL
 2 01 TATSWSWS*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLFNSGSKPTAFAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMMVVIAP					
g562	MASPSSLFNSGSKPTAFAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMMVVIAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPTTVASTSSPPGAEMRTFFAP					
g562	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTASAKR					
g562	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTASAKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRLPLALTATSWSWSX					
g562	PCTVSNLVRWALVSRLPLALTATIWSWSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

a562.seq
 1 ATGGCAAGCC CGTCGAGTTT GTCTTTCAAT TCGGGCAGTA CCAAACCGAC
 51 GGCTTTTGCC GCGCCAGTTT TGGTCGGAAT CATGTTTCC ACGCCGCTGC
 101 GGGCGCGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTG
 151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
 201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
 251 TGGAAACGAC GGTGATGTCG GCGGTCAGGA TGCTGTCGTT CACGCCGTAC
 301 ACGACGGTTG CATCGACATC GTCGCGGCCC GGTGCGGAAA TGAGGACTTT
 351 TTTCGCGCCG CTTTCCAGAT GAACTTTGGC TTTTCTTTG CTGGTGAACG
 401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTCTTT CCACGGCAGT
 451 TCGGCAGGGT TGCCGGTCNA GAAGAANGG ATTTTGTGCG CGTTGACGAT
 501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGACCG
 551 TGTCGAATTT GGTGAGGTGG GCGTTGTTT CAAGGCTGCC GCTGGCGTTG
 601 ACGGCGACGA TTTGGAGTTG GTCTTGA

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

a562.pep
 1 MASPSSLFNSGSKPTAFAPVLVGIMFS TPLRARRRSL WRTSVTVWSL
 51 VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALETTVMS AVRMLSFTPY
 101 TTVASTSSPP GAEMRTFFAP LSR*TLAFSL LVNAPVHSMT KSTPSSFHGS
 151 SAGLRVXXKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL
 201 TATIWSWS*

m562/a562 96.6% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLFNSGSKPTAFAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMMVVIAP					
a562	MASPSSLFNSGSKPTAFAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMMVVIAP					
	10	20	30	40	50	60

849

	70	80	90	100	110	120
m562. Pep	LTMP TLSLNTLATGERQLVVQEALETTVMSAVRTLSEFTPYTTVASTSSPPGAEMRTFFAP					
a562	LTMP TLSLNTLATGERQLVVQEALETTVMSAVRMLSEFTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562. Pep	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMRLPPSWDTSASKR					
a562	LSRXTLAFSLLVNAPVHSMTKSTPSSFHGSAGLRVKKXGILSPLTMRLPPSWDTSASKR					
	130	140	150	160	170	180
	190	200	209			
m562. Pep	PCTVSNLVRWALVSRLPLALTATSWWSX					
a562	PCTVSNLVRWALVSRLPLALTATIWSWX					
	190	200				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563.seq

```

1  ATGAACAAAA CCCTCTATCG TGTGATTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGGTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTCTTTTAT GTTTGGCTTT
201 GGGTACCGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCCc tACTTCGGCa ggGGTTTCTG TTAATCAATA
351 TGCCCGATTT GATGTGGGTA ATcgCGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GGCGGTTGGA TTCAAGGCAA TCCTTGTTG
451 ACAAGGGGCG AAGCACGTGT GGTTGTAAAC CAAATCAACA GCAGCCATCC
501 TTCACAAC TG AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAAGTCG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTAAAGATAA GGCAAGGCAA TGCTGTAATC GCCGGACACG
701 GTTTGGATGC CCGTGATACC GATTTCACAC GTATTCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTC GTAATCAAGG
801 GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGGCACGATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAAGTCAA TATCCGCAGT CAAGCCTTTG AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 ACATGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCCTGAACA ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTCAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTCAGG CAAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGCTGATAA TAAACTGGAT ATTGCGTTAC AAGATGATTT
1251 TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACCTTGC AAGCAGGAAA ACGCATTTCG
1351 ATTAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1401 CGGTACGACA GACATTGGCA CGCAGCACAA TTAAACCAAT AGAGGCTTGA
1451 TTGACGGACA ACAAACCAA ATCCAAGCCG GGCAAATGAA TAATATCGGT
1501 ACAGGTCGGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
1551 CAATCAAGAT GAAACCGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
1601 TGAATTTAGG CATTGAACAA TTAAATAACC GTGAAAACAG TCTGATTAC
1651 AGCGGTAACG ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGACCAAGC
1701 CACAGGCAAA GCCCAAAGGA TACACAATGC CGGCGCAATC ATTGAAGCTG
1751 CAGGCAAAAT GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT
1801 TTGAAAACGC AGTTGGTAGA AACAGGGCGC GAGCGTATTG TTGATTACGA
1851 AGCATTGGGA CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG
1901 GCTGGTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAAC TG CCGCTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTCAACA GCGACAGCCG AATCATTGCC

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2101 GCGCGCCAAT TGCTTGTGCA AACAGAAAAA GACGGTTTGC ATAACGAGCA
2151 AACCTTTTGC GAGAAGAAAG TCTTCAGCGA AAATGGTAAG TTGCACAAC
2201 ACTGGCGTGC GCGTCGTAAA GGACATGATG AAACAGGGCA TCGTGAACAA
2251 AATTATACTT TGCCGAGGA AATCACACGC GACATTTTAC TGGGTTTATT
2301 TGCCTATGAA TCGCATAGCA AAGCATTAAAG CCGTCATGCG CCCAGCCAAG
2351 GCACTGAGTT GCCACAAAGT AACCGGGATA ATATCCGTAC TCGGAAAAGC
2401 AACGGTATTT CGCTACCCTA TACGCCCAAT TCTTTTACCC CATTACCCGG
2451 CAGCAGCTTA TACATTATCA ATCCTGCCAA TAAAGGCTAT CTTGTTGAAA
2501 CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGGGTAG TGACTATATG
2551 CTGGGCAGCC TCAAACTAGA CCCAAACAAT TTACATAAAC GTTTGGGTGA
2601 TGGTTATTAC GAGCAACGTT TAATCAATGA ACAATCGCA GAGCTGACAG
2651 GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA ATTTAAAGCC
2701 TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC TCAGCGTTGG
2751 CATTGCATTA AGTGCCGAGC AAGCAGCGCA ACTGACCAGC GATATTGTTT
2801 GGTGGGTACA AAAAGAAGTT AAACCTCCTG ATGGCGGCAC ACAAACCGTA
2851 TTGATGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGGCA TAGACGGTAA
2901 AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT TCAGGCAGCC
2951 TGAAAAAATC AGGCACGATT GCAGGGCGCA ATGCGCTTAT TATCAATACC
3001 GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA AATCAGCGGT
3051 TACGGCCACA CAAGACATCA ATAATATTGG CGGCATTCTT TCTGCCGAAC
3101 AGACATTATT GCTCAATGCG GGTAACAACA TCAACAACCA AAGCACGGCC
3151 AAGAGCAGTC AAAATGCACA AGGTAGCAGC ACCTACCTAG ACCGAATGGC
3201 AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA GCGCAGGCAG
3251 GCAAGACAT CAACATCATT GCGGTCAAA TCAGCAATCA ATCAGATCAA
3301 GGGCAAAACC GGCTGCAGGC AGGACGCGAC ATTAACCTGG ATACGGTACA
3351 AACC GGCAAA TATCAAGAAA TCCATTTTGA TGCCGATAAC CATACCATCC
3401 GAGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA AGGCGATGTT
3451 ACCCtatTGT CAGGGAATAA TCTCAATGCC AAAGTGCCG AAGTCGGCAG
3501 CGCAAAAGGC ACACTTGCCG TGTATGCTAA AAATGACATT ACTATCAGCT
3551 CAGGCATCCA TGCCGGCCAA GTTGATGATG CGTCCAAACA TACAGGCAGA
3601 AGCGCGGGCG GTAATAAATT AGTCATTACC GATAAAGCCC AAAGTCATCA
3651 CGAAACTGCT CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT GTATTGCAGG
3701 CAGGAAACGA TGCCAACATC CTTGGCAGTA ATGTTATTTC CGATAATGGC
3751 ACCCGGATTC AAGCAGGCAA TCATGTTTCG ATTGGTACAA CCCAACTCA
3801 AAGCCAAAGC GAAACCTATC ATCAAACCCA AAAATCAGGA TTGATGAGTG
3851 CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA AGAAAACCAA
3901 TCCCAAAGCA ACCAATATAC AGGCAGTACC GTAGGCAGCC TGAAAGGCGA
3951 TACCACCATT GTTGCAAGCA AACACTACGA ACAAAACGGC AGCAACGTTT
4001 CCAGCCCTGA GGGCAACAAC CTTATCAGCA CGCAAAAGTAT GGATATTGGC
4051 GCAGCACAAA ACCAATTAAA CAGCAAAACC ACCCAAACCT ACGAACAAAA
4101 AGGCTTAACG GTGGGCATTG AGTTCGCCCG TTACCGATTG GGCACAACAA
4151 GCGATTGCCG TAGCACACAA AGCAGCAAAC AAGTCGGACA AAGCAAAAAC
4201 GACCGCGTTA ATGCCATGGC GGCTGCCAAT GCAGGTTGGC AGGCCTATCA
4251 AACAGGCAAA GGCGCACAAA ACTTAGCCAA TGGTACAACC AATGCCAAAC
4301 AAGTCAGCAT CTCATAACC TACGGCGAAC AGCAAAACCG ACAAAACACC
4351 CAAGTTCAAG CCAATCAAGC CCAAGCGAGT CAAATTCAAG CAGGCGGCAA
4401 AACTACCCCT TATTGCCGAA GGTGCGGCGA ACAATCCAAT ATCAACATCA
4451 CAGGCTCAGG TGTTTCAGGC AGAGCAGGAA CCGGCCTGAT TGCCGATAAG
4501 CAAATCCATC TGCAATCAGC CGAGCAAAGC AATACCGAAC GCAGCCAAAA
4551 CAAATCAGCA GGCTGGAACG CAGGTGCTGC CGTATCATTG GGACAAGGAG
4601 GCTGGTCATT AGGCGTTGCC GCAGGCGGCA ATGTCGGCAA AGGCTACGGC
4651 TATGGCGATA GCGTAACCCA CCGCCATAGC CATATTGGCG ACAAAAGCAG
4701 CCAAACCCCT ATCCAAAGTG GTGGCGATAC CATCATCAA GGCAGCGAAG
4751 TACGCGGCAA AGGCGTACAA GTCAATGCCA AAAACCTAAG CATTCAAAGT
4801 GTACAAGATA GAGAACTTA TCAAAGCAA CAACAAAACG CCGGTGCACA
4851 AGTTACCGTA GGTATGGCT TCAAGTGCCAG TGCGGATTAC AGCCAAAGCA
4901 AAATCCGAGC CGACCATGCT TCGGTAACCG AGCAAAGCGG TATTTATGCC
4951 GGAGAAGACG GCTATCAAT CAAGGTCGGA AACCATAACG GCCTCAAAGG
5001 CGGCATCATC ACCAGCAGCC AAAGCGCAA AGACAAGGTT AAAAACCGAT
5051 TCAGCACAGG CACACTCGCC GGCAGTGATA TTCAAATTA CAGCCAATAC
5101 GAAGGAAAAA GTTTTGGATT GGGTGCCAGC GTTGCCGTAA GCGGCAAAAC
5151 ACTGGGACAG GGCACAAAA ATAAACCTCA AGACAAACAC CTGACAAGCA

5201 T'AGCCGATAA AAACGGCGCA AGTTCATCAG TAGGGTACGG CAGCGACAGC
 5251 GACAGTCAAA GCAGCATCAC AAAAAGCGGC ATCAATACCC CCAAAAACAT
 5301 T'CAAAATCACA GACGAAGCCG CACAAATCAG GCTGACAGGC AAAATAGCGG
 5351 CACAAACCAA AGCCGATATT GATACAAACG TAACCACAGA CACCGCCGAA
 5401 CGACATTTCGG GCAGCCTGAA AAACATATTT GACAAAGATA GAGTGCAAAG
 5451 T'GAACTGGAT TTACAAAgaa CCGTCAGCCA AGATTTTAGT AAAAATGTTC
 5501 AACAAACCAA TACCGAGATT AACCAACATT TAGACAACT CAAAGCAGAC
 5551 AAGAAGCAG CCGAAACAGC AGCAGCCGAG GCATTAGCCA ATGGCGATAT
 5601 GGAAGCTGCC AAACGCAAAG CCCATGAAGC TCAAGATGCG GCAGCAAAAG
 5651 CAGATAATTG GCAACAAGGC AAAGTCATT TCAACATGTT AGCCTCAGGT
 5701 TTAGCTGAG CGACCCAAAG CGGAGCgggc ATCGCTGCGG CTACCGCATC
 5751 GCCagacGTA TCGTATGCGA TTGGACAGCA CTTTAAagaT TTAGCCGGTC
 5801 AAAACCGCAA TGGCAAACCT ACCGCCAGTC AagaAACCGC TCACGTTCTT
 5851 GCCCACGCGG TATTAGGAGC AGCGGTTGCC GCAGCATGAG GCAACAATGC
 5901 CCGCGCAGGA GCATTGGGTG CCGGCGGGTc ggAagcggCC GCCCAATCA
 5951 TCGGCAAATG GCTGTACGGC AAAGGAGAcg gcggcagccT GAATgaggag
 6001 gaaaAAGaga CCGTTTCGGC GATTACAAGG ATGCTGggta cGgctGCCGG
 6051 ACAGCTGAG GGAAACTCGT CCGCCGATGC TGTGTGGGT TGTTTTcaaa
 6101 cggctTCaga TTTCGCTTCC TCTTTTTCAT ATCTATAAA CATGTGA

This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:

g563.pep..

1 MNKTLRVIF NRKRGAVVAV AETTKREGKS CADSGSGSVY VKSVSFIPTH
 51 SKAFCSALG FSLCLALGTV NIAFADGIIT DKAAPKTQQA TILQTGNIP
 101 QVNIQTPTSA GVSVNQYAQF DVGNRGAILN NSRSNTQTQL GGWIQGNPWL
 151 TRGEARVVVN QINSSHPSQL NGYIEVGRR AEVVIANPAG IAVNGGGFIN
 201 ASRATLTGQ PQYQAGDFSG FKIRQGNVAV AGHGLDARDT DFTRILLYAN
 251 KITLISTAEQ AGIRNQGLF ASSGNVAIDA NGRLVNSGTM AAANVQDMNN
 301 TAEHKVNIRS QAFENSGTAV SQGTQIHSQ SIQNTGKLLS AGTEDLAVSG
 351 SLNNQNGEIA TNQQLIHDG QQSTVVIDNT NGTIQSGRDV AIQAKSLNN
 401 GTLAADNKLD IALQDDFYVE RKIVAGNELS LSTRGSLKNS HTLQAGKRIR
 451 IKANLNDNAV QGNIQSGGTT DIGTQHNLN RGLIDGQQT IAGQMNIG
 501 TGRIYGDNIA IAATRLDNQD ENGTGAAIAA RENLNLGIEQ LNNRENSLIY
 551 SGNDMAVGA LDNDQATGK AQRIHNAGAI IEAAGKMRIG VEKLHNTNEH
 601 LKTQLVETGR ERIVDYEAFG RHELLREGTQ HELGWFVYNN ESDHLRTPDG
 651 VAHENWHKYD YEKVTQETQV TGTAPAKIIA GSDLIIDSKA VFNSDSRIIA
 701 GGQLLVQTEK DGLHNEQTFG EKKVFSNGK LHNWYRARRK GHDETGHREQ
 751 NYTLPEEITR DISLGSFAYE SHSKALSRHA PSQGTLPQS NRDNIRTAKS
 801 NGISLPYTPN SFTPLPGSSL YIINPANKGY LVETDPRFAN YRQWLGSDDY
 851 LGSLLKLPNN LHKRLGDGYE EORLINEQIA ELTGHRRLDG YONDEEQFKA
 901 LMDNGATAAR SMNLVSGIAL SAEQAAQLTS DIVVLVQKEV KLPDGGTQTV
 951 LMPQVYVRVK NGGIDGKGAL LSGSNTQINV SGSLKNSGTI AGRNALIINT
 1001 DTLDNIGGRI HAQKSAVTAT QDINNIGGIL SAEQTLILLNA GNNINNQSTA
 1051 KSSQNAQSS TYLDRMAGIY ITGKEKGVL AQAQKDINII AGQISNQSDQ
 1101 GQTRLQAGRD INLDTVQTGK YQEIHFDADN HTIRGSTNEV GSSIQTQKDV
 1151 TLLSGNNLNA KAEVGSAGK TLAVYAKNDI TISSGIHAGQ VDDASKHTGR
 1201 SGGGNKLIVIT DKAQSHHETA QSSTFEGKQV VLQAGNDANI LGSNVISDNG
 1251 TRIQAGNHVR IGTQTQSQS EYHQYQKSG LMSAGIGFTI GSKTNTQENQ
 1301 SQSNEHTGST VGLKGDTTI VASKHYEQTG SNVSSPEGNN LISTQSMFIG
 1351 AAQNQLNSKT TQTYEQKGLT VGIQFARYRF GTTSDCRSTQ SSKQVQSKN
 1401 DRVNAMAAN AGWQAYQTGK GAQNLANGTT NAKQVSISIT YGEQQRQTT
 1451 QVQANQAQAS QIQAGGKTTL YCRRCEQSN INITGSGVSG RAGTGLIADK
 1501 QIHLQSAEQS NTERSQNKSA GWNAGAASF GQGGWSLGVA AGGNVKGYG
 1551 YGDSVTHRHS HIGDKGSQTL IQSGGDTIIG GAQVRGKGVQ VNAKNLSIQS
 1601 VQDRETYQSK QONAGAQTV GYGFSASGDY SQSKIRADHA SVTEQSGIYA
 1651 GEDGYQIKVG NHTGLKGGII TSSQSAKDKG KNRFTGTGLA GSDIQNYSQY
 1701 EGKSFGLGAS VAVSGKTLGQ GAKNKPQDKH LSTIADKNGA SSSVGYGSDS
 1751 DSQSSITKSG INTPKNIQIT DEAAQIRLTG KIAAQTKADI DTNVTDTAE
 1801 RHSGSLKNIF DKDRVQSELD LQRTVSQDFS KNVQQTNTI NQHLDKLAD
 1851 KEAAETAFAE ALANGMETA KRKAHEAQDA AAKADNWQQG KVILNMLASG
 1901 LAEPTQSGAG IAAATASPDV SYAIGQHFQD LAGQANGLK TASQETAHVL
 1951 AHAVLGAAVA AAXGNAPAG ALGAGGSEAA APIIGKWLYG KGDGGSLSNAE
 2001 EKETVSAITR MLGTAAGAAE GNSSADAVWG CFQTASDFAS SFSYPIN*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq..

```
1  A TGAATAAAAA CTCTCTATCG TGTAATTTTC AACCGCAAAC GTGGGGCTGT
51  GGTAGCCGTT GCTGAAACTA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGATTCAGG CAGCGCTCAT GTGAAATCTG TTCCTTTTGG TACTACTCAT
151 GCACCTGTTT GTCGTTCAAA TATCTTTTCT TTTTCTTTAT TGGGCTTTTC
201 TTTATGTTTG GCTGTAGGTA CGGCCAATAT TGCTTTTGCT GATGGCATT A
251 TTGCTGATAA AGCTGCTCCT AAAACTCAAC AAGCCACGAT TCTGCAAAAC A
301 GGTAAACGGCA TACCGCAAGT CAATATTCAA ACCCCTACTT CGGCAGGGGT
351 TTCTGTTAAT CAATACGCCC AGTTTGATGT GGGTAATCGC GGGGCGATTT
401 TAAACAACAG CCGCAGCAAC ACCCAAACAC AGCTAGGCGG TTGATTCAA
451 GGTAAATCCTT GGTGCGAAG GGGCGAAGCA CGTGTGGTTG TAAACCAAAT
501 CAACAGCAGC CATTCTTCAC AAATGAATGG CTATATTGAA GTGGGCGGAC
551 GACGTGCAGA AGTCGTTATT GCCAATCCGG CAGGGATTGC AGTCAATGGT
601 GGTGGTTTTA TCAATGCTTC CCGTGCCACT TTGACGACAG GCCAACCGCA
651 ATATCAAGCA GGAGACCTTA GCGGCTTTAA GATAAGGCAA GGCAATGTTG
701 TAATCGCCGG ACACGGTTTG GATGCCCGTG ATACCGATT CACACGTATT
751 CTCAGTTATC ATTCCAAAAT TGATGCACCC GTATGGGGAC AAGATGTTG
801 TGTCGTCGCG GGACAAAACG ATGTGGTTCG AACAGGTAAT GCACATTGCG
851 CTATTCTCAA TAATGCTGCT GCCAATACGT CAAACAATAC AGCCAACAAC
901 GGCACACATA TCCCTTATT TCGGATTGAT ACAGGCAAAAT TAGGAGGTAT
951 GTATGCCAAC AAAATCACCT TGATCAGTAC GGCCGAGCAA GCAGGCATTC
1001 GTAATCAAGG GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA
1051 AATGGCCGTT TAGTCAATAG TGGCAGCATG GCTGCCGCCA ATGCCAAAGA
1101 TACCGATAAT ACAGCGGAAC ACAAAGTCAA TATCCGAGT CAGGGCGTTG
1151 AAAACAGCGG TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAG
1201 TCGATTCAAA ACACTGGCAC ATTATTGTCC TCAGGCGAAA TATTGATTCA
1251 CAATTGCGGC AGCCTGAAAA ATGAAACATC AGGCACCATT GAAGCCGCTC
1301 GTTTGGCTAT TGATACCGAC ACACTTAATA ATCAAGGCAA ACTCTCTCAA
1351 ACAGGTTTCA AAAAATCCA TATTGATGCA CAAGGCAAAA TGGATAACCG
1401 TGGCCGCATG GGTTTACAAG ATACCGCACC AACCGCGTCA AATGGTTCAA
1451 GCAATCAAAC CGGCAATAGT TACAATGCAT CTTTCCATT C ATCCACTACC
1501 ACACCAACAA CGGCAACAGG TACGGGTACT GCAACCGTTT CTATATCAAA
1551 CATAACTGCG CTAACCTTTG CTGATGGGAC AATTGCGACT CATGGTGCAC
1601 TGGATAATTC AGGCAGTATT ATTGCCAATG GTCAAACAGA TGTTAGTGCG
1651 CAACAAGGTT TAAATAATGC AGGACAAATA GACATTATC AGTTAAATGC
1701 AAAAGGTTTG GCGTTTGACA ATCACAATGG AACAATTATC AGTGATGCGG
1751 TCCACATTCA AGCCGGCAGC CTGAATAATC AAAATGGCAA CATCACAACA
1801 CGCCAACAGT TAGAGATTGA AACCGATCAA CTGGATAACG CTCATGGCAA
1851 GTTATTATCA GCAGAAATAG CGGATTTAGC CGTTTCAGGC AGCCTGAACA
1901 ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT TCACGATGGT
1951 CAGCAATCTA CCGCTGTCAT TGATAATACG AATGGCACGA TACAATCAGG
2001 CCGTGATGTT GCTATTCAGG CAAAATCGTT ATCCAACAAC GGCACACTTG
2051 CCGCTGATAA TAAACTGGAT ATTGCGTTAC AAGATGATT TTAGTGTAGAA
2101 CGCAATATCG TGGCGGGCAA TGAATTGTG CTAGTACAC GAGGCAGCCT
2151 GAAAAATTCA CATACTTTGC AAGCAGGAAA ACGCATTGCG ATTAAAGCAA
2201 ATAACCTTGA TAATGCAGCA CAAGGCAACA TTCAATCCGG CGGTACGACA
2251 GACATTGGCA CGCAGCACAA TTAAACCAAT AGAGGCTTGA TTGACGGACA
2301 ACAAACCAAA ATCCAAGCCG GGCAAATGAA TAATATCGGT ACAGGTCGGA
2351 TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA CAATCAAGAT
2401 GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGTGAAAACC TGAATTTAGG
2451 CATCGGACAA TTAACAACCC GTGAAAACAG TCTGATTAC AGCGGTAACG
2501 ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGGCCAAGC CACAGGCAAA
2551 GCCCAAAGGA TACACAATGC CGGCGCAACC ATTGAAGCTG CAGGCAAAAT
2601 GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT TTGAAAACGC
2651 AGTTGGTAGA AACAGGGCGC GAGCATATTG TTGATTACGA AGCATTGGA
2701 CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG GCTGGTCTGT
2751 CTATAACGAT GAATCAGACC ACTTACGCAC CCCTGATGGA GCGGCGCATG
2801 AAAATTGGCA TAAATACGAT TATGAAAAAG TCACCCAAA AACCAGTT
2851 ACCCAAACTG CGCCAGCCAA AATCATTTC GGTAAATGATT TAACCATTGA
2901 TGGTAAAGAA GTATTTAATA CCGATAGCCA AATCATTGCT GGTGGCAATC
2951 TCATTGTACA AACAGAAAAA GACGGTTTGC ATAACGAGCA AACCTTGGC
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3001 GAAAAGAAAG TATTCACTGA AAATGGCAAA TTACACAGCT ATTGGCGTGA
3051 GAAACATAAA GGACGAGACT CAACGGGACA TAGCGAACAA AATTACACTT
3101 TGCCCGAGGA AATCACACGC AACATTTTAC TGGGTTTATT TGCCTATGAA
3151 TCGCATCGCA AAGCATTAAAG CCATCATGCG CCCAGCCAAG GCACTGAGTT
3201 GCCGCAAAAGC AACGGTATTT CGCTACCCTA TACGTCCAAT TCTTTTACCC
3251 CATTACCCAG CAGCAGCTTA TACATTATCA ATCCTGTCAA TAAAGGCTAT
3301 CTTGTTGAAA CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGCGGTAG
3351 TGAATATATG CTGGACAGCC TCAAACTAGA CCCAAACAAT TTACATAAAC
3401 GTTTGGGTGA TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA
3451 GAGCTGACAG GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA
3501 ATTTAAAGCC TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC
3551 TCAGCGTTGG CATTGCATTA AGTGCCGAGC AAGTAGCGCA ACTGACCAGC
3601 GATATTGTTT GGTGTTGACA AAAAGAAGTT AAGCTTCCTG ATGGCGGCAC
3651 ACAAAACCGTA TTGGTGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGACA
3701 TAGACGGTAA AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT
3751 TCAGGCAGCC TGAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT
3801 TATCAATACC GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA
3851 AATCAGCGGT TACGGCCACA CAAGACATCA ATAATATTGG CGGCATGCTT
3901 TCTGCCGAAC AGACATTATT GCTCAACGCA GGCAACAACA TCAACAGCCA
3951 AAGCACCACC GCCAGCAGTC AAAATACACA AGGCAGCAGC ACCTACCTAG
4001 ACCGAATGGC AGGTATTTAT ATCAGAGGCA AAGAAAAAGG TGTTTTAGCA
4051 GCGCAGGCAG GAAAAGACAT CAACATCATT GCCGGTCAAA TCAGCAATCA
4101 ATCAGAGCAA GGGCAAAACC GGCTGCAAGC AGGGCGCGAC ATTAACCTAG
4151 ATACGGTACA AACCAGCAAA CATCAAGCAA CCCATTTTGA TGCCGATAAC
4201 CATGTTATTC GCGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA
4251 AGGCGATGTT ACCCTATTGT CAGGGAATAA CCTCAATGCC AAAGCTGCCG
4301 AAGTCAGCAG CGCAAAACGGT AACTCGCTG TGTCTGCCAA AAATGACATC
4351 AACATCAGCG CAGGCATCAA CACGACCCAT GTTGATGATG CGTCCAAACA
4401 CACAGGCAGA AGCGGTGGTG GCAATAAATT AGTCATTACC GATAAAGCCC
4451 AAAGTCATCA CGAAACCGCC CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT
4501 GTATTGCAGG CAGGAAACGA TGCCAACATC CTTGGCAGCA ATGTTATTTT
4551 CGATAATGGC ACCCAGATTC AAGCAGGCAA TCATGTTGCG ATTGGTACAA
4601 CCCAAACTCA AAGCCAAAGC GAAACCTATC ATCAAACCCA GAAATCAGGA
4651 TTGATGAGTG CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA
4701 AGAAAACCAA TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCT
4751 TGAAAGGCGA TACCACCAT GTTGCAGGCA AACACTACGA ACAAATCGGC
4801 AGTACCGTTT CCAGCCCGGA AGGCAACAAT ACCATCTATG CCCAAAGCAT
4851 AGACATTCAA GCGGCACACA ACAAATTAAG CAGTAATACC ACCCAAACCT
4901 ATGAACAAAA AGGCCTAAG GTGGCATTCA GTTCGCCCGT TACCGATTTG
4951 GCACAAACAAG CGATTGCCGT AGCACAAGAG AGCAAACAAG TCGGACAAAG
5001 CAAAACGAC CGCGTTAATG CCATGGCGGC TGCCAATGCA GGCTGGCAAG
5051 CCTATCAAA AGGTAAGAGT GCACAAAAT TAGCCAATGG TACAACCAAT
5101 GCCAAACAAG TCAGCATCTC CATAACCTAC GGCGAACAGC AAAACCGACA
5151 AACCACCCAA GTTCAAGCCA ATCAAGCCCA AGCGAGTCAA ATTCAAGCAG
5201 GTGGTAAAC CACATTAATC GCCACAGGCG CAGCAGAACA ATCCAATATC
5251 AACATCGCAG GCTCAGATGT TGCCCGCAAA GCAGGCACAA TCCTGATTGC
5301 CGATAACGAC ATCACACTCC AATCAGCCGA GCAAAGCAAT ACCGAACCGG
5351 GCCAAAACAA ATCGGCAGGC TGGAACGCAG GTGCTGCCGT ATCATTGCGA
5401 CAAGGAGGCT GGTCAATTAG CGTTACCGCA GGCGGCAATG TCGGCAAAAG
5451 CTACGGCAAT GCGCAGACGA TCACCCACCG CCATAGCCAT ATCGGCGACA
5501 AAGGCAGCCA AACCTTATC CAAAGCGGTG GCGACACTAC CATCAAAGGC
5551 GCGCAAGTAC GCGGCAAGG CGTACAAGTC AATGCCAAAA ACCTAAGTAT
5601 TCAAAGCGTA CAAGATAGAG AAACCTATCA AAGCAAACAA CAAAACGCCA
5651 GTGCACAAGT TACCGTAGGT TATGGCTTCA GTGCCGGTGG CGATTACAGC
5701 CAAAGCAAAA TCCGAGCCGA CCATGTTTCA GTAACCGAGC AAAGCGGTAT
5751 TTATGCCGGA GAAGACGGCT ATCAAATCAA GGTGGAAGC CATACAGACC
5801 TCAAAGGCGG CATCATCACC AGTACCCAAA GCGCAGAAGA CAAGGGTAAA
5851 AACCGCTTTC AGACGGCCAC CCTCACCCAT AGCGACATCA AAAACACAG
5901 CCAATACAAA GCGGAAAGTT TTGGATTGGG CGCAAGTGCG TCCATAAGCG
5951 GCAAAACACT GGGACAGGCG GCACAAAATA AACCTCAAAA CAAACACCTG
6001 ACAAGCGTAG CCGATAAAAA CAGCGCAAGT TCATCAGTGG GTTATGGCAG
6051 CGACAGCGAC AGTCAAAGCA GCATCACAAA AAGCGGCATC AACACCCGCA

6101 ACATTCAAAT CACCGACGAA GCCGCACAAA TCCGGCTGAC AGGCAAAACA
 6151 GCGGCACAAA CCAAAGCCGA TATTGATACA AACGTAACCA CAGACACCGC
 6201 CGAACGACAT TCGGGCAGCT TGAAGAACAC CTTCAACAAA GAAGCGGTGC
 6251 AAGTGAACCT GGATTACAA AGAACCGTCA GCCAAGATTT TAGTAAAAAT
 6301 GTTCAACAAG CCAATACCGA GATTAACCAA CATTAGACA AACTCAAAGC
 6351 AGACAAAGAA GCAGCCGAAA CAGCAGCAGC CGAGGCATTA GCCAATGGCG
 6401 ATATGGAAAC TGCCAAACGC AAAGCCCATG AAGCTCAAGA TCGGGCAGCA
 6451 AAAGCAGATA ATTGGCAACA AGGCAAAGTC ATTCTCAACA TGTTAGCCTC
 6501 AGGTTTAGCT GCGCCGACCC AAAGCGGAGC GGGCATCGCT GCGGCTACCG
 6551 CATCGCCAGC CGTATCGTAT GCGATTGGAC AGCATTTTAA AGATTTAGCC
 6601 GGTCAAAACG CGAATGGTAA ACTAACCGCC AGTCAAGAAA CCGCACACGT
 6651 TCTTGCCAC GCGGTATTAG GAGCAGCGGT TGCCGAGTA GGAGACAACA
 6701 ATGCTCTAGC AGGAGCATTG AGTGC GGCG GGTGCGAAGC GGCTGCGCCT
 6751 TACATCAGCA AATGGTTATA CGGCAAAGAA AAAGGAAGCG ACTTAACGGC
 6801 GGAAGAGAAA GAGACTGTAA CAGCGATTAC AAATGTATTG GGTACGGCTA
 6851 CGGGTGCGGC AGTCGGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
 6901 AATGCGCAAA GTGCGGTGGA GAATAATGAT ACTGTAGAGC AAGTGAAATT
 6951 TGCTCTTAGG CACCCTAGAA TTGCTATTGC AATTGGATCT GTACATAAAG
 7001 ATCTTGCTC TACATTAGAG CCTAATATTT CAACAATTGC TTCAACTTTT
 7051 CAATTAAATT TATTTCTTAA TAGTGAATTT GGTGGTGAAG GTGGAGTTGG
 7101 CAATGCATTG AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTTG
 7151 GCAAAGATAT TGCTGTTAAA GTAGGAAATA GTCATGAAAG TGGGGAAAAA
 7201 ATTAATTATT CTATAAGACG TAATCTTTCA TTAGATAAAG CAGATGAAAT
 7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TTAAATACCA
 7301 ATAGGTAAAC CACAAAAGAG TTAGTTGGAT TAATTCTGGA AACTTATAAA
 7351 AATAATGGTT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
 7401 TGTAAGAAAA AGATTATCTG AAAAAGATTA CCAGAATACA AGCAATATAT
 7451 TGATTCACTT AGATAATACT GGTGCCGGAT TAAAATTCA GCAGAGGAGA
 7501 AAACAAATCA GAGCACAAT TTCAGCCAGA CAATGGAGAA GATAA

This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563.pep..

1 MNKTLRVIF NRKRGAVVAV AETTKREGKS CADSDSGSAH VKSVFPGTTH
 51 APVCRSNIFS FSLGFSCL AVGTANIAFA DGIADKAAP KTOQATILQT
 101 GNGIPQVNIQ TPTSAGVSVN QYAQFDVGNR GAILNNSRSEN TOTQLGGWIO
 151 GNPWLARGEA RVVNVQINSS HSSQMNGYIE VGGRRAEVVI ANPAGIAVNG
 201 GGFINASRAT LTTGQPOYQA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI
 251 LSYHSKIDAP VWGQDVRVVA GQNDVVATGN AHSFILNNA ANTSTNTANN
 301 GTHIPLFAID TGKLGMYAN KITLISTAEQ AGIRNQGLF ASSGNVAIDA
 351 NGRLVNSGTM AANAADTDN TAEHKVNIRS QGVENSQTAV SQGTQIHSQ
 401 SIQNTGTLIS SGEILIHNSG SLKNETSGTI EAARLAIDTD TLNNQKLSQ
 451 TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQTGNS YNASFHSSTT
 501 TPTTATGTGT ATVSISNITA PTFADGTIRT HGALDNGSSI IANGQTDVSA
 551 QOGLNAGQI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT
 601 RQQLIETDQ LDNAHGKLLS AEIADLAVSG SLNNQNGEIA TNQQLIHDG
 651 QOSTAVIDNT NGTIQSGRDV AIQAKSLSN GTLAADNKLD IALQDDFYVE
 701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT
 751 DIGTQHNLTN RGLIDGQOTK IQAGQMNNIG TGRIYGDNIA IAATRLDNQD
 801 ENGTGAAIAA RENLNLGIGQ LNNRENSLIY SGNDMAVGGA LDTNGQATGK
 851 AQRIHNAGAT IEAAGKMLG VEKLHNTNEH LKTQLVETGR EHIVDYEAFG
 901 RHELLREGTO HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
 951 TOTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
 1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEEITR NISLGSPAYE
 1051 SHRKALSHHA PSQGTLPQS NGISLPYTSN SFTPLPSSL YIINPVNKGY
 1101 LVETDPRFAN YRQLGSDYM LDSLKLDPN LHKRLGDGY EQRLINEQIA
 1151 ELTHRRDLG YQNDDEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS
 1201 DIVLVQKEV KLPDGGTQTV LVPQVYVRV NGDIDKGAL LSGSNTQINV
 1251 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQSAVTAT QDINNIGGML
 1301 SAEQTLILLNA GNNINSQSTT ASSQNTQSS TYLDRMAGIY ITGKEKGVLA
 1351 AQAGKDINII AQQISNQSEQ QTRLQAGRD INLDTVQTSK HQATHFDADN
 1401 HVIRAGSTNEV GSIQTKGDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI
 1451 NISAGINTTH VDDASKHTGR SGGGNKLVT DKAQSHHETA QSSTFEGKQV
 1501 VLQAGNDANI LGSNVISDNG TQIQAGNHVR IGTTQTQSQS EYHQTQKSG

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1551 LMSAGIGFTI GSKTNTQENQ SQSNEHTGST VGS LKGDTTI VAGKHYEQIG
1601 STVSSPEGNN TIYAQSIDIQ AAHNKLSNT TQTYEQKGLT VAFSSPVTDL
1651 AQQAIAVAQS SKQVQSKND RVNAMAANA GWQAYQTGKS AQNLANGTTN
1701 AKQVSISITY GEQONRQTTQ VQANQAQASQ IQAGGKTTLI ATGAAEQSN
1751 NIAGSDVAGK AGTILIADND ITLQSAEQSN TERGQNKASG WNAGA AVSFG
1801 QGGWSLGVTA GGNVGKGYGN GDSITHRSH IGDKGSQTLI QSGGDTTIKG
1851 AQVRGKGVQV NAKNLSIQSV QDRETYQSKQ QNASAQVTVG YGFSAGGDYS
1901 QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGGIIT STQSAEDKGK
1951 NRFQTATLTH SDIKNHSQYK GESFGLGASA SISGKTLGQG AQNKPNKHL
2001 TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051 AAQTKADIDT NVTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
2101 VQANTEINQ HLDKLKADKE AAETAAREAL ANGDMETAKR KAHEAQDAAA
2151 KADNWQQGKV ILNMLASGLA APTQSGAGIA AATASPAVSY AIGQHFKDLA
2201 GQNANGKLT A QETAHVLAH AVLGA AVAAV GDNALAGAL SAGGSEAAAP
2251 YISKWLYGKE KGSDLTAEK ETVTAITNVL GTATGA AVGN SATDAAGGSL
2301 NAQSAVENND TVEQVKFALR HPRIAIAGS VH KDPGSTLE PNISTIASTF
2351 QLNLFNPSEF GEGGVGNF RHLVWQATIT REFGKDI AVK VGNSHESGEK
2401 INYSIRRLS LDKADEMIDQ LNNEIGREIA LNTNRLNTKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNILHLDNT GAGFKIQRR
2501 KQIRAQISAR QWRR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563.ng) from *N. gonorrhoeae*:

m563/g563

	10	20	30	40	50	
g563 . pep	MNKTL YRVIFNRKRGAVVAV AETTKREGKSCADSGSGSVYVKSVSFIPTH-----SKAF					
m563 . pep	MNKTL YRVIFNRKRGAVVAV AETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS					
	10	20	30	40	50	60
	60	70	80	90	100	110
g563 . pep	FSALGFSLCLALGTVNIAFADGIIITDKAAPKTQQTILQTGNGI PQVNIQTPTSAGVSVN					
m563 . pep	FSLGLFSLCLAVGTANIAFADGIIADKAAPKTQQTILQTGNGI PQVNIQTPTSAGVSVN					
	70	80	90	100	110	120
	120	130	140	150	160	170
g563 . pep	QYAFQDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE					
m563 . pep	QYAFQDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQMNGYIE					
	130	140	150	160	170	180
	180	190	200	210	220	230
g563 . pep	VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIRQGNVVIAGHGL					
m563 . pep	VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLGFKIRQGNVVIAGHGL					
	190	200	210	220	230	240
	240					
g563 . pep	DARDTDFTRIL-----					
m563 . pep	DARDTDFTRILSYHKSIDAPVWGQDVRVVAGQNDVVATGNAHSPILNNAANTSNNNTANN					
	250	260	270	280	290	300
	250	260	270	280	290	
g563 . pep	-----LYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGMT					
m563 . pep	GTHIPLFAIDTGKLGMYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGMT					
	310	320	330	340	350	360

856

	300	310	320	330	340
g563.pep	AAANVQDMNNTAEHKVNIRSQAFENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----				
	: : : : :				
m563.pep	AAANAKDTDNTAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLSSGEILIHNSG				
	370	380	390	400	410 420

g563.pep					
m563.pep	SLKNETSGTIEAARLAIDTDTLNNQKLSQTGSQKLHIDAQGKMDNRGRMGLQDTAPTAS				
	430	440	450	460	470 480

g563.pep					
m563.pep	NGSSNQTGNSYNASPHSSTTTPTTATGTGTATVSISNITAPTADGTIRTHGALDNSGSI				
	490	500	510	520	530 540

g563.pep					
m563.pep	IANGQTDVSAQQGLNNAQQIDIHQLNAGSAFDNHNGTIISDAVHIQAGSLNNQNGNITT				
	550	560	570	580	590 600

g563.pep	-----EDLAVSGSLNNQNGEIATNQQLIIHDGQQSTVVIDNT				
	:				
m563.pep	RQOLEIETDQLDNAHGKLLSAEIALAVSGSLNNQNGEIATNQQLIIHDGQQSTAVIDNT				
	610	620	630	640	650 660

g563.pep	390	400	410	420	430 440
	NGTIQSGRDVAIQAKSLSNGTLAADNKLDIALQDDFYVERKIVAGNELSLSTRGSLKNS				
	:				
m563.pep	NGTIQSGRDVAIQAKSLSNGTLAADNKLDIALQDDFYVERNIVAGNELSLSTRGSLKNS				
	670	680	690	700	710 720

g563.pep	450	460	470	480	490 500
	HTLQAGKRIRIKANNLDNAVQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQIQAGQMNNIG				
	:				
m563.pep	HTLQAGKRIRIKANNLDNAAQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQIQAGQMNNIG				
	730	740	750	760	770 780

g563.pep	510	520	530	540	550 560
	TGRIYGDNIAIAATRLDNQDENGTTGAIAAARENLNLGIEQLNNRENSLIYSGNDMAVGGA				
	:				
m563.pep	TGRIYGDNIAIAATRLDNQDENGTTGAIAAARENLNLGIGQLNNRENSLIYSGNDMAVGGA				
	790	800	810	820	830 840

g563.pep	570	580	590	600	610 620
	LDTNDQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGRERIVDYEAFG				
	:				
m563.pep	LDTNGQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGREHIVDYEAFG				
	850	860	870	880	890 900

g563.pep	630	640	650	660	670 680
	RHELLREGTQHELGFVYNNESDHLRTPDGAHENWHKYDYEKVTQETQVTGTAPAKIIA				
	:				
m563.pep	RHELLREGTQHELGWSVYNDES DHLRTPDGAHENWHKYDYEKVTQKTQVTGTAPAKIIS				
	910	920	930	940	950 960

	690	700	710	720	730 740

859

	1950	1960	1970	1980	1990	2000
g563 . pep	TASQETAHVLAHAVLGA AVAAAXGNNAPAGALGAGGSEAAAPIIGKWLYGKGDGGSLSNAE					
m563 . pep	TASQETAHVLAHAVLGA AVAAVGDNNALAGALSAGGSEAAAPYISKWLYGKEKGSDLTAE					
	2210	2220	2230	2240	2250	2260
	2010	2020	2030	2040	2049	
g563 . pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFQTASDFASSFSYPINMX					
m563 . pep	EKETVTAITNVLGATGA AVGNSATDAAQGSLSNAQSAVENNDTVEQVKFALRHPRIATAI					
	2270	2280	2290	2300	2310	2320
m563 . pep	GSVHKDPGSTLEPNISTIASTFQLNLFNPFSEFGGEGVGNAFRHVLWQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

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m564 . seq
1  ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51  GATAGCCGTT GCTGAAAATG CCAAACGCGA GGGCAAAAAC ACAGCCGACA
101 CCCAAGCTGT AGGTATTTTG CCAAATGATA TTGCGGGCTT TCGCGGTTT
151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTT
201 TGCCCTTATC CTGACTTCTT CTCTGCTAC TGCCCAAGGT ATCGTTGCCG
251 ACAAATCCGC ACCTGCACAG CAACAGCCTA CCATCCTGCA AACAGGTAAC
301 GGCATACCGC AAGTCAATAT TCAAACCCCT ACTTCGGCAG GGGTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA
401 ACAGTCGCAG CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT
451 CCTTGGTTGG CAAGGGGCGA AGCAGCTGTG GTTGTAACCC AAATCAACAG
501 CAGCCATTCT TCACAACTGA ATGGCTATAT TGAAGTGGGC GGACGACGTG
551 CAGAAGTCGT TATTGCCAAT CCGGCAGGGA TTGCAGTCAA TGGTGGTGGT
601 TTTATCAATG CTTCCCGTGC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTAAATCG
701 CCGGACACGG TTTGGATGCA CGTGATACCG ATTACACACG TATTCTCAGT
751 TATCATTCCA AAATTGATGC ACCCGTATGG GGACAAGATG TTCGTGTCCT
801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTATTC
851 TCAATAATGC TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAACGGCACA
901 CATATCCCTT TATTTGCGAT TGATACAGGC AAATTAGGAG GTATGTATGC
951 CAACAAAATC ACCTTGATCA GTACGGTCTGA GCAAGCAGGC ATTCGTAATC
1001 AAGGGCAATG GTTTGCCTCA GCCGGCAATG TGGCAGTGAA TGCTGAGGGT
1051 AACTGGTCA ACACGGGCAT GATTGCAGCG ACGGGAGAAA ATCATGCGGT
1101 TTCACTTCAT GCCCGCAATG TTCATAATAG CGGTACGGTT GCCTCACAGG
1151 ATGATGCCAA TATTCACAGC CAGACGCTGG ACAATTCAGG TACGGTCTTA
1201 TCCTCAGGTC GATTGACTGT TCGTAATTTA GGCGTCTGA AAAACCAAAA
1251 CAACGGTACG ATCCAGGCTG CCCGCTTAGA TATGTCAACA GGTGGTTTGG
1301 ATAACACAGG TAATATTACT CAAACAGGTT CACAAGCATT GGATTTGGTA
1351 TCTGCCGGCA AATTCGATAA CAGTGGCAAG ATTGGTGTA GTGACGTTCC
1401 ACAGACCGGT TTGAATCCCA ATCCATCAGT CATACCACAG ATTCCGAGTA
1451 CTGCAACAGG TTCAGGCAGC AGCACTGTCT CGGTATCTAA GCCTGGTTCA
1501 AACAAATCCG TTTCACCTAC AGCACCTGCA AAAAATCTAC CCGTAGGACG
1551 CATTCAAACA ACAGGAGCAT TTGACAATGC AGGATCAATT AATGCGGGTG
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1851 CCGCTTGAGC AATGATAAAA AAGGCAATAT TCGAGCTGCA CATTACAGC
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1951 ACCGTTACCA CCAAGAATAA TCTTCGCAAT ACAGGAAAAG TTTCTGTTGC
2001 ACCACTGAAT ACCGAAGGTC AGACTCTAGA TAATACGCGC GGACGTATAG
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2101 CATATTACTG CTACCGAACA ACTGACTATC AATAGTCGAA ATGTAGACAA
2151 CCAAAACGGC AAACCTCTAT CTGCAAACCA AGCACAATTA GCTGTTTCAG
2201 ACGGCCTATA CAACCAACAT GGTGAAATTG CCACCAACCG GCAGTTGTCT

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2251 ATTACGATA AAAATCAAAA CACTTTGGCG TTAACAATG CGGATGGCAC
2301 GATTCAATCT GCCGGTAATG TATCGCTACA AGCCAAATCA CTCGCCAACA
2351 ATGGCACATT AACAGCCGGT AACAACTGG ATATTGCTTT GACGGACGAT
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2501 AACTCAATGC CGGCAATATA GATAACCAAG TTACAGGCAA AATTATTGGT
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2601 GATCAACAGC GACGGTTTGA CCCACATCGG TGCAGGTCAA ACCCTGACCA
2651 ACACCGGGAC AGGCAAAATC TATGGCAACC ATATTGCCCT GGACGCGCAA
2701 ATACTGCTTA ACCGGGAAGA AACGACGGAA GGCAGTACCA AAGCGGGGCG
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3251 AAAATTGGCT GAACAAAGAC AGCCGGATTG TAGTAGGCGG GCGTATTATC
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3901 GCTCTGATGG ACAACGGCCT TACTGCTGCC AAAACATTG GTCTCACCCC
3951 AGGTATCGCC TTGAGTGCAG AGCAAGTTGC CCGCTTAAT TCAGATATCG
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4051 GTAATGGTTC CTAAAGTCTA TGCCCTGGCG CGCAAAGGTG ATCTCAATAC
4101 CTCCGGTGGC CTGATTAGTG CCGAACAGT CTTACTTAAA CTGCAAAACG
4151 GCAACCTGAC TAACAGCGGT ACCATTGCGG GCGCAGAGGC CGTACTCATC
4201 CAGGCACGGA ATATTAAACAG CAACGGTAAC ATTCAAGCCG ACCAAATCGG
4251 CTTAAAAGCT GAAAAAAGTA TCAATATCGA CGGCGGGCAG GTACAAGCAG
4301 GCAGACTGCT GACTGCCCAA GCGCAAAATA TCAACCTTAA CGGTACAACC
4351 CAAACTTCCG GTAATGAACG TAACGGCAAT ACCGCCATCG ATCGTATGGC
4401 CGGCATTAACT GTGGTCGGAA GCCATACCTGA ACAAGTAGAT AACAGAACTT
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4501 GCCACCGTCT CTAACCAAGT TAAAGACGGC ACTACCCAAA TTACCGCCGG
4551 CAATAATCTC AACCTCGGCA CCATCCGTAC CGAACATCGC GAAGCCTATG
4601 GTACATTAGA TGACGAGAAC CATCGCCATG TCCGCCAAAG TACCGAAGTC
4651 GGCAGCAGTA TCCGCACGCA AAACGGCGCA CTGCTTAGAG CCGGTAACGA
4701 CTTAAAAATC CGCCAAGGCG AACTGGAGGC CGAAGAAGGC AAAACCGTCC
4751 TTGCCGAGG ACGTGATGTC ACTATCAGCG AAGGACGCCA AATAACCGAA
4801 CTGGATACCT CCGTAAGCGG AAAAAGCAAA GGCATCCTTT CCAGTACCAA
4851 AACACACGAC CGCTACCGCT TCAGTCATGA TGAAGCAGTC GGCAGCAACA
4901 TCGGCGGCGG CAAAATGATT GTTGCAGCCG GGCAGGATAT CAATGTACGC
4951 GGCAGCAACC TTATTTCTGA TAAGGGCATT GTTTTAAAAG CAGGACACGA
5001 CATCGATATT TCTACTGCCC ATAATCGCTA TACCGGCAAT GAATACCACG
5051 AGAGCAAAAA ATCAGGCGTC ATGGGTACTG GCGGATTGGG CTTTACTATC
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5151 AGGCAGCATT ATAGGACGCC TGAATGGAGA CACCGTTACA GTTGCAGGAA
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5301 CACTGACTAC GCCCATACCC AGGAACAAAA AGGCCTTACC GTCGCCCCA
5351 ATGTCCCGGT TGTCCAAGCT GCACAAAAT TCATACAAGC AGCCCAAAT
5401 TGGGGCAAAA GTAAAAATA ACGCGTTAAT GCCATGGCTG CAGCCAAATGC
5451 TGCAATGGCAG AGTTATCAAG CAACCCAACA AATGCAACAA TTTGCTCAA
5501 GCAGCAGTGC GGGACAAGGT CAAAACAACA ATCAAGCCCC CAGTATCAGT

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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
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5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
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6101 GTTACGGATT CAGTGCAAGC GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAAACCCAG AGCCGCTACG AAGGCAGAAG
6351 CTTCCGCATA GCGCGCAGTT TCGACCTGAA CCGCGGCTGG GACGGCACGG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
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6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAACAGCT TCGACAAAGA
6651 CGCGGTGCGC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCC
6701 AAGCGCGAAG CGCCCAAGCC GTAGCGGCCG TTGCCGACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCTGCT TGGAGGCCGA
6801 ACTGCAAAAC ACGGACAGCG AAGCCGAAAA AGCCGCCTTC CGCGCATCCC
6851 TCGGCCAAGT AAACGCCATAT CTTGCCGAAA ACCAAAGCCG CTACGACACC
6901 TGGAAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCAGGCGG
6951 ACTGACGACC GGCAGCCTCG GCGGCATACT GGCCGCGCGC GGCACCTCCC
7001 TTGCCGCACC GTATTTGGAC AAAGCGGCGG AAAACCTCGG TCCGCGGGGC
7051 AAAGCGGCGG TCAACGCACT GGGCGGTGCG GCCATCGGCT ATGCAACTGG
7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGTAAGATTGG AACAATAGGC
7151 AGCTGCATCC GAAAGAAATG CGGTTGGCCG ACAAATATGC CGAAGCCCTC
7201 AAGCGCGAAG TTGAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
7251 GGCAATGAGA ATCCGCAGGC AGATACTGCG TTGGGTGGAC AAAGGTTCCC
7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AAGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
7551 CGTTGCCGAA GGAAGTACGA GCCTTGTCAG CCCCATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAGGCATC CGCAACCTGA AAAACATCAA GCCGACAGTT
7651 ACCGGCAGCG ATCCCTTATT GCGGGTGCG GGAATATCC GTATCCCTGC
7701 AAACGGCAAT GTTGCAGAGG GGGACAGGAT TCCGGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep

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1 MNRTLYKVVF NKHRNCMAIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51 IHSISVISFS LSLLLGSALE LTSSSATAQG IVADKSAPAQ QOPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIOGN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQPQYQAGD LSGFKIROGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW GQDVRVWAGQ NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGGMVANKI TLISTVEQAG IRNQGWFAE AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGRLTVRNL GRLKNQNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVSDVPQTG LNPNSVIPQ IPSTATSGS STSVSVKPGS
501 NNPVSPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLGNSGSL
551 NNAKLRVSGD SFNNTVKGKL QAHLAVNTQ TAKNSGHLT QTGKIDNREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIRAA HLQDLTAGLH NAGNILADSG
651 TVTTKNNLRN TGKVSVARLN TEGQTLDNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVDNQNG KLLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

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901 ILLNREETTE GSTKAGAI AA RKRLDIGAKE IHNQEGALLS SEGIFAVGNR
951 LDEQHHAAGM ADTFVNGSAG LEVQGDALMS VRNMQNINNH FKTETYLAKA
1001 EKQVRDYTVL GQNTYYQAGK DGLFDNSQGG KDQTTATFHL KNGSRIEANO
1051 WHVRDYHIET YKERIENRP AHITVGGDLT ASGQNLWLNK SRIVVGGRII
1101 TDDLNOKEIT NQSTTGKGRD DAVGTQWDSV TKKGWYSGRK RQRRTERNHT
1151 PYHDTQLFTH DFDTPVSVIQ QNAASPSFQP AASAIKLIDG VSTAANGVQR
1201 IHTGNVSVLN NATVTLPNSS LYTHHPDNKG WLVTDPQFA DYRRWLGS DY
1251 MLQQLQLDTN HLHKRLGDBG YEQKLVNEQI HQLTGYRRLD GYRSDEEQFK
1301 ALMDNGLTAA KTFGLTPGIA LSAEQVARLT SDIVWMENQT VTLSDGSTQT
1351 VLVPKVYALA RKGDLNTSGG LISAEQVLLK LQNGNLNLSG TIAGRQAVLI
1401 QARNINSNGN IQADQIGLKA EKSINIDGGQ VQAGRLLTAQ AQNLNNGTT
1451 QTSGNERNNGN TAIDRMAGIN VVGSHTQVD NRTSDGILSL HASNDINLNA
1501 ATVSNOVKDG TTQITAGNNL NLGTIRTEHR EAYGTLDDEH HRHVRSSTEV
1551 GSSIRTQNGA LLRAGNDLKI RQGELEAEEG KTVLAAGRDV TISEGRQITE
1601 LDTSVSGKSK GILSSTKTHD RYRFSHDEAV GSNIGGGKMI VAAGQDINVR
1651 GSNLISDKGI VLKAGHDIDI STAHNRYTGN EYHESKSKGV MGTGGLGFTI
1701 GNRKTTDDTD RTNIVHTGSI IGSNLGDTVT VAGNRYRQTG STVSSPEGRN
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1801 VGKSKNKRNV AMAAANAQWQ SYQATQOMQO FAPSSSAGQG QNNNQSPSIS
1851 VSITYGEQKS RNEQKRHYTE AAASQIIGKG QTTLAATGSG EQSNINITGS
1901 DVIGHAGTAL IADNHIRLQS AKQDQSEQSK NKSSGWNAGV AVKIGNGIRF
1951 GITAGGNIGK GKEQGGSTTH RHTHVGSTTG KTTIRSGGDT TLKGVQLIGK
2001 GIQADTRNLH IESVQDTETY QSKQONGNVQ VTVGYGFSAS GSYRQSKVKA
2051 DHASVTGQSG IYAGEDGYQI KVRDNTDLKG GIITSSQSAE DKGKNLQFTA
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2151 YGSDGDSKNS TTRSGVNTHN IHITDEAGQL ARTGRTAKET EARIYTGIDT
2201 ETADQHSGLH KNSFDKDAVA KEINLQREVT KEFGRNAQA VAAVADKLGN
2251 TQSYERYQEA RTLLEAELQN TDSEAEEKAA RASLGQVNAY LAENQSRYDT
2301 WKEGGIGRSI LHGAAGGLTT GSLGGILAGG GTSLAAPYLD KAAENLGPAG
2351 KAAVNALGGA AIGYATGGSG GAVVGANVDW NNRQLHPKEM ALADKYAEAL
2401 KREVEKREGR KISSQEAAMR IRRQILRWVD KGSQDGYTDQ SVISLIGMKG
2451 EDKALGYTDW YRDYGARNPQ TYNDPKLFEE YRRQDKPEYR NLTWLHSGTK
2501 DTKIRQGERK NEEFALNVAE GLTSLVNPNP RIKVPILAGI RNLKNIKPTV
2551 TGSDDL LAGA GNIRIPANGN VAKGDRIPTD ALASKGIKHK DRKDQLEKK*

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Computer analysis of this amino acid sequence gave the following results:

Homology with fha

m564/fha

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ID FHAB_BORPE STANDARD; PRT; 3591 AA.
AC P12255;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE FILAMENTOUS HEMAGGLUTININ. . . .

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SCORES Init1: 190 Initn: 524 Opt: 594
 Smith-Waterman score: 866; 21.7% identity in 2427 aa overlap

		10	20	30	40	50	60
m564	.pep	MNRTLYKVVF	NKHNKCMIAVA	ENAKREGKNTAD	TQAVGILPNDI	AGFAGFIHSIS	VISVISFS
		: : : :	: : : :	: : :	: : :	: : :	: : :
fhab_borpe		MNTNLYRLV	FSHVRGMLVP	VEHCTV-G-NT	FCGRTRG---	QARSGARATSL	SVAPNALA
		10	20	30	40	50	

		70	80	90	100	110	119
m564	.pep	LSLLLG-SAL	LITSSSATAQ	GIVADKSAPA	QQOQTILQ	TGNGIPQVNI	QTPTSAGVSVNQ
		: : : : :	: : : : :	: : : :	: : : :	: : : :	: : : :
fhab_borpe		WALMLACTG	LPLVTH---A	QGLV-----	P-QGQTQV	LQGGNKVPV	VNIADPNSSGGVSHNK
		60	70	80	90	100	

		120	130	140	150	160	170	179
m564	.pep	YAQFDVGNR	GAILNNSRNT	QTQQLGGWI	QGNPWLARGE	ARVVVNQINS	SHSSQLNGYIEV	
		: : : : :	: : : :	: : : :	: : : :	: : : :	: : : :	
fhab_borpe		FQQFNVANP	GVVFNNGLT	DGVSRI	GALTKNPNL	TR-QASAILA	EVTDTPSRLAGTLEV	
		110	120	130	140	150	160	

863

	180	190	200	210	220	230	239
m564 .pep	GGRRAEVVIANPAGIAVNGGGFINASRATLT	TAQPQYQAGDLSGFKIRQGNVVIAGHGLD					
fhab_borpe	YGKGADLIIANPNGISVNGSLTLNASNLTLT	TGRPSVNGGRI-GLDVQQTVTIERGGVN					
	170	180	190	200	210	220	
	240	250	260	270	280	290	
m564 .pep	ARDTDYTRILSYHISKIDAPV---WGQ---	DVRVVAGQNDVAATGDAHSPILNNAANTSN					
fhab_borpe	ATGLGYFDVVARLVKLQGAUSSKQKPLADIA	VVAGANRYDHATRRATPI----AAGARG					
	230	240	250	260	270	280	
	300	310	320	330	340	350	
m564 .pep	NTANNGTHIPLFAIDTGKLGMYANKITLIST	VEQAGIRNQGWFFASAGNVAVNAEGKLV					
fhab_borpe	AAAGA-----YRIDGTAAGAMYGKHITLV	SSDSGLGVRQLGS-LSSPSAITVSSQGEIA					
	290	300	310	320	330		
	360	370	380	390	400	410	
m564 .pep	NTGMIAATGENHAVSLHARNVHNSGTVASQ	DDANIHSQTLDNSGTVLSSGRLTVRNIGRL					
fhab_borpe	---LGDATVQRGPLSLKGAGVVSAGKLASG	GGGAV---NVAGGAVKIA---SASSVGNL					
	340	350	360	370	380		
	420	430	440	450	460	470	
m564 .pep	KNQNNGTIQAARLDMSTGGLDNTGNITQT	GSQALDLVSAGKFDNSGKIGVSDVPQTGLNP					
fhab_borpe	AVQGGGKVQATLLNAG-----GTLVSGRQ	AVQLGAASSRQALS VNAGGALKADKLSA					
	390	400	410	420	430		
	480	490	500	510	520	530	
m564 .pep	NPSV-IPQIPSTATGSGSSTVSVSKPGSNN	PVSPAPAKNYAVGRIQTGAFD-NAGSIN					
fhab_borpe	TRRVDVDGKQAVALGSASSNALSVRAGGA	-----LKAGKLSATGRDLVDGKQAVTLG	SV				
	440	450	460	470	480	490	
	540	550	560	570	579		
m564 .pep	AGGQIDIAAQNGLGNSGSLNAAKLTVSG	-----DSFNNT-----VKGKLQAHDLAVNT					
fhab_borpe	SDGALSVSAGGNLRANELVSSAQLEVRGQ	REVALDDASSARGMTVVAAAGALAARNLQ	SKG				
	500	510	520	530	540	550	
	580	590	600	610	620	630	
m564 .pep	QTAKNSGHLTQTGKIDNRELH--NAGEIA	ANNLTLIHSGRLSNDKKGNIRAAHLQ	LQ	DTA			
fhab_borpe	AIGVQGGGAVSVANANSDAELVRGRGQ	VDLHDLAARGADISGEGRVNIGRARS	SD	SVK			
	560	570	580	590	600	610	
	640	650	660	670	680	690	
m564 .pep	GLHNAGNILADSGTVTTKNNLRNTGKVS	VARLNTGQTLDNTRGRIEAEVTNIQ	SQ	QLTN			
fhab_borpe	-VSAHGALSIDSMTALGAIGVQAGGSV	SAKDMRSRGAVTVSGGG-----AVNLG	DVQ---				
	620	630	640	650	660		
	700	710	720	730	740	750	
m564 .pep	QSGHITATEQLTINSRNVNDNQNGKLLS	ANQAQLAVSDGLYNQHGEIATNRQLS	IH	DKNQ			
fhab_borpe	SDGQVRATSAGAMTVRDV-----AAA	DLALQAGDALQAGFLKSAGAMTVN	GRDAV				
	670	680	690	700	710		

864

m564	.pep	760	770	780	790	800	810
		TLALNNADGTIQSAGNVSLQAKSLANNGTTLTAGNKLDIALTD	DFVVERDLTAGKQL-NLS				
fhab_borpe		RL-----DGA-HAGGQLRVSSDGOALGSLAAKGELTVSAARAATVA-EL---KSLDNIS					
		720	730	740	750	760	
m564	.pep	820	830	840	850	860	870
		IKGRLLK-NHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLNSDGLT					
fhab_borpe		VTGGERVSVQSVNSASRVAISAHGALD---VGKV--SAKSGIGLE---GWGAVGADSL-					
		770	780	790	800	810	
m564	.pep	880	890	900	910	920	930
		HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETEGSTKAGATAARKRLDI-GAKEIHN					
fhab_borpe		--GSDGAISVSGRDAVRVDQARSLADISLG---AEGGATLGAVEAAGSIDVRGGSTV--					
		820	830	840	850	860	
m564	.pep	940	950	960	970	980	990
		QEGALLSSEGIFAVGNRLDEQHHAGMADTFVNGSAGLEVQGDALMSVRNMQINNHFKT					
fhab_borpe		AANSLHANRDVRVSGK--DAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV					
		870	880	890	900	910	920
m564	.pep	1000	1010	1020	1030	1040	1050
		ETYLAKAEK--QVRDYTVLGQNTYYQAGKDGLFDNSQGQKDOTTATFHLKNGSRIEANQ-					
fhab_borpe		ALQSAKASGTLHVQGGHLDLGTAAVGAVDV---NGTGDVVRVAKLVSDAGADLQAGRS					
		930	940	950	960	970	
m564	.pep	1060	1070	1080	1090	1100	
		--WHVRDYHIETYKERIENRPAHITVGGDLTASGQNWLNKDSRIVVGGRITDDLNQKE					
fhab_borpe		MTLGIVDTTGLQARAQQKLELGSVKSDGGLQAAAGGALSAAAEVAGALELS---GQGV					
		980	990	1000	1010	1020	1030
m564	.pep	1110	1120	1130	1140	1150	1160
		ITNQSTTGKGRDVAVGTDQWDSVTKKGWY--SGRKRQRRTERNHTPYHDTQLFTHDFDTPV					
fhab_borpe		TVDRASASRARIDSTGSGVIGALKAGAVEAASPRRARRALR-----QDFFTPG					
		1040	1050	1060	1070	1080	
m564	.pep	1170	1180	1190	1200	1210	1220
		SVI---QQNAASPSFQPAASAIKLIDGVSTAAVNGQRIHTGNVSVLNNATVTLPNSSLYT					
fhab_borpe		SVVVRAQGNVTVGRGDPHQGVLAQGGDIIMDA--KGGTLLLNDALTENGTVTISADSAVL					
		1090	1100	1110	1120	1130	1140
m564	.pep	1230	1240	1250	1260	1270	1280
		THPDNKGWLVETD-PQFADYRRWLGS DYMLQQLQDLTNHLHKRLGDGYEQKL VNEQI HQ					
fhab_borpe		EHSTIESKISQSVLAAKGDKGKPAVSVKVAKKLFL--NGTLRAVNDN--NETMSGRQIDV					
		1150	1160	1170	1180	1190	
m564	.pep	1290	1300	1310	1320	1330	1340
		LTGYRRLDGYRSDEEQFKALMDNGLTAAKTFLGTPG-IALSAEQVARLTS DIVWMENQTV					
fhab_borpe		VDGRPQI-----TDAVTGEARKDES VVSDAALVADGGFIVVEAGELVSHAGGIGNGRNK--					
		1200	1210	1220	1230	1240	1250

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m564	.pep	1350	1360	1370	1380	1390	1400
		TLSDGSTQTVLVPKVYALARKGDLNTSGGLISAEQVLLKLQNGNLNSGTIAGROAVLIQ					
		: :: :		: :: :	: :: :	: :: :	: :: :
fhab_borpe		--ENGASVTVRTT-----	GNLVNKGYSAGKQGVLEV--	GGALTNEFLVGS	SDGTORIE		
		1260	1270	1280	1290	1300	
m564	.pep	1410	1420	1430	1440	1450	
		ARNINSNGNIQ-----	ADQIGLKAESINIDGGQVQAGRLLTAQ----	AQNINLNGTT			
		: :: :	: :: :	: :: :	: :: :	: :: :	
fhab_borpe		AQRIENRGTFQSQAPAGTAGALVVKAAEAIVHDGVMATKGEMQIAGKGGGSPTVTAGAKA					
		1310	1320	1330	1340	1350	1360
m564	.pep	1460	1470	1480	1490	1500	
		QTSGNERNGNTAI--	DRMAGINVV--	GSHTQVDNRTSD--	GILSLHASNDINLNAATVSNQV		
		: :: :	: :: :	: :: :	: :: :	: :: :	
fhab_borpe		TTSANKLSVDVASWDNAGSLDIKKGGAQVTVAGRYAEHGEVSIQGDYTVSADATLAAQV					
		1370	1380	1390	1400	1410	1420
m564	.pep	1510	1520	1530	1540	1550	
		--KDGTQITAGNNLNLGT--	IRTE---	HREAYGTLDDENHRHVRQST-----	EVGS		
		: :: :	: :: :	: :: :	: :: :	: :: :	
fhab_borpe		TQGGGAANLTSRHDTRFSNKIRLMGPLQVNAGGPVSNVTGNLKVREGVTVTAASFDNETGA					
		1430	1440	1450	1460	1470	1480
m564	.pep	1560	1570	1580	1590	1600	
		SIRTQNGALLRAGNDLKIRQGELEAEKGKTVLAAGRDV--	TISEGRQITELDTS---	VSG			
		: :: :	: :: :	: :: :	: :: :	: :: :	
fhab_borpe		EVMAKSATLTTSGAARN--	AGKMVQKEAATIVAASVSNPGTFTTAGKDITVTSRGGFDNEG				
		1490	1500	1510	1520	1530	
m564	.pep	1610	1620	1630	1640	1650	1660
		K---SKGILSSTKTHDRYR---	SHDEAV--	GSNIGGGKMIVAAGQDINVRGNSNLISDKGI			
		: :: :	: :: :	: :: :	: :: :	: :: :	
fhab_borpe		KMESNKDIVIKTEQFSNGRVLDAKHDLTVTASGQADNRGSLKAGHDFTVQAQRI--	DNSG				
		1540	1550	1560	1570	1580	1590
m564	.pep	1670	1680	1690	1700	1710	
		VLKAGHDIDISTAHNRYTG-----	NEYHESKKS	GVMGTGGLGFTIGNRKTDDTDRTNIV			
		: :: :	: :: :	: :: :	: :: :	: :: :	
fhab_borpe		TMAAGHDATLKAHLRNTGQVVAGHDIHIINSAKLENTGRV--	DARNIDIALDVADFTN--				
		1600	1610	1620	1630	1640	1650
m564	.pep	1720	1730	1740	1750	1760	1770
		HTGSIIGSLNGDVTTVAGNRYRQT----	GSTVSSPEGRNTVTAKSIDVEFANNRYATDYA				
		: :: :	: :: :	: :: :	: :: :	: :: :	
fhab_borpe		-TGSLYAEHDA-TLTLAQGTQORDLVVDQDHILPVAEGTLRVKAKSLTTEIETGNPGSLIA					
		1660	1670	1680	1690	1700	1710
m564	.pep	1780	1790	1800	1810	1820	1830
		HTQEQKGLTVALNVPVQAAQNFIAQAAQNVGKSKNKRVNAMAAANAA--	WQSYQATQQMQQ				
		: :: :	: :: :	: :: :	: :: :	: :: :	
fhab_borpe		EVQE-----	NIDNKQA----	IVVGKDLTSL--	SAHGNVANEANALLWAAGELTVKAQN		
		1720	1730	1740	1750		
m564	.pep	1840	1850	1860	1870	1880	1890
		FAPSSSAGQGQNNNQSPSISVSITYGEQKSRNEQKRHYTEAAASQIIGKGQTTLAATGSG					
		: :: :	: :: :	: :: :	: :: :	: :: :	
fhab_borpe		ITNKRAALIEAGGNARLTAVALNKLGRIRAGEDMHLDD--	APRI----	ENTAKLSGEV			
		1760	1770	1780	1790	1800	1810
m564	.pep	1900	1910	1920	1930	1940	1950
		EQSNINITGSDVIGHAGTALIADNHIRLQSAKQDGSEQSKNKS	SGWNAGVAVKIGNGIRF				
		: :: :	: :: :	: :: :	: :: :	: :: :	
fhab_borpe		QRKGVQDVGGGEHGRWSGIGYVNYWLRAGNGKKAGT-----	IAAPWYGGDLTAEQSLIEV				
		1820	1830	1840	1850	1860	

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		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKGKEQGGSTTHRHVGVSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
				::		::	::::
fhab_borpe		GKDLYLNAGARKDE-----HRHL-----LNEGVIQAGGHGIGG-----DVDNRSV-					
		1870	1880	1890	1900		
		2020	2030	2040	2050	2060	
m564	.pep	IESVQDTETTYQSKQQNGNVQVTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE					
		::::	::	::	::	::	::
fhab_borpe		VRTVSAMEYFKTLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTY					
		1910	1920	1930	1940	1950	1960
		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGNLFQTATLTASDIQNS--RYEGRSFGIGGS					
		::::				::::	::
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPMPKA-----PELDLRGHTLESAEGRKI-FGEY					
		1970	1980	1990	2000	2010	
		2130	2140	2150	2160	2170	
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYSGDSDSKNSTTRSGVNTNHIHITDEAG					
		::	::	::	::	::	::
fhab_borpe		KKLQGEYEKAKMAVQAVEAYGEATRRVHDQLG-----QRYGKALGGMDAETKEVDGIIQ					
		2020	2030	2040	2050	2060	2070
		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGRTAKETEARIYTGIDTETADQHSGLKNSFDKDAVAKEINLQREVTKFGRNAA					
		::	::	::	::	::	::
fhab_borpe		EFAADLRTVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPRVT--LAKALS					
		2080	2090	2100	2110	2120	
		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAAVADKLGNTQSYERYQEARTLE-AELQNTDSEAEKAAFRASLGQVNAYL-----					
		::	::	::	::	::	::
fhab_borpe		AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYFKEQTVLAAGAGLTLNNGAIHNGENA					
		2130	2140	2150	2160	2170	2180
		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDYTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGTSLAAPYLDKAAENLGPAGK					
		::::	::	::	::	::	::
fhab_borpe		AQNRGRPEGLKIGAHSA TSVSGSFDALRDVGLEKRLDIDDALAAVLVNPHIFTRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1  atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accattttcg cccgtcccag accggcggct tccaatactt
101 ccctgcgttt cgcctcgccg aacgacaccg gctcgcttgc acttctggct
151 acctgcacgc gtgcgatgtc caagtcgagc gcgaaatagc gaatatcctc
201 tttggcgcaa gacgcgtccg accgtctgcc cgcccctgcc gaagccgaca
251 atcagcacat gatcagactt gtcctatcgt tccaccaaca tgctgtgcag
301 atcgagcgac ttcattgtccc agcttga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1  MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1  ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA

```

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```

251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
  51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
 101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSGETISSCP
 151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSFA NTSSIAN SIN
 201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

              10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
              |||||
g565           MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
              10      20      30      40      50      60

              70      80      90      100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDL LMVSTSILCRSSDFMSQLDLTKRPTSASLP
              |||||
g565           AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
  1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
  51 CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
 101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
 151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
 201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCTGCGC AAGCCGACAA
 251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
 301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
 351 ATCGCTGCCG CCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
 401 CCGCCGTCGC CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCG
 451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
 501 AGCCGTTTGG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
 551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
 601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
  51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
 101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSSETISSCP
 151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSFA NTSSIAN SIN
 201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

              10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
              |||||

```

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```

a565      MDSTLSKTCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60

           70      80      90      100     110     120
m565.pep  AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
           |||||||||||||||||||||||||||||||||||||||||||||||||||
a565      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120

           130     140     150     160     170     180
m565.pep  PKRKGAIIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           |||||||||||||||||||||||||||||||||||||||||||||||||||
a565      PKRKGAIIIDSRTAAVAACSHSSETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180

           190     200     210
m565.pep  KAMANTTSAFNTSSSIANSINTCRQPPINAX
           |||||||||||||||||||||||||||
a565      KAMANTTSAFNTSSSIANSINTCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct ttccagacgg cattttgtat ggggggtaac
51  ggttggtcag cccgagtagc tcctgcatat cgtacaaacc cgttttgccg
101 tttacccaaa ctgcggcgcg gacggcaccg gcggcaaaagg tcatgcggct
151 gccggctttg tgggtgattt ccacgcgttc gccgtcgggtg gcgaagaggg
201 cgggtgtggtc gccgactatg tcgcctgcgc ggacgggtggc aaagccgatg
251 gtggaaggat cgcgcggacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcgccggc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51  AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAHSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTGTTAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTGGCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACC GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATTT CCACGCGCTC GCCGTGCGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCTGCGC GGACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDNCGA DGTGGKGHAA
51  AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAHSA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDNCGADGTGGKGHAAAGLVGDFHAL
           |||||||||||||||||||||||||||||||||||||||||||||||

```

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```

g566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10      20      30      40      50      60
           70      80      90      100     110
m566 . pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g566      AVGGEEGGVVADYVACADGGKADGRRISVAFAAVNGALFEVAAERAGDDFAHSX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566 . seq
1  ATGCCGTCTG  AACAATATCT  TTTCAGACGG  CATTTTGTAT  GGGGGTTAAC
51  GGTTGTTTCTG  CCCGAGTACG  TCCTGCATAT  CGTACAAACC  CGTTTTACCG
101 TTTACCCAAA  CTGCGGCGCG  GACGGCGCGG  GCGGCAAAGG  TCATGCGGGT
151 GCTTGCCTTG  TGGGTGATT  CCACGCGCTC  GCCGTCGGTG  GCGAAGAGGG
201 CCGTGTGGTC  GCCGACGATG  TCGCCCGCGC  GGACGGTGGC  AAAGCCGATG
251 GTGGACGGAT  CGCGCGGGCC  GGTGTGGCCT  TCGCGCCCGT  AAACGGCGCA
301 TTGTTTGAGG  TCTCTGCCGA  GCGCGCCGGC  GATGACTTCG  CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566 . pep
1  MPSEQYLFRR  HFVWGLTVVQ  PEYVLHIVQT  RFTVYPNCGA  DGAGGKGHAA
51  ACLVGDFHAL  AVGGEEGGVV  ADDVARADGG  KADGGRIARA  GVAFAAVNGA
101 LFEVSAERAG  DDFAHA*

```

m566/a566 94.0% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566 . pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
           10      20      30      40      50      60
           70      80      90      100     110
m566 . pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      AVGGEEGGVVADDVARADGGKADGRRIRAGVAFAAVNGALFEVSAERAGDDFAHAX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567 . seq..
1  atgcgacgac  gggcagcggc  atcgacaagg  cgggtttgca  gtccggcggt
51  tatcaggtct  tattggcgga  tgcggacgtg  cagtcggcgg  cggtacgcag
101 caaagagggc  ggatacggcg  tgttgggtgc  gaacgcgcgc  gcttgccggc
151 gcggaaatcg  agctggtgca  ggaaatcgcc  cggaagtgc  gttgaaaaaa
201 cgcgctcaag  gcagtgccgg  aagattacga  cttatcctg  atcgactgtc
251 cgccttcgct  gacgctgtg  acgcttaacg  gcttggtggc  ggcggggcgg
301 gtgattgtgc  cgatgttggt  cgaatattac  gcgctggaag  ggatttccga
351 ttgattgctg  accgtgcgca  aaatccgtca  ggcggtcaat  cccgatttgg
401 acatcacggg  catcgtgcgt  acgatgtacg  acagccgcag  caggctgggt
451 gccgaagtca  gcgaacagtt  gcgcagccat  ttcggggatt  tgctttttga
501 aaccgccatc  ccgcgcaata  tccgccttgc  ggaagcgccg  agccacggta
551 tgccggtgat  ggcttacgac  gcgcaggcaa  agggtgccaa  ggcgtatctt
601 gccttggcgg  acgaactggc  ggcgaggggt  tcggggaaat  ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567 . pep
1  MRRRAAATR  RVCSPAFIRS  YWAMRTCSRR  RYAAKRADTA  CWVRTRALAG
51  AEIELVQEIA  REVRKLNALK  AVAEDYDFIL  IDCPPSLTLL  TLNGLVAAGG
101 VIVPMLCEYY  ALEGISDLIA  TVRKIRQAVN  PDLDITGIVR  TMYDSRSRLV
151 AEVSEQLRSH  FGDLLFETAI  PRNIRLAEAP  SHGMPVMAYD  AQAKGAKAYL
201 ALADELAARV  SGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTGCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGCAGTCGG CGGCGGTACG CAGCAAAGAG GCGCGATACG
251 CTGTGTTGGG TCGGAACCGC GCGCTGGCCG GCGCGGAAAT CGAACTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGA
351 AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTT GGACATCACG GGCATCGTGC
551 GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCCGGGA TTGCTTTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701 ACGCGCAGGC AAAGGTACC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 GCGGCGAGGG TGTCGGGGAA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
1  MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51  GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVLGANR ALAGAEIELV
101 QEIAREVRLK NALKA VEEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAGT KAYLALADEL
251 AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m567/g567 98.2% identity in 168 aa overlap

m567.pep 60      70      80      90      100      110      119
          G V Y Q V L L G D A D V Q S A A V R S K E G G Y A V L G A N R A L A G A E I E L V Q E I A R E V R L K N A L K A V E E D
g567      A F I R S Y W A M R T C S R R R Y A A K R A D T A C W V R T R A L A G A E I E L V Q E I A R E V R L K N A L K A V A E D
          20      30      40      50      60      70

m567.pep 120      130      140      150      160      170      179
          Y D F I L I D C P P S L T L L T L N G L V A A G G V I V P M L C E Y Y A L E G I S D L I A T V R K I R Q A V N P D L D I
g567      Y D F I L I D C P P S L T L L T L N G L V A A G G V I V P M L C E Y Y A L E G I S D L I A T V R K I R Q A V N P D L D I
          80      90      100      110      120      130

m567.pep 180      190      200      210      220      230      239
          T G I V R T M Y D S R S R L V A E V S E Q L R S H F G D L L F E T V I P R N I R L A E A P S H G M P V M A Y D A Q A K G
g567      T G I V R T M Y D S R S R L V A E V S E Q L R S H F G D L L F E T A I P R N I R L A E A P S H G M P V M A Y D A Q A K G
          140      150      160      170      180      190

m567.pep 240      250
          T K A Y L A L A D E L A A R V S G K X
g567      A K A Y L A L A D E L A A R V S G K X
          200      210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTGCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGAGTTT GCAGTCCGGC GTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GCGCGATACG
```

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```

251 GCGTGTGGG TGCGAACCGC GCGCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCC GATTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCATTG GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCCGGGA TTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGGCGAGGG TGTCGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
  1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
 51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GGYVGLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKG KAYLALADEL
251 MARVSGK*

```

m567/a567 97.7% identity in 257 aa overlap

```

              10      20      30      40      50      60
m567.pep      MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKAGLQSG
              |||
a567           MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
              10      20      30      40      50      60

              70      80      90      100     110     120
m567.pep      VYQVLLGDADVQSAAVRSKEGGYAVLGGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
              |||
a567           VYQVLLGDADVKSAAVRSKEGGYGVLGANRALAGAEIELVQEIAREVRLKNALKAVAEDY
              70      80      90      100     110     120

              130     140     150     160     170     180
m567.pep      DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
              |||
a567           DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
              130     140     150     160     170     180

              190     200     210     220     230     240
m567.pep      GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAGT
              |||
a567           GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKG
              190     200     210     220     230     240

              250
m567.pep      KAYLALADELAARVSGKX
              |||
a567           KAYLALADELMARVSGKX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
  1 atgctcaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
 51 gataccttgc agaactctgc gattaaagcg ttcgcggtcg cccaatattt
101 tcaggcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaaaggc
151 tgtaaaaaca gcccatcag gaacgaaact tcgtcttcgg ggcgacgcca
201 gttttcggtt gaaaaggcaa acacggtcag atattgcacg cccagtttgg
251 cgcaatgctt caccatattt tccaacgcgt ccaagccgcg tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggccgt tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcg

```

401 tgctgctctt catatctgcc tttcgcggtt cggcggtcaa atgccgtctg
451 aacgccgcgc cgtga

This corresponds to the amino acid sequence <SEQ ID 1690; ORF 568.ng>:

g568.pep

1 MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL
151 NAAP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1691>:

m568.seq

1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC
51 GATGCCTTGC AGAATCTGCC GGTGAAGCG TTCGCGGCTG CCCAATATCT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAAACT TCGTCTTCGG GCGGCGGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGGCCTGCG
401 TGCTGCTTT CATGTCTGCC TTTGCGGTT CGGCATTCAA ATGCCGCTCTG
451 AACGCCGAAC CGTGCAGGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATAGAGA
651 CCGGCGCTTC TTCCGCTTCG CCGCGTACGA CTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTT AGTCCCAAGT TTGA

This corresponds to the amino acid sequence <SEQ ID 1692; ORF 568>:

m568.pep..

1 MLRVRPVLFA VNASASSMPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVVGIA AHVADRDAAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m568/g568 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
g568	MLRVRPVLFAVKASASSIPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAASKPRLCPIMRGRKRFFAQRPLPSIITA					
g568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAASKPRLCPIIRGRKRFFAQRPLPSIITA					
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
g568	MCLGMAVCSKMVCVLLFISAFRGSFAFKCRLNAAPX					
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568 . seq
1  ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CGCCTCTTC
51  GATGCCCTTC AGGATTGAC GGTGAAGCG TTCGCGGCTG CCCAGTATT
101 TCAGGCGCAT ATTGTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTCGCGGTT CCGCATTCAA ATGCCGTCTG
451 AACGCCGAAC CGTGCAGGT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTC AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568 . pep
1  MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCTIF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSFAFKRL
151 NAEPCLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

m568 . pep	10	20	30	40	50	60
a568	10	20	30	40	50	60
m568 . pep	70	80	90	100	110	120
a568	70	80	90	100	110	120
m568 . pep	130	140	150	160	170	180
a568	130	140	150	160	170	180
m568 . pep	190	200	210	220	230	240
a568	190	200	210	220	230	240
m568 . pep	250					
a568	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569 . seq..
1  atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgtgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgogggc
101 tgattgccct gaccgccttg tgggagtatg cccgatggc cggtttgtgc
```

874

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151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
201 tgcctatgcg ggcggctgga tgctgcctaa ttgggttgg tatgttgtt
251 tggcattttg gctcgccgtt atgcctttgt ggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctggcttt tgctcatgcc
351 gttttggttc gcgctcgat ccctggcgcc cgcattccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

```

g569.pep
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51  KIETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

```

m569.seq..
1  ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51  GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
101 TGATTGCCCTT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGTTTT TCGGCGTGGT
201 TGCCTATGCG GCGCGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTITG GCTCGCGGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCACACGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCTGCGCCC GCATCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCGATAT TTGCGGTAT
451 TTCAGCGCGA AGGCGTTCCG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCEA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTGGTGTCTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAAGCTGCT GCCCGGACAC GCGCGGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

```

m569.pep..
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51  KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVVWADICAY
151 FSGKAFGKHK IAPAI SPKSWEGAIGGAVC VAVYMTAVRS AGWLAFTDGTW
201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRDTSLS
251 IAVISVYAAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
m569.pep	TLVFGVVAYAGGWMLPNLVVYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
g569	TLVFGVVAYAGGWMLPNLVVYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
	70	80	90	100	110	120
m569.pep	ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPKSWEGAIGGAVC					
g569	ALVSLAPASRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

```

a569.seq
1  ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51  GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

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875

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151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGCTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTGG TATGTTGTTT
251 TGGCATTGTT GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGCGCG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTGCA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGGCGGTGT TCGACCGCAC CGACAGCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569 . pep
1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALLAL WEYARMGGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRTDSL
251 IAVISVYAAM MSVLN*

```

m569/a569 99.6% identity in 265 aa overlap

	10	20	30	40	50	60
m569 . pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGGLCKIKTNHYLAA					
a569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGGLCKIKTNHYLAA					
	10	20	30	40	50	60
m569 . pep	70	80	90	100	110	120
	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
a569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
	70	80	90	100	110	120
m569 . pep	130	140	150	160	170	180
	ALVSLRPHPDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEAIGGAVC					
a569	ALVSLRPHPDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEAIGGAVC					
	130	140	150	160	170	180
m569 . pep	190	200	210	220	230	240
	VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLESWLKRAAGIKDSSKLLPGH					
a569	VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLESWLKRAAGIKDSSNLLPGH					
	190	200	210	220	230	240
m569 . pep	250	260				
	GGVFDRTDSLIAVISVYAAMMSVLNX					
a569	GGVFDRTDSLIAVISVYAAMMSVLNX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

```

g570 . seq . .
1 atgatccgtt tgaccgcgc gtttgccgcc gccctgatcg gtttatgctg
51 caccacaggc gcgcacgccg acaccttcca aaaaatcggc tttatcaaca
101 ccgagcgcat ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacy
151 ctggacggcg aattttccgc ccgtcaggac gaattgcaaa aactgcaacy
201 cgaaggcttg gatttggaaa ggcagctcgc cggcgcaaaa cttaaggacy
251 caaaaaaggc gcaagccgaa gaaaaatggc gcgggctggt cgaagcgttc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtgttgc tccctccagc aaaacgccaa ccgcgtcatc gtcaaaatcg

```

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
 451 acccaatagc acgttacgga cagcgtcatt aaagaaatga acgcccgtg
 501 a

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

1 MTRLTRFAAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
 51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
 101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
 151 TQYDVTDSVI KEMNAR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

1 ATGACCCGTT TGACCCGCGC GTTTCGCCG GCTCTGATCG GTTGTGCTG
 51 CACCGCAGGC GCGCACGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
 151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTTGAAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
 501 A

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

1 MTRLTRFAAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAP
 101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQNVIIYVN
 151 TQYDVTDSVI KEMNAR*

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLTLDSEFSARQD					
g570	MIRLTRFAAAALIGLCCTTAGAHADTFQKIGFINTERIYLESKQARNIQKTLTLDGEFSARQD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAPFRKKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLDKAKKAQAEKWRGLVEAPFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX					
g570	SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

1 ATGACCCGTT TGACCCGCGC GTTTCGCCG GCTCTGATCG GTTGTGCTG
 51 CACCGCAGGC GCGCACGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
 151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTTGAAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

a570.pep
 1 MTRLTRAF~~AA~~ ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
 101 RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
 151 TQYDVTDSVI KEMNAR*

m570/a570 97.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRAF AA AALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
a570	MTRLTRAF AA AALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA					
a570	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRVI V KIAKQEGYDVILQNVIVNTQYDVTDSVIKEMNARX					
a570	SLQQNANRVI V KIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

g571.seq (partial)
 1 atgcgcttt tccgagtaaa ccgatttgtt gttaccgttt tcggcgccgg
 51 t~~at~~aggttct gccgtccac acgctgcctg cgctcgcaaa caggctcagg
 101 cggacggtgc gtgcgtcttt cgcaccgggc atcggaaga gcagctcggc
 151 ggagacgttg gctttttgt tgcgcgcgta gctgatttt tcgccgtatt
 201 cgtcatacac tttcgggccc agcgtgcgcg tttcgtagcc gcgcacogaa
 251 cccagggccc cgcgtagaa gttttcaaag aaggggattt ctttggttct
 301 gcgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
 351 ttttgc...

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

g571.pep (partial)
 1 MRVFRVNRV VTVFGGGIGS AVPHAACVGK QAQADGACVF RTGHRREQLG
 51 GDVGF~~F~~VAAV ADFFAV~~F~~VIH FRAERAAVFA AHRTQAAAVE VFKEGDFFGS
 101 AVAARNADFA AEHQREGFA...

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

m571.seq
 1 ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCGG CCGGTCGCGG
 51 AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
 101 GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
 151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CGGTAGCTGA
 201 TTTTTCGCCC GTATTGCTCA TAGACTTTCG GACCGAGCGT GCCGCTTTCG
 251 TATCCGCGCA CCGAACCCAG GCCGCGCCG TAGAAGTTT CAAAGAAGGG
 301 GATTTCCTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
 351 GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACCAGT TGGTGTGTGG
 401 GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTCCGCGTT
 451 CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

m571.pep
 1 MGIAGAVNL NPAAGRGTAV VVGVFAVPHA ACVGKQAQAD GARVFRAGHR
 51 EEQLGGDVGF FVA~~A~~VADFFA VFVIDFRTER AAFVSAHRTQ AA~~A~~VEVFKEG
 101 DFFGSAVAAR NADFA~~A~~EHQR EGFAQGE~~E~~PG LVVGGGVVLQ FAARQGD~~F~~GV
 151 HARQVAARRP *

878

m571/g571 93.1% identity in 102 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVLNPAAGRGTAVVVVGFVAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
g571      MRVFRVNRFFVTVFVGGGIGSAVPHAACVKGQAQADGACVFRTGHREEQLGGDVGF
      10      20      30      40      50

      70      80      90      100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
g571      FVAAVADFFAVFVIHFRAERAAAFVAAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
      60      70      80      90      100     110

      130     140     150     160
m571.pep  EGFAQGEEPLVVGGGVVLQFAARQDGFVHARQVAARRPX
g571      EGFA
      119

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```

a571.seq
1  ATGGGTATTG CCGGCGCCGT AAATGTTTGT AACCTGCCG CCGGTCGCGG
51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTGCCC CCGTAGCTGA
201 TTTTTCGCC GTATTCGTCA TACACTTTCG GACCGAGCGT GCCGCTTTCG
251 TATCCGCGCA CCGAACCCAG GCCGCGCCG TAGAAGTTTT CAAAGAAGGG
301 GATTCTTTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGGTTTTG CTTAAGGGGA AGAACCAGT TTGGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTGCTGCCG GGCAGGGCGA TTTCGGCGTT
451 CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:

```

a571.pep
1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVKGQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAAVADFFA VFIHFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQ EGFA*GEEPL VVGGGVVLQ FAAGQDGFV
151 HARQVAARRP *

```

m571/a571 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVLNPAAGRGTAVVVVGFVAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
a571      MGIAGAVNVLNPAAGRGTAVVVVGFVAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
      10      20      30      40      50      60

      70      80      90      100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
a571      FVAAVADFFAVFVIHFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
      70      80      90      100     110     120

      130     140     150     160
m571.pep  EGFAQGEEPLVVGGGVVLQFAARQDGFVHARQVAARRPX
a571      EGFAQGEEPLVVGGGVVLQFAAGQDGFVHARQVAARRPX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq..

879

```

1  atgtgcgcca tcgtcggggc ggcggggctg ccttccgcgc tcgcagcggc
51  gcaaaaaggc aaaaccattt atctggcaaa caaagaaacg ctggtggttt
101 ccggcgcggt gtttatggaa accgcccgcg caaacggcgc ggcagtgttg
151 ccgctcgaca gcgaacacaa cgccattttc caagttttgc cgcgcgatta
201 caacagaccgt ctgaacgaac acggcatcga ttcgattatc ctgaccgctt
251 ccggcgggccc gtttttaaca accgatttaa gcacgttcga cagcattacg
301 ccgagcgagg cgtcaaaaca cccaattgg cgtatggggc gcaaaatctc
351 cgtcgattca gccactatgg caaacaaggg cttggaactg attgaagcgc
401 attggtcgtt caactgtccg ccgcacaaac tcgaagtcgt catccatccc
451 caatccgtga tacacagtat ggtgcgctac cgcgacggct cgtgctggc
501 gcaactgggc aatcccgaata tgcgaacgcc catcgctat tgtttgggt
551 tgcccgagcg catcgattcg ggtgtcggca aactcgattt cggcgcttg
601 tcgcgctga ctttccaaa gcccgacttc ggcgcttcc cctgcctgaa
651 gttcgcctat gaaaccataa acgcaggcgg agccgcgccc tgcgtattga
701 acgcgcgcaa cgaaacgcc gtcgcgcct ttttgacgg acagattaag
751 ttaccgaca ttgccaaaac cgtcgccac tgtctgcac aagacttttc
801 aaacggcatg ggcgatatag aaggactgtt ggcgaagat gcccgacac
851 ggcgacaagc gcgggcattt atcggcacac tgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1714; ORF 572.ng>:

g572.pep..

```

1  MCAIVGAAGL PSALAAQKG KTIYLANKET LUVSGALFME TARANGAAVL
51  PVDSEHNAIF QVLPRDYDR LNEHGIDSII LTASGGPFLT TDLSTFDSIT
101 PEQAVKHPNW RMGRKISVDS ATMNKGLLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGKLDLFDAL
201 SALTFFQKPDF GRFPCLKFAY ETINAGGAAP CVLNAANETA VAAFLDGQIK

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1715>:

m572.seq..

```

1  ATGTGCGCCA TCGTCGGGCG GGTGGGGCTG CTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGGCAAA CAAAGAAACG CTGGTGGTTT
101 CCGGCGCGGT GTTTATGGAA ACCGCCCGTG CAAACGGCGC GGCAGTGTCTG
151 CC CGTCGACA GCGAACACAA CGCGTTTTTC CAAGTTTTGC CGCGCGATTA
201 CGCGCGCGGT CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCCC GTTCTGACC GCCGATTAA ACACGTTTGA CCGCATTACG
301 CC CGCCCAAG CGGTCAAACA CCCCATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCCGTGA TACACAGCAT GGTGCGCTAC CCGACGGCT CCGTGTGGC
501 GCAACTGGGC AATCCOGATA TCGAAGCGCC CATCGCTTAT TGTTTGGGT
551 TGCCCGAGCG CATCGATTGC GGTGTGGCG ACCTGGATT TCGACGATTG
601 TCCGCGCTGA CTTCCAAA GCGCGACTTT GACCGCTTCC CCGCTGTGAG
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCG AGCCGCGCCC TGCCTATTGA
701 ACGCGGCCAA CGAAGCGGCC GTCGCGCCT TTTTGGACGG ACAGATTAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAC TGTCTTGCAC AAGACTTTTC
801 AGACGGCATA GCGATATAG GGGGCTCTT GCGCAAGAT GCCCGGACAC
851 GCGCACAAAG CCGAGCATTT ATCGGCACAC TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1716; ORF 572>:

m572.pep..

```

1  MCAIVGAVGL PSALAAQKG KTIYLANKET LUVSGALFME TARANGAAVL
51  PVDSEHNAIF QVLPRDYAGR LNEHGIASII LTASGGPFLT ADLNTFDRIT
101 PAQAVKHPNW RMGRKISVDS ATMNKGLLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGKLDLFDAL
201 SALTFFQKPDF DRFPCLRLAY EAMNAGGAAP CVLNAANETA VAAFLDGQIK
251 PTDIAKTVAH CLAQDFSDGI GDIGGLLAQD ARTRAQARAF IGTLR*

```

m572/g572 92.9% identity in 295 aa overlap

```

          10      20      30      40      50      60
m572.pep  MCAIVGAVGLPSALAAQKGKTIYLANKETLUVSGALFMETARANGAAVL PVDSEHNAIF
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572      MCAIVGAVGLPSALAAQKGKTIYLANKETLUVSGALFMETARANGAAVL PVDSEHNAIF
          10      20      30      40      50      60

          70      80      90     100     110     120
m572.pep  QVLPRDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572      QVLPRDYDRLNEHGIDSII LTASGGPFLTTDLSTFDSITPEQAVKHPNWRMGRKISVDS

```

880

	70	80	90	100	110	120
	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDQKLEVVHPQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
g572	ATMANKGLELIEAHWLFNCPDQKLEVVHPQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGLDFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
g572	CLGLPERIDSGVGLDFGALSALTFOKPDFGRFPCLKFAYETINAGGAAPCVLNAANETA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGGIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
g572	VAAFLDGGIKFTDIAKTVAHCLAQDFSDGMDIEGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```
a572.seq
1  ATGTGCGCCA TCCTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGGCGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCGTG CAAACGGCGC GGCAGTGCTG
151 CCGTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTCG CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCC GTTTCTGACC GCCGATTAA ACACGTTTCA CAGCATTACG
301 CCGACCAAG CGGTCAAACA CCCCATTGG CGTATGGGAC GCAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTGGC
501 GCAACTGGGC AATCCCGATA TCGGAACGCC TATCGCTTAT TGTGTGGGT
551 TGCCCGAGCG CATCGATTGG GGTGTCGGCG ACCTGGATTG CGACGCATTG
601 TCCGCGCTGA CCTTCCAAA GCCCGACTTT GACCGCTTCC CCTGCCTGAA
651 GCTCGCTTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TGCCTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCTT TTTTGGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAT TGTCTTTCAC AAGACTTTTC
801 AGACGGCATA GCGACATAG GGGGGCTCTT GCGCAAGAT GCCCGGACAC
851 GCGACAAGC GCGGGCATT ATCGGCACAC TGCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

```
a572.pep
1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAVF QVLPRDYTGR LNEHGIASII LTASGGPFLT ADLNTFDSIT
101 PDQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVHP
151 QSVIHSMVRY RDGSLAQLG NPD MRTPIAY CLGLPERIDS VVGDLDFDAL
201 SALTFOKPDF DRFPCLRLAY EAMNAGGAAP CVLNAANEAA VAAFLDGGIK
251 FTDIAKTVAH CLSQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*
```

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572.pep	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF					
a572	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m572.pep	QVLPRDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS					
a572	QVLPRDYTGRLNEHGIASII LTASGGPFLTADLNTFDSITPDQAVKHPNWRMGRKISVDS					
	70	80	90	100	110	120

881

	130	140	150	160	170	180
m572. pep	ATMMNKGLELIEAHWLFNCPDPKLEVVIHQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPDPKLEVVIHQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572. pep	CLGLPERIDSGVGDLDLFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAAEAA					
a572	CLGLPERIDSGVGDLDLFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAAEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572. pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIAKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1  atgccctgtt tgtgccgect taatcgcaat atcggcagtt tccaaatcac
51  gaatctcacc gaccataatg atgtccgggt cctgacgcag gaaagacttc
101 aaagcagcgg caaaagtcag accctgctta tcattgacgt taacctgatt
151 gatgcccgcc aggttaaatct cggcagggtc ttccgcccgt gcaatattta
201 ccgactccgt attcaaaata ttcaaacagg tatagagcga cacogtctta
251 ccggaacccg tcggaccggg taccagcacc atcccgttaag gacggtgaat
301 cgcttccaac aacaattttt tctggaacgg ctcaaaacgg agctggtcga
351 tgttcaaga cgccgcatcg gaattcaaaa tccgcatcac gaccttttcg
401 ccaaacagcg tcggcaatgt gctgacacgg aaatcgacag gcttgccgcc
451 cttttgaag gtcagctgca tcctaccgtc ctgcggatc cgtttttcgg
501 aaatgtccaa acgcgacatt acctaatcc ggaagcaag ctgcccctt
551 accgcaatgg gcggctgaac cacctcggg agctgcccgt ccacacggaa
601 accgatacgc gcattgtgtt cgtaaaactc gaaatggatg tcggatgccc
651 cgtctacgaa ggcacccgac aaagtattat ggataaacct cggaacaggg
701 ccgtctcttg cctcctcgtc gtcgatatac aggggtgtgg tttcctcttc
751 ctcttgcccc tccccaaagt cctgaagcag cgtatgtcaa cggaaccca
801 ccaatcgag caaacccgcc aactggtcat cctcgacaat gaccaactca
851 accgcaatcc ctgcggcaga aaccgttttc tgaatttgcg gcattctgggt
901 cggatcggaa accgcaaaaa atactttgtc gcccccaggg aaaaccggca
951 cacagtggaa ctccaccatc tgcctcctcg tcaacacccc catcagcacc
1001 ctgtggcgcg gataatgacg caaatcaaga atcgaataac tgaacaccct
1051 cgcaatcaat gccgcaagcg acttgggcga aatgacaccg tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1  MPCLCRINRN IGSFQITNLT DHNDVRVLTO ERLQSSGKSQ TLLIIDVNL
51  DARQVNLRV FRRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVRTVN
101 RFQQQFFLER LKTELVDVQR RGIGIQPHH DLFQKRRQC ADTEIDRLAA
151 LLKGQLHPTV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTRIVFVKL EMDVGCPATQ GIRQSPMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTTRTHPIE QTRQLVILDN DQLNRNPGCR NRFLNLRHLG
301 RIGNRKRYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1  ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG GCCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCGCGCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACCGTGAAT
301 CGCTACCAAC aCaw.TTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTGAAGG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GTGAAGCAAG CTGCCCCCTT

```

```

551  ACCGCAATGG GCGGCTGAAC CACCTGCGG AGCTGCCCGT CCACACGGAA
601  ACCGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651  CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701  CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCCTCTTC
751  CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801  CCAATCGAG CAAACCCGCC AACTGGTCAT CCTGACAAT GACCAACTCA
851  ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTTGCG GCATCTGTGT
901  CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951  CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

```

m573.pep..
1  MPCLCLRNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
51  DARQVNLGRV FRRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHXFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKQQLHPAV LRYPPFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPPAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/g573 95.9% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCLRNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
g573	MPCLCLRNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m573.pep	FRRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVMRYQHXFFLKR LKTELVDVQR					
g573	FRRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVMRYQHXFFLKR LKTELVDVQR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK					
g573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHTEITDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRAVFCLLV					
g573	LPPYRNGRLNHLAELPVHTEITDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
g573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300
	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHHLLLRQHHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
g573	RIGNRKKYFVAPTENRHTVELHHLLLRQHHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

883

a573 . seq

```

1 ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51 GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCGG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACCGTGAAT
301 CGCTTCCAAC AACAATTTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGAAGAGCAAG CTGCCCCCTT
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCCGAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTTC
751 CTCCTGCCCC TCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATAATTGTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573 . pep

```

1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51 DARQVNLGRV FRRCNIRYLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPPAQ GIRQSLMDKP RNRVAFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKRYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573 . pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQ TLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
m573 . pep	FRRCNIRYLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN RYQHFFLKR LKTELVDVQR					
a573	FRRCNIRYLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN RFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
m573 . pep	FRRCNIRYLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN RYQHFFLKR LKTELVDVQR					
a573	FRRCNIRYLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN RFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
m573 . pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
a573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
m573 . pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
a573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
m573 . pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRVAFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRVAFCLLV					
	190	200	210	220	230	240
m573 . pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRVAFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRVAFCLLV					
	190	200	210	220	230	240
m573 . pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300
m573 . pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300

884

	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573						
	RIGNRKKYFVAPTENRHTVELHLLLRQHHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360

m573.pep	NDTVX
a573	NDTVX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1 atgctgcccga atctgccaaa cagccttaag aaagccgata tggacaacga
51 attgtggatt atcctgctgc cgattatcct tttgcccgtc ttcttcacga
101 tgggctgggt tgcgcgccgc gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc cttcgggatt ttataaaagc ctggacgctt tggtcgaccg
201 caa cagcggg cgcgccgcaa gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaac cttaccctcg gcaaacttta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cggacaatgc tcgattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 act accaaag cgcggtttg gtgatcgtg ccgaacagat tttttgggg
451 ctgcaagacg gtgaaatggc gcgtgaagcc agacagcacc tgcataat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccaacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcgttt
651 caatgtcggc aaggcactcg aagccaacaa aaaatgcacc cgcgccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgcgcgcgtc
751 gaagcctatg ccgcccacga gcagcaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaacgc tctgacagga tatatgcaga cgtttcccga acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg ctttaagggcg agaaagaagc
951 cgcgcaaacg gcgctcgagc ttgtccgcgc caagcccgac cttaacggcg
1001 tgt accgcct gctcggttg aaactcagcg atttggatcc ggcttgaaa
1051 gccgatgcgc acatgatgcg ttcggttacc ggacggcagc tccagcgagc
1101 cgt gatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcaactgtcc cgctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagtttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1 MLEPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51 KSI PSGFYKS LDALVDRNSG RAARELAENV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFELAQFYC
201 ELAQALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVYEKSL LKGEKEAAQT AVELVRRKPD LNGVYRLGL KLSDLPDPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1 ATGCGCCCGA ATCTACCAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51 ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCCGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTGAAC CTCACCTCG GCAAACCTTA CCGCCAGCGT
301 GGCAGAAACG ACAAAGCCAT CAACATACAC CGGACAATGC TCGATTCTCC
351 CGATACGGTC GCGGAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGG
451 CTGCAAGACG GTAAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGTAAGC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTCGATG TCGCGCGTTT

```

651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCGCGCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGGC AGAAAGAAGC
951 CGCGCAAAAC GCCGTCGAGC TTGTCCGCGC CAAGCCCGAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AAACCTCAGC ATATGAATCC GGCTTGGAAA
1051 GCCGATGCCG ACATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCTTTTCT
1151 GGCACTGCCC CGCCTGCAAC AAATGGCAGA CGTTTACCCC GAATAAAATC
1201 GAAGTTTAA

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

1 MRPNLNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51 KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGKMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQAAALFKS NFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GKPEEGLNRLTG YMQTFPELDL
301 INVVEKSLLL KCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSMDNPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFPNKI
401 EV*

m573/g573 97.8% identity in 402 aa overlap

m574.pep	10	20	30	40	50	60
	MRPNLNSLK	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA	KSIPSGFYKS
g574	MLPNLNSLK	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA	KSIPSGFYKS
	10	20	30	40	50	60
m574.pep	70	80	90	100	110	120
	LDALVDRNSG	RAARELAEVV	DGRPQSYDLN	LTLGKLYRQR	GENDKAINIH	RTMLDSPDTV
g574	LDALVDRNSG	RAARELAEVV	DGRPQSYDLN	LTLGKLYRQR	GENDKAINIH	RTMLDSPDTV
	70	80	90	100	110	120
m574.pep	130	140	150	160	170	180
	GEKRARVLFE	LAQNYQSAGL	VDRAEQIFLG	LQDGKMAREA	RQHLLNIYQQ	DRDWEKAVET
g574	GEKRARVLFE	LAQNYQSAGL	VDRAEQIFLG	LQDGKMAREA	RQHLLNIYQQ	DRDWEKAVET
	130	140	150	160	170	180
m574.pep	190	200	210	220	230	240
	ARLLSHDDQT	YQFEIAQFYC	ELAQAAALFKS	NFDVARFNVG	KALEANKKCT	RANMILGDIE
g574	AQLLSHDEQT	YQFEIAQFYC	ELAQAAALFKS	NFDVARFNVG	KALEANKKCT	RANMILGDIE
	190	200	210	220	230	240
m574.pep	250	260	270	280	290	300
	HRQGNFPAAV	EAYAAIEQQN	HAYLSMVGEK	LYEAYAAQ GK	PEEGLNRLTG	YMQTFPELDL
g574	HRQGNFPAAV	EAYAAIEQQN	HAYLSMVGEK	LYEAYAAQ GK	PEEGLNRLTG	YMQTFPELDL
	250	260	270	280	290	300
m574.pep	310	320	330	340	350	360
	INVVEKSLLL	KCEKEAAQT	AVELVRRKPD	LNGVYRLLGL	KLSMDNPAWK	ADADMRSVI
g574	INVVEKSLLL	KCEKEAAQT	AVELVRRKPD	LNGVYRLLGL	KLSMDNPAWK	ADADMRSVI
	310	320	330	340	350	360
m574.pep	370	380	390	400		
	GRQLQRSVMY	RCRNCHFKSQ	VFFWHCPACN	KWQTFPNKIEV		
g574	GRQLQRSVMY	RCRNCHFKSQ	VFFWHCPACN	KWQTFPNKIEV		
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1  ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACCTTA CCGCCAGCGT
301 GCGGAAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTCGATG CCGCGCGTTT
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCGCTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGCGGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCGC CAAGCCCGAC CTCAACGGCG
1001 TGTACCGCCT GCTTGGTTTG AAACCTCAGC ATTTGGATCC GGCTTGAAAA
1051 GCGGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACAA GTCTTTTCTT
1151 GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1  MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINMH QTLSDSPDTT GAKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQGK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSLDLPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFQSQ VFFWHCPACN KWQTFTPNKI
401 EV*
```

m574/a574 97.5% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLKKADMDNELWIIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
a574	MRPNLPNSLEKADMDNELWIIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
	10	20	30	40	50	60
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINIHRTMLDSPDTV					
a574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINMHQTLSDSPDTT					
	70	80	90	100	110	120
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINIHRTMLDSPDTV					
a574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINMHQTLSDSPDTT					
	70	80	90	100	110	120
m574.pep	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
a574	GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
m574.pep	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
a574	GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFVARFNVGKALEANKKCTRANMILGDIE					
a574	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFVARFNVGKALEANKKCTRANMILGDIE					

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	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pép	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKPEEGLNRLTGYMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKPEEGLNRLTGYMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pép	INVVYEKSLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDMNPAWKADADMMSVI					
a574	INVVYEKSLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDLDPWKADADMMSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pép	GRQLQRSVMYRCRNCHFSQVFFWHCPACNKWQTFFTPKNKIEVX					
a574	GRQLQRSVMYRCRNCHFSQVFFWHCPACNKWQTFFTPKNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

g575.seq (partial)

```

1  ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51  cccgtcaaaca gtccgctttc ggtttcttct tccgcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggcaacttc actggctgtt tccgcaacag
151 gttcggaaac ggtgttacgg gtttcgtcgg tccgcgtgtc gatggcagaa
201 gcggcggctt cttggggggg cggattcggc agcggtttcc gatgcggcag
251 tatttcgacg ggttacaggt cgggttggtc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggttcgggt cgaacggccg gttttccgc
351 ttttgcctcg ggccgggcaa cttttgttc aggttttca accggttttt
401 cgacagggtt ctctatcggg ttctccacag ttgctctgtt ggacggttca
451 gacggcatgg atgcagtttc ggctttgggt ttccgcgttt cgggtttggg
501 ttgttcgcgt ttgatttttt tgggtgctgc cgtttgatc ctgttcagat
551 tcggaatgtg a*
```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

g575.pép (partial)

```

1  ..MPCLRRQAAR CTNRRIDRQT VRFRFLLRQK FVRQVRQVR RQLHWLFPQQ
51  VRKRCYRFRF SACRWQKRRL LGGADSAAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGSG RTAGFSAFAS GAATFASGFS TGFSTGFSIG PSTVACLDGS
151 DGMDAVSALG FAVCGLGCSA LIFLGAAALI LFRFGM*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

m575.seq..

```

1  ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTTGTG GGAGAAATCG GTATCGACCG TTTCCGTTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTGACAGG
201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CAGCTGTCT GTGGATTCTGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAATGCC GTTTTGCGCG GCTGCCAGGC TGTGAAATC
351 CAAGTCGATG CGGTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGT
401 TTGCCGATAA CTCCTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGCG GATTAAATGCC GCGCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACCGCGCA ACAGACCGTC AAACAGTCCG CTTTCGTTTT
701 CTTCTTCGGC AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCCGTCG GCGTGTGAT GGCAGAACCG GCGGCTTCTT GGGGGGCGGA
801 TTCGGCAGCG GTTTCGATG CGGCAGTATT TGCAGCGGGT ACAGGTTTCG
851 GTCGAACGGC CGGTTTTTCC GCTTTTGCTT CGGGCGCGGC AACTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTTCGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTTTGGGTT
1001 GTTCCGCTTT GATCCTGTTT AGATTGGAA TGTGA
```

This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

m575.pep
 1 MVS GEEAFRK PASPEGEAGF AEA VSSVPIW LFEGR LSEKS VSTVSGLFSA
 51 VWATDSGSGV SMTISTGLYG LKVS GSYTLS VDSMAFQSAS ARFWVSSSCV
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVC FADN SSS DSPSKASVSF
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
 201 RKSSSRAINA APPPASSKVY EPPNRPNSP LSVSSSAETC STGSETALPV
 251 SSVGVSM AEA AASWGADSAA VSDAAVFAAG TSGRTAGFS AFASGAATFA
 301 SGFSTGPFSTV ACLDGS DGM AVSALGFAVC GLGCSALILF RFGM*

m575/g575 70.2% identity in 114 aa overlap

	240	250	260	270	280
m575.pep	SSAETCSTGSETALPVSSGVSM AEAASWGADSAAVSDAAVFAAGTG-----				
g575	LHWLFPPQVRKRCYRFRRSACRWQKRRLGGADSAAVSDAAVFAAGTGPGWRSVAEAGVS				
	50	60	70	80	90

	290	300	309	310	320
m575.pep	-----SGRTAGFSAFASGAATFASGFGTGFST-----VACLDGS DGM DAVSALGFA				
g575	DTAGLGSRTAGFSAFASGAATFASGFGTGFSTGFSIGFSTVACLDGS DGM DAVSALGFA				
	110	120	130	140	150

	330	340
m575.pep	VCGLGCSALI-----LFRFGMX	
g575	VCGLGCSALIFLGAAALILFRFGMX	
	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

a575.seq
 1 ATGGTTTCGG GCGAGGAAGC CTT CAGGAAG CCTGCCAGTC CGGAGGGTGA
 51 GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
 101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
 151 GTTTGGGCGA CAGATTCGGG TCGGGCGGTG TCGATGACGA TTTTCGACAG
 201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
 251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
 301 AGTGCGCCGG ATAAAATGCC GTTTTGCGCG GCTGCCAGGC TGTCGAAATC
 351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
 401 TTGCCGACAA CTCTTCTTCA GATTCCCCAT CTAAGGCAAG TGTGTCGTTT
 451 ACATCGTTTT TCGGAGCGGG TCGGGCGGTT GCCGGAGTTT CGACTTCGGC
 501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
 551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
 601 CGCAAAGCA GCAGCAGGGC GATCAATGCC GCGCCTCCGC CGGCAAGCAG
 651 CAAGGTGTAC GAACGCGCGA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG
 701 AAACCTGTTT GACAGGTTCT GAAACGGCGT TACCGGTTTC GTCGGTCGGC
 751 GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT
 801 TTCCGATGCG GCAGTATTTG CAGCGGTGAC AGGTTCCGGT CGAACGCGCG
 851 GTTTTTCGCG TTTTGCTTCG GCGCGGCGAA CTTTGTCTTC AGGTTTTTCA
 901 ACCGTTTCT CTACCGTTGC CTGTTTGAC GGTTCGGACG GCATGGATGC
 951 GGTTCGGCT TTGGGTTTCG CCGTTTGC GG TTTGGGTTGT TCCGCTTTGA
 1001 TCCTGTTTCA ATTCCGAATG TGA

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

a575.pep
 1 MVS GEEAFRK PASPEGEAGF AEA VSSVPIW LFEGR LSEKS VSTVSGLFSA
 51 VWATDSGSGV SMTISTGLYG LKVS GSYTLS VDSMAFQSAS ARFWVSSSCV
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVC FADN SSS DSPSKASVSF
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
 201 RKSSSRAINA APPPASSKVY EPPNRPNSP LSVSSSAETC STGSETALPV
 251 VSM AEAASW GADSAAVSDA AVFAAGTGS RTAGFSAFAS GAATFASGFS
 301 TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM *

889

m575/a575 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
m575. Pep	MVSGEAEFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
a575	MVSGEAEFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m575. Pep	SMTISTGLYGLKVGSGSYTLSDVSMFAQSASARFWVSSSCVSAPDKMPFCAAARLSKSKSM					
a575	SMTISTGLYGLKVGSGSYTLSDVSMFAQSASARFWVSSSCVSAPDKMPFCAAARLSKSKSM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m575. Pep	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR					
a575	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m575. Pep	SGSSSGTDSSVRRRLDWARRKSSSRINAAPPPASSKVYEPNRPNSPLSVSSSAETC					
a575	SGSSSGTDSSVRRRLDWARRKSSSRINAAPPPASSKVYEPN----SPLSVSSSAETC					
	190	200	210	220	230	
	250	260	270	280	290	300
m575. Pep	STGSETALPVSSVGVSMMAEAAASWGADSAAVSDAAVFAAGTGSGRTAGFSAFASGAATFA					
a575	STGSETALPVSSVGVSMMAEAAASWGADSAAVSDAAVFAAGTGSGRTAGFSAFASGAATFA					
	240	250	260	270	280	290
	310	320	330	340		
m575. Pep	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
a575	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
	300	310	320	330	340	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1 ..atgggcgtgg acatcgagcgt ctccctgaaa caaatgaagg aacagggcgc
51 ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttcttcgagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 caggggtgaag gcaaacagcc gacaaaagac gacatcgta ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccgcc caccctccct ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcgg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactgggtc aaatcggcgc acccgaaaac
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1 ..MGVDIGRSLK QMKEQGAIEID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51 FLQEQQAKAV EKHKADAKAN KEKGEAFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1 ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

```

890

```

51   GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301  CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
451  GTGATTCCGG GTTGACCGA AGCGTACAG CTTCTGAAAG AAGGCGGCGA
501  AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551  GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep.. (partial)

```

1   ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

```

              10      20      30      40      50      60
m576.pep      MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ
              |||
g576           MGVDIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ
              10      20      30      40      50

              70      80      90      100     110     120
m576.pep      EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITQ GEGKQPTKDDIV
              |||
g576           EQQAKAVEKH KADAKANKEK GEAFLENAA EDGVKTTASGLQYKITQ GEGKQPTKDDIV
              60      70      80      90      100     110

              130     140     150     160     170     180
m576.pep      TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE
              |||
g576           TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE
              120     130     140     150     160     170

              190     200     210     220
m576.pep      QGAGDKIGPN ATLVFDVKLV KIGAPENAPAK QPAQVDIKK VN*
              |||
g576           QGAGEKIGPN ATLVFDVKLV KIGAPENAPAK QPDQVDIKK VN*
              180     190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCCGCGC TTCTTCCGCG CAGGCGGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA

```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
 701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

a576. pep
 1 MNTIFKISAL TISAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LQYKITKQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

m576. pep				10	20	30
				MQQASYAMGV	DIGRSLKQMK	EQGAEIDLKV
a576	CGKKEAAPAS	ASEPAASSA	QGDTSSIGST	MQQASYAMGV	DIGRSLKQMK	EQGAEIDLKV
	30	40	50	60	70	80

m576. pep		40	50	60	70	80	90
	FTEAMQAVYD	GKEIKMTEE	QAEVMMKFL	QEQQAKAVE	KHKADAKAN	KEKGEAFLE	NAA
a576	FTEAMQAVYD	GKEIKMTEE	QAEVMMKFL	QEQQAKAVE	KHKADAKAN	KEKGEAFLE	NAA
	90	100	110	120	130	140	

m576. pep		100	110	120	130	140	150
	KDGVKTTAS	GLQYKITK	QEGGKOPT	KDDIVTVE	YEGRLIDG	TVFDSSKAN	GGPVTFPL
a576	KDGVKTTAS	GLQYKITK	QEGGKOPT	KDDIVTVE	YEGRLIDG	TVFDSSKAN	GGPVTFPL
	150	160	170	180	190	200	

m576. pep		160	170	180	190	200	210
	VIPGWTEGV	QLLKEGGE	ATFYIPSN	LAYREQAG	DKIGPNAT	LVFDVKLV	KIGAPENAP
a576	VILGWTEGV	QLLKEGGE	ATFYIPSN	LAYREQAG	DKIGPNAT	LVFDVKLV	KIGAPENAP
	210	220	230	240	250	260	

m576. pep		220
	KQPAQVDIKK	VNX
a576	KQPAQVDIKK	VNX
	270	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

g576-1. seq
 1 ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTCCG CCGCTTTGGC
 51 ACTTTCCGCC TCGGCGAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
 101 CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTTCTCAAT CGGCAGCAGC
 151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
 201 ACAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGATG
 251 CCATGCAGGC AGTGTATGAC GGCAAGAAA TCAAATGAC CGAAGAGCAG
 301 GCCCAGGAAG TGATGATGAA ATTCTGCGAG GAGCAGCAGG CTAAAGCCGT
 351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
 401 TCCTGAAGGA AATGCCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
 451 CTGCAGTACA AAATCACCAA ACAGGGTGAA GGCAACAGC CGACAAAAGA
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
 551 TCGACAGCAG CAAAGCCAAC GGCGCCCGCG CCACCTTCCC TTTGAGCCAA
 601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
 701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

g576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
201 VI PGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFVDKLV
251 KIGAPENAPA KQPDQVDIKK VN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

m576-1.seq

```

1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCG CCGCTTGGC
51  ACTTTCCGCC TGGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGCGGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGCGGACG CGAAGGCCAA TAAAGAAAAA GCGGAAGCCT
401 TTCTGAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AATCACCAC ACAGGCCGAA GGCAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCACAGCAGC CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGCGGCGCA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

m576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VI PGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFVDKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASAAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
g576-1.pep	DIGRSLQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	KADAKANKEKGEAFLENAAKDGVKTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLEKGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
g576-1.pep	ATLVFVDKLVKIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFVDKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq

```

1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  AC'TTTCCGCC TCGGCGAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC
151 ATGAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GC'AAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CC'ATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GC'TCAGGAAG TCATGATGAA ATTCTTCAG GAACAACAGG CTAAAGCCGT
351 AG'AAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TT'CTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CT'GCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CG'ACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TC'GACAGCAG CAAAGCCAAC GCGCGCCCGG TCACCTTCCC TTTGAGCCAA
601 GT'GATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GC'GACAAATG CCGGCCGAAC GCCACTTGG TATTGATGT GAAACTGGTC
751 AA'ATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CA'TCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENA KDGVRTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLSAALALSACGRKEAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGRKEAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLQMKEQGAEIDLKVFTEAMQAVYDQKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLQMKEQGAEIDLKVFTEAMQAVYDQKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLENAKDGVRTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAKDGVRTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577. seq..
1 atggaagga gcggtgtatt tggtaaaatt gtcggcaatc gcataactccg
51 tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaactaac gcaatccttg ttcagagtgc gaagctgtcc gtgcggcggt
151 tttatttacg gagcaaacat gaaacttatc tataccgtca tcaaatcat
201 tatcctgctg ctcttcctgc tgcttgccgt cattaatatg gatgccgtta
251 ccttttccta tcttcggggg cagagtgtca atctgccgct gattgtcgta
301 ttgttcggcg cgtttgtcgt cggcatcgtg ttcggaatgt ttgccctggt
351 cggcgcgctg ctgtccttgc gcggcgaaaa cagccgctg cgtgcggaag
401 tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgccgata
451 caaatgctg ccgaatctgc caaacagcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577. pep
1 MERSGVFGKI VGNRILRMP EHAAYFPKP CKSFKLTQSW FRVRSCPCGW
51 FIYGANMKLI YTVIKIILL LFLLLAVINM DAVTFSYLPQ QSVNPLPLIV
101 LFGAFVVGIV FGMFALFGR LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151 QNAESAQKP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577. seq..
1 ATGGAAAGGA ACGGTGTATT TGGTAAAATT GTCGGCAATC GCATACTCCG
51 TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAAACTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTACG GAGCAACAT GAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCCGT CATTAAATACG GATGCCGTTA
251 CCTTTTCCTA CCTGCCGGGG CAAAATTTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CATTTGTAGT CGGTATTATT TTTGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGC CGCTTTG ACGGGGAAG AGCTGACCGC ACCACCGGCG
451 CAAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577. pep..
1 MERNGVFGKI VGNRILRMSS EHAASYPKP CKSFKLAQSW FRVRSCLGW
51 FIYGANMKLI YTVIKIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIV
101 LFGAFVVGII FGMFALFGR LSLRGENGRL RAEVKKNARL TGKELTAPPA
151 QNAPESTQKP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m577/g577 88.1% identity in 160 aa overlap

	10	20	30	40	50	60
m577. pep	MERNGVFGKIVGNRILRMSSEHAASYPKPCKSFKLAQSWFRVRSCLGWFIYGANMKLI					
g577	MERSGVFGKIVGNRILRMPSEHAAYFPKPCKSFKLTQSWFRVRSCPCGVFIYGANMKLI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m577. pep	YTVIKIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFAGFVVGIIFGMFALFGR					

895

```

|||||
g577  YTVIKIIILLFLLAVINMDAVTFSYLPQSVNLPLIVVLFGAFVVGIVFGMFALFGRL
      70      80      90      100     110     120

      130     140     150     160
m577 .pep  LSLRGENRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
|||||
g577  LSLRGENSRLRAEVKKSARLSGQKLTAPPIQNAAESAKQPX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577 .seq
1  ATGGAAGGA ACGGTGTATT TGGTAAATTT GTCGGCAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAACCTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCC GGGCGGCGTT
151 TTTATTTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCTGT CATTAATACG GATGCCGTTA
251 CCTTTTCCTA CCTGCCGGGG CAAAAATTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CGTTTGTCGT CGGCATCGTG TTCGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAATGCGC CCGAATCTGC CAAACAGCCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577 .pep
1  MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSEKLAQSW FRVRSCTPGGV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENRL RAEVKKNARL TGKELTAPPA
151 QNAPESAKQP *

```

m577/a577 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m577 .pep  MERNGVFGKIVGNRILRMSSSEHAAASYPKPCKSEKLAQSWFRVRSCLGGVFIYGANMKLI
|||||
a577  MERNGVFGKIVGNRILRMSSSEHAAASYPKPCKSEKLAQSWFRVRSCTPGGVFIYGANMKLI
      10      20      30      40      50      60

      70      80      90      100     110     120
m577 .pep  YTVIKIIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIIFGMFALFGRL
|||||
a577  YTVIKIIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIVFGMFALFGRL
      70      80      90      100     110     120

      130     140     150     160
m577 .pep  LSLRGENRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
|||||
a577  LSLRGENRLRAEVKKNARLTGKELTAPPAQNAPESAKQPX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578 .seq..
1  atgggaaagc tcgacatcgg gatattgttt gccgatttct tcaaagattt
51  cgcgccacag ttcggtggtt tccaaaacgt tggctttgcc tacggagcag
101 acttttttgc tgcgtttttg ggcggattgg aaggccacgt gggcgatgcg
151 gcggatttcg ctttcgctgt atttcattgt gttgtagcct tcgtgttcgc
201 cgtttttcaa aacacggatg ccgcgcggtt cgcgaaata aatatcgccg
251 gtaagtccgc gcacaatcaa aatatccaaa ccggcaacga tttcaggcct
301 gagcgtggag gcgttggtta a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578 .pep
1  MGKLDIGILF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGHVGD
51  ADFAFVFGH VVAFVFAVFQ NTDAARFABI NIAGKFAHNQ NIQTGNDPRL

```

101 ERGGVG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

```
m578.seq -
1  ATCGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCTT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTCG TCGGTTTTTG GCGGATTGG AAGGCAACAT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCAG AACGCGGATG CCGCGCGGTT CGCCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGCAACGA TTTCAGGCTT
```

This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

```
m578.pep -
1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNMGNT
51  ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
101 QRGGVG*
```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
g578	MGKLDIGILFADFFKDFAPQGGFQNVGFAYGADFFAAFLGGLEGHVGDADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
g578	VVAFAFAVFQNTDAARFAEINIAGKFAHNQNIQTGNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

```
a578.seq
1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCTT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTCG TCGGTTTTTG GCGGATTGG AAGGCGACGT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCAG AACACGGATG CCGCGCGGTT CGCCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G
```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

```
a578.pep
1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGDVGN
51  ADFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*
```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
a578	MGKLDIRVFFADFFKDFAPQGGFQNVGFAYGADFFAAFLGGLEGDVGNADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

```
g579.seq..
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
```


897

```

51 TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCTTAA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCCT CCCGTTCAAA GTCGGCGACT
251 TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGCCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

g579.pep..

```

1 MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51 GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLTTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

m579.seq..

```

1 ATGAGGCGCG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51 TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCCT CCCGTTCAAA GTCGGCGACT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

m579.pep..

```

1 MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51 GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLTTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
g579	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM					
g579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	: : : : :					
g579	GNSIVNRSSLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	: : : : :					
g579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```
a579.seq
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTGTCTCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCCGG GCGCTGATTA TCCTGTTCG CCCGTTCAA GTCGCGGATT
251 TTATCCGCGT CCGCGGTTTT GAAGGATATG TCCGAGAGAT TAAATGGTG
301 CAGACTTCTT TCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCCACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTCAAAA
501 CGAAGAGCGG CAGGCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGCACAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```
a579.pep
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQORDIHIIN S*
```

m579/a579 100.0% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	: : : : :					
a579	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	: : : : :					
a579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	: : : : :					
a579	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	: : : : :					
a579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:

g579-1.seq

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```

1  A TGGACTTCA AACAAATTGA TTTTTCAC CTGATCAGTG TTTCCGGTTG
51  G GGGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCGG
101 C GCTGCTTAT TTTCTTGGTC GGGAAATGGG CGGCGAAACG CATTGTCGCC
151 G TAATAGAGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 T TTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 C CGCATTGGG ACGGTTGGGC GTTTCACAA CATCCGTAAC CGCCTTAATC
301 G GCGGCGCGG GTTGGCGGT GCGTGTGCC TTAAGACC AGCTGTCCAA
351 T TTTGCCGCC GCGCGCTGA TTATCTGTT CCGCCCGTTC AAAGTCGGCG
401 A CTTTATCCG TGTCGGCGGT TTTGAAGGAT ATGTCGGGA AATCAAAATG
451 G TGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 C AGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCCAGC CTGCCGCTT
551 G CCGCGCCCA AGTGATAGTC GCGTCGATT ACAACTGCGA TTTGAAAGTG
601 G CGAAAGAGG CGGTGTTGAA AGCCGCCGTC GAACACCCCT TGAGCGTTCA
651 A AACGAAGAG CGGCAGCCG CCGCTACAT CACCGCCTTG GCGGACAATG
701 C CATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 C TGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 T ATCAACATC CCGTTCCGCG AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  M D F K Q F D F L H L I S V S G W G H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A
51  V M R A A M T R A Q V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I
101 G G A G L A V A L S L K D Q L S N F A A G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M
151 V Q T S L R T T D N E E V V L P N S V M G N S I V N R S S L P L C R A Q V I V G V D Y N C D L K V
201 A K E A V L K A A V E H P L S V Q N E E R Q A A Y I T A L G D N A I E I T L W A W A N E A D R W T
251 L Q C D L N E Q V V E N L R K V N I N I P F P Q R D I H I I N S *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1  A T G G A C T T C A A A C A A T T T G A T T T T T A C A C T G A T C A G T G T T T C C G G T T G
51  G G A G C A T C T G G C T G A A A A G G C G T G G G C G T T C G G G C T G A A C C T T G C C G C G
101 C G C T G C T T A T T T T T T G G T C G G A A A T G G G C G G C G A A C G C A T T G T C G C T
151 G T G A T A G A G G C G G C G A T G A C G C G C G C A G G T C G A T G C C A C G C T G A T T A G
201 T T T T T G T G T A A T G T T G C C A A T A T C G G C T T A T T G A T T T T G T G A T T A T T G
251 C C G C A T T G G G C A G A T T G G G C G T T T C C A C A A C A T C C G T A A C C G C T T A A T C
301 G G C G G C G C G G G T T T G G C G G T G C G T T G T C C T G A A A G A C C A G C T G T C C A A
351 T T T T G C C G C G G G C G C A C T G A T T A T C C T G T T C G C C C G T T C A A A G T C G G C G
401 A T T T T A T C C G C G T C G G C G G T T T G A A G G A T A T G T C G G A G A G A T T A A A A T G
451 G T G C A G A C T T C T T G C G G A C G A C C G A C A C G A A G A G T C G T G C T G C C C A A
501 C A G C G T G G T G A T G G C A A C A G C A T C G T C A A C G T T C C A C A C T G C C G C T G T
551 G C C G C G C C C A A G T G A T A G T C G C G T C G A T T A C A A C T G C G A T T T G A A A G T G
601 G C G A A A G A G G C G T G T T G A A A G C C G C G T C G A C A C C C C T T G A C G T T C A
651 A A A C G A A G A G C G G C A G G C T G C C G C T A C A T C A C C G C C T T G G C G A C A A T G
701 C C A T C G A A A T C A C A T T A T G G C T T G G G C A A A C G A A G C A G A C C G C T G G A C G
751 C T G C A A T G C G A C T T G A A C G A A C A A G T G G T C G A A A C C T C C G C A A A G T C A A
801 T A T C A A C A T C C C G T T C C G C G A A C G C G A C A T A C A C A T C A T C A A T T C T T A A

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  M D F K Q F D F L H L I S V S G W E H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A
51  V M R A A M T R A Q V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I
101 G G A G L A V A L S L K D Q L S N F A A G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M
151 V Q T S L R T T D N E E V V L P N S V M G N S I V N R S T L P L C R A Q V I V G V D Y N C D L K V
201 A K E A V L K A A V E H P L S V Q N E E R Q A A Y I T A L G D N A I E I T L W A W A N E A D R W T
251 L Q C D L N E Q V V E N L R K V N I N I P F P Q R D I H I I N S *

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	M D F K Q F D F L H L I S V S G W E H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A V M R A A M T R A Q					
g579-1	M D F K Q F D F L H L I S V S G W G H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A V M R A A M T R A Q					
	10	20	30	40	50	60
m579-1.pep	V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I G G A G L A V A L S L K D Q L S N F A A					
g579-1	V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I G G A G L A V A L S L K D Q L S N F A A					
	70	80	90	100	110	120
m579-1.pep	V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I G G A G L A V A L S L K D Q L S N F A A					
g579-1	V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I G G A G L A V A L S L K D Q L S N F A A					
	70	80	90	100	110	120
m579-1.pep	G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M V Q T S L R T T D N E E V V L P N S V M G N S I V N R S T					
	130	140	150	160	170	180

900

```

|||||
g579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180
          190      200      210      220      230      240
m579-1.pep LPLCRAQVIVGVVDYNDLKVAKAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
g579-1  LPLCRAQVIVGVVDYNDLKVAKAVLKAAAEHPLSVQNEERQPAAYITALGDNAIEITLW
          190      200      210      220      230      240
          250      260      270      280
m579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQDIHIINSX
          |||||
g579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

```

a579-1.seq
1  ATGGACTTCA AACAAATTGA TTTTTCAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTGTGTC GGAAATGGG CGGCGAAACG CATTGTCCGC
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGGCGCGGG GTTGGCGGTT GCGGTGTGCC TTGAAAGACC AGCTGTCCAA
351 TTTTGC CGCG GCGCGCTGA TTATCCTGTT CCGCCCGTTC AAAGTCGCGG
401 ATTTATCCG CGTCGCGGTT TTTGAAGGAT ATGTCCGAGA GATTAATG
451 GTGCAGACTT CTTTGCAGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCACAA CTGCCGCTGT
551 GCGCGGCCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCGGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCCG CGGCCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACCGGACAT ACACATCATC AATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

```

a579-1.pep
1  MDFKQDFDLH LISASGWEHL AEKAWAFGLN LAAALLIFLV GKWAARKIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVLPNSV MGNISVNRST LPLCRAQVIV GVDYNDLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
a579-1.pep MDFKQDFDLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWAARKIVAVMRAAMTRAQ
          |||||
m579-1  MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAARKIVAVMRAAMTRAQ
          10      20      30      40      50      60
          70      80      90      100     110     120
a579-1.pep VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALS LKDQLSNFAA
          |||||
m579-1  VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALS LKDQLSNFAA
          70      80      90      100     110     120
          130     140     150     160     170     180
a579-1.pep GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRST
          |||||
m579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRST
          130     140     150     160     170     180
          190     200     210     220     230     240
a579-1.pep LPLCRAQVIVGVVDYNDLKVAKAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
m579-1  LPLCRAQVIVGVVDYNDLKVAKAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          190     200     210     220     230     240
          250     260     270     280
a579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQDIHIINSX

```

901

m579-1 |||||
 AWANEADRWTLQCDLNEQVVENLRKVNINIFPQRDIHIINSX
 250 260 270 280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

g580.seq
 1 atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
 51 cgcgctgcag cccatttcga tggcaaggca gacttcgccc atcatgtcgc
 101 caacggttcgg accgacaatg ccgcccgcga tgatgcggcc ggtttcggca
 151 tcgaaaaatca gcttggtaaa gcggtgtcgc caacggttgg caatcgcacg
 201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg
 251 ctttggcaga caattcgggt tcaccgaccc atgccacttc gggggaagtg
 301 tag

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

g580.pep..
 1 MDSPKVGC GW MVLPSAASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
 101 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

m580.seq..
 1 ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGTTTTCGC CGATGTCTGC
 51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
 101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCGGCA
 151 TCAAAAATCA GCTTGGTAAA GCCGTTGTCG CAACGTTGG CAATCGCACG
 201 GCCGGAAGCC GCCACGGGA AGTTGGCTTT GGTGATTTG CGGCCGAGG
 251 CTTTGGCGGA CAGTTCGGTT TCGCCACCC ACGCCACTTC GGGGAAGTG
 301 TAG

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

m580.pep..
 1 MDSPKVGC GW MVLPSAASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
 101 *

m580/g580 97.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGC GW MVLPSAASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA SKISLVKPLS					
g580	MDSPKVGC GW MVLPSAASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA SKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEVX					
g580	QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

a580.seq
 1 ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGTTTTCGC CGATGTCTGC
 51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCTGC
 101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCAGCA
 151 TCAAAAATCA GCTTGGTGAA ACCATTGTCG CAACGTTGG CAATCGCACG
 201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTG CGGCCGAGG
 251 CTTTGGCAGA CAATTCGGTT TCGCCACCC ATGCCACTTC AGGAGAAGTG
 301 TAA

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

a580.pep
 1 MDSPKVGC GW MVLPSAASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

101 *

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
	10	20	30	40	50	60

	70	80	90	100
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPTHATSGEVX			
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPTHATSGEVX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1  atgcacttcg cccagcttgt gggtaaaccc ggtatagaac aaaatacgtt
51  ctgtcgctcg ggttttaccg gcatcgatat gggcggaaat accgatgttg
101 cggtagacggc tgatcggggg cttacgagcc attttattag cctttcaaaa
151 ttagaaacgg aagttagaga atgctttgtt ggcttcagcc atacggtgta
201 cttcttcacg tttttcaac gcacggccac ggccttcgga cgcataatc
251 aactcgctcg ccaaacgcag atccatggat ttctcaccac gtttcggggc
301 cgcgtcgcga acccaacgca ttgccaaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ INHPLTTFAG
101 RVANPTHQCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1  ATGCACCTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51  CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CCGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151 TTAGAAACGG AAGTGAAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTCACG GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGLTSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAQADRGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60

	70	80	90	100	110
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLLTFAGRANPAHCQSQTAX				
g581	GFSHTVYFFTFFQRTATAFGRINQLACQTQIHGFLLTFAGRANPAHCQSQTAX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

a581.seq

```

1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51 CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTCAC GCACCGCCAC GGCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

a581.pep

```

1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTQADRG LTSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRG	LTSHFISLSKLETEVRECFV				
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTQADRG	LTSHFISLSKLETEVRECFV				
	10	20	30	40	50	60

	70	80	90	100	110
m581.pep	GFSHTVYFFTFFQRTATAFG	RINQFACQTQVHGFLLTFAG	RINPAHCQSQTAX		
a581	GFSHTVYFFTFFQRTATAFG	RINQFACQTQVHGFLLTFAG	RINPAHCQSQTAX		
	70	80	90	100	110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

g582.seq..

```

1 atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
51 agagaccgcg ctgcaatgcg ccgctttgac ggacaatggt acgcgtttgg
101 cgtgtttacga caggattttt gcggcacagc ttccgtcttc ggcagggcag
151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttggat aagggcagag cgtcattgt tgttgaaaaa ggcggggatg
251 cgcttctcgc cgacagtgcg ggcgaaaccc ccgatatcta tacgcctttg
301 agcctgatgt acgacttgga caaaaacgat ttgcgcgggc tggtcggcgt
351 acgcgaacac aatccgatgt accttatgcc gttttggtat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttccggacagc agaaacgtgc ggaacccaaa ttgcaggttt cgttcaaaag
501 caaaattgcc gaaaatttgt ttaaaacccg ccgcgatctg tggttcggct
551 acacccaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601 ccgttccgca atacggatta caaacctgaa atttctctga cccagcctgt
651 gaagggcgat ttgccgttcg gcggcaggct gcgtatgctc ggtgcgggtt
701 ttgtccacca gtccaacgga cagagccgtc ccgaatcgcg ttctggaac
751 aggatattat ccattggcagg catggaatgg ggcaaattga cggtgattcc
801 gcgcgtgtgg gtgcgtgctg tcgatcagag ccgcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggatgagg acgtgaagct gcagtaccgc
901 ctgaaacgaca ggcagaatgt gtattccgta ttgcgttaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttcogatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggatc gggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

g582.pep ..

```

1 MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51 EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMPPFW NNSPNYAPSS PTRGTTVQEK
151 FGQKRAETK LQVSPFSKIA ENLFKTRADL WFGYTQSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEV GKLTVIPRVW VRAFDQSGDK NDNPDIDYDM GYGDKVLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKVVVRG FHGYGESLID
351 YNHKQNGIGI GLMPNDWDGI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTATTACGA CAGGATTTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CCGTCATTGT TGTGAAAAAA GCGGGGGATG
251 CGCTTCTCTG CGACAGTGC GCGGAAACCG CCGACATCTA TAGCCTTTG
301 AGCCTGATGT ACGACTTGA CAAAAACGAT TTGCGCGGGC TGTGCGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCG
401 CCAACTATGC CCCGGGTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAACCAAA TTGCAGGTTT CGTTCAAAAG
501 CAAATTTGCC GAAGATTGT TTAATAACCG CCGGATCTG TGGTTCGGCT
551 ACACCCAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCCGCA ATACGGATTA CAAACCTGAA ATTTTCTGTA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTG GCGGCAGGCT CGGTATGCTC GGTGCGGGT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTGCCT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CACTATATG GGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTTCGGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGCGATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVPVWV VRAFDQSGDK NDNPDADYIM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGLKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *
```

m582 / g582 98.6% identity in 370 aa overlap

m582.pep	10	20	30	40	50	60
m582.pep	MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
g582	MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
m582.pep	70	80	90	100	110	120
m582.pep	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
g582	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
m582.pep	130	140	150	160	170	180
m582.pep	NPMYLMPLWYNNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL					
g582	NPMYLMPLWYNNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAENLFKTRADL					
m582.pep	190	200	210	220	230	240
m582.pep	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
g582	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
m582.pep	250	260	270	280	290	300
m582.pep	QSRPESRSWNRIYAMAGMEWGKLTVPVWVRAFDQSGDKNDNPDADYIMGYGDVKLQYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVPVWVRAFDQSGDKNDNPDADYIMGYGDVKLQYR					
m582.pep	310	320	330	340	350	360
m582.pep						
g582						

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```

m582.pep  LNDQRNVSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          |||||
g582      LNDQRNVSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          |||||
g582      GLMFNDWDGIX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.s eq
1   ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
1 01 CGTGTTACGA CAGGATTTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
1 51 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
2 01 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GGCGGGGATG
2 51 CGCTTCTGCG CGACAGTGGC GCGGAAACCG CCGACATCTA TACGCCTTTG
3 01 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGCGCGT
3 51 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
4 01 CCAACTATGC CCCGGGTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
4 51 TTCGGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTCAAAAG
5 01 CAAAATTGCC GAAGATTGTG TTAACACCCG CCGGATCTG TGGTTCGGCT
5 51 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
6 01 CCGTTCCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
6 51 GAAGGCGGAT TTGCCGTTCC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
7 01 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
7 51 AGGATTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CGGTGATTCC
8 01 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CGGCGATAAA AACGACAATC
8 51 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
9 01 CTGAACGACA GGCAGAATGT GTATCCGTA TTGCGCTACA ATCCCAAAAC
9 51 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTTCGATT AAGGGCAAAC
10 01 TCAAAGCGCT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
10 51 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
11 01 GGACGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1   MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
1 01 SLMYDLKND LRLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
1 51 FGQOKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
2 01 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
2 51 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDKVLQYR
3 01 LNDQRNVSV LRYNPKTGYG AIEAAYTFPI KGLKGVVRG FHGYGESLID
3 51 YNHKQNGIGI GLMFNDLDGI *

```

m582/a582 100.0% identity in 370 aa overlap

```

          10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          |||||
a582      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          10      20      30      40      50      60

          70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSIMYDLKNDLRLLGVREH
          |||||
a582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSIMYDLKNDLRLLGVREH
          70      80      90      100     110     120

          130     140     150     160     170     180

```

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```

m582.pep      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAEDLFKTRADL
|||||
a582          NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAEDLFKTRADL
              130      140      150      160      170      180

              190      200      210      220      230      240
m582.pep      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRLMGAGFVHQSNQ
|||||
a582          WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRLMGAGFVHQSNQ
              190      200      210      220      230      240

              250      260      270      280      290      300
m582.pep      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
|||||
a582          QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
              250      260      270      280      290      300

              310      320      330      340      350      360
m582.pep      LNDRONVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
|||||
a582          LNDRONVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
              310      320      330      340      350      360

              370
m582.pep      GLMFNDLDGIX
|||||
a582          GLMFNDLDGIX
              370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg accaaagcca aatatttacc catcttgccct tctgtgcctt
51  ttgcgggatt ggagccgtaa ctgccggcaa tgcactgcat aatcgatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgagac tgtaaccgat gcccagcgtt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgcg aaatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaaacgca ctcaacgcac cgctcatcgc cgcgcccggg ttgtcggcgg
351 ttacgcgggt tactgcgacc aaccgcagcg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcggca atcacaccga caaacatagc
451 cagcagcgctc caagcctgag gcttgacccc gtcgggtacg ggcagtgccca
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIHRH RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRLLD VGYGQCQNQG AQYCGNGEGY RFETQFHID LKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCgcgc GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTTCGGA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTGCGCGG
351 TTACGCGGGT TACTGCGACC AACCAGACGG CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACGAGGCG GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA

```

551 CCCAATTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAA~~A~~AAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..
1 MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
151 QQRPSLRLDV VGYGQCQNG AQYCGNGEGY RFETQFHHD LKKDRPEKS
201 EK*

m583 / g583 98.5% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					
g583	MIIDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					
	10	20	30	40	50	60
m583.pep	AQRFSKNGDK QISDTHPQP CFEQTARNH NCDGNQPNQRI GERTQRIahr RARFVGGYAG					
g583	AQRFSKNGDK QISDTHPQP CFEQTARNH NCDGNQPNQRI GERTQRIahr RARFVGGYAG					
	70	80	90	100	110	120
m583.pep	AQRFSKNGDK QISDTHPQP CFEQTARNH NCDGNQPNQRI GERTQRIahr RARFVGGYAG					
g583	AQRFSKNGDK QISDTHPQP CFEQTARNH NCDGNQPNQRI GERTQRIahr RARFVGGYAG					
	70	80	90	100	110	120
m583.pep	YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG QQRPSLRLDV VGYGQCQNG AQYCGNGEGY					
g583	YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG QQRPSLRLDV VGYGQCQNG AQYCGNGEGY					
	130	140	150	160	170	180
m583.pep	YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG QQRPSLRLDV VGYGQCQNG AQYCGNGEGY					
g583	YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG QQRPSLRLDV VGYGQCQNG AQYCGNGEGY					
	130	140	150	160	170	180
m583.pep	RFETQFHHD LKKDRPEKSEKX					
g583	RFETQFHHD LKKDRPEKSEKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq
1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51 TTGCGGGATT GGAGCCGTAA CTGCCGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCAGCCC TGTTTTGAGC
251 AAACGCGCG AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCACGCAT CGCTCATCGC CGCACC CGGT TTGTCGCGG
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAAGGC GCACAATACT GCGCAATGG CGAGGGGTAT CGGTTTGAAA
551 CCCAATTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep
1 MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
151 QQRPSLRLDV VGYGQCQNG AQYCGNGEGY RFETQFHHD LKKDRPEKS
201 EK*

m583/a583 99.0% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					

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```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRNGSQQQFGKSETVTD
           10      20      30      40      50      60
           70      80      90      100     110     120
m583.pep  AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQPQNRIGERTORIAHRRARFVGGYAG
           |||||
a583      AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQPQNRIGERTORIAHRRTRFVGGYAG
           70      80      90      100     110     120
           130     140     150     160     170     180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
           |||||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
           130     140     150     160     170     180
           190     200
m583.pep  RFETQFHHIDLRRKKDRPEKSEKX
           |||||
a583      RFETQFHHIDLRRKKDRPEKSEKX
           190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

g584.seq..

```

1  atgctgcgtt ctattttggc ggcttccctg ctggcggtat cttttcggc
51  ggcggtgag gcattgaatt acaatattgt cgaattttcc gaatcgccg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcgcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttgta aaaaattcaa
201 caatttcacc agaaaatcga aaaatggtag ctttaaaacc gaattggtat
251 cgcgcgatgc gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag gcggaggcca gggattttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tgcgttgaa
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgccgtttt gcgtttcaag gcgcgtgccg aaaaactggc
501 gggcggttctg ggtgcgtccg gttataaaat cgtcaaattg aattttgggc
551 aaatcggcag ccatattgag ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggtg cggattcagc
651 cgcaccgggt gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

g584.pep Length:..

```

1  MLRSILAASL LAVSFPAAE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  EGRDKNVANA EFVKKFNNFT RSKNGSFYKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAERFK AEGRDFDALN RFIADVQTD SLEDTFDFVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
201 RAMPMAASVN MKGTDAAAPG VEEISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

m584.seq..

```

1  ATGTTGCGTC TTGTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATGT CGAATTTTCC GAATCGGCGG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAATTCAA
201 CAAGTTCATC AGAAAATCGA AAAATGGTAG CTTTAAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTTAAG GTCGAAGGTA GAGATTTTGA
351 TGAGTTAAAC CGTTTATTG CCGATATTC AAGCAGATGC GCGTTGGMAT
401 ATACGGATT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCATCAG
451 GTCAGCAAGG ATGCCGTTT GCCTTTCAAG GCGCGTCCG AAAAGTTGGC
501 GGGCGTTTGG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCGCG
651 CGCGCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTCACT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

m584.pep..

```

1 MLRLVLAASL SAVSFPAABE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51 EGRDKNVNA EFKKFNKFI RSKNGSFKT ELVSRAMPY QYTNRRRIQ
101 TGWEERAEFK VEGRDDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

      10      20      30      40      50      60
m584.pep MLRLVLAASLSAVSFPAABEALNYNIVEFSSESAGVEVAQDTMSARFQVTAEGRDKNVNA
      ||| :|||
g584      MLRSILAASLLAVSFPAABEALNYNIVEFSSESAGIEVAQDTMSARFQVAEGRDKNVNA
      10      20      30      40      50      60

      70      80      90     100     110     120
m584.pep EFKKFNKFIKRSKNGSFKTSLVSRAMPYQYTNRRRIQTGWEERAEFKVEGRDDELN
      ||| :|||
g584      EFKKFNKFNTRKSKNGSFKTSLVSRAMPYQYTNRRRIQTGWEERAEFKAEGRDDELN
      70      80      90     100     110     120

      130     140     150     160     170     180
m584.pep RFIADIQADAALXYTDFHVSRRRNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL
      ||| :|||
g584      RFIADVQTDASLEDTFVSRRRNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL
      130     140     150     160     170     180

      190     200     210     220     230
m584.pep NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVEEISISVNGTVQFX
      ||| :|||
g584      NFGQIGSHIAGDGA VRAMLRAMPMAASVNMKGTD SAAPGVEEISISVNGTVQFX
      190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

```

a584.seq
1 ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51 .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTACAC AGAAAATCAA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TCGGTTGAAC CGTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAT CGTCAAATTG AATTTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGCGCGC AAGCGTCAAT ATGGAGGGTG CGGATTCGCG
651 CGGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

```

a584.pep
1 MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51 EGRDKNVNA EFKKFNKFI RSKNGSFKT ELVSRAMPY QYTNRRRIQ
101 TGWEERAEFK VEGRNFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

      10      20      30      40      50      60
m584.pep MLRLVLAASLSAVSFPAABEALNYNIVEFSSESAGVEVAQDTMSARFQVTAEGRDKNVNA
      ||| :|||
a584      MLRSILAASLL-----IVEFSSESAGVEAVQDTMSARFQVTAEGRDKNVNA
      10      20      30      40

```

910

	70	80	90	100	110	120
m584 . pep	EFVKKFNKFIKRSKNGSFKTELVSRSAMPQYQYTNRRRIQTGWEERAEFKVEGRDFDELN					
a584	EFVKKFNNFTRKSKNGSFKTELVSRSAMPQYQYTNRRRIQTGWEERAEFKVEGRNFDALN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584 . pep	RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADAALXYTDFHVSRRERNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584 . pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt  tccaacgcat  ttctgccaca  ttttgccggt  ttatcgctctg
51  cgcaatcttt  gtggcgagtt  tttctttttg  gctggtgcag  aacacccttg
101  ccgaaaacca  attcaaccaa  cgccgcacca  tcgaaaccac  attgatgggc
151  agcattatgt  ccgcattcaa  gacacggggc  gacaacggcg  cgcgcgaaat
201  cctgaccgaa  tggaaaaaca  gcccgtcttc  atccgccgtt  tacgtcatac
251  agggcgacga  gaaaaaagac  atcttaaac  gctatatcga  caattacacc
301  atagaacgag  cccggtctgt  tgcgcacaac  aacccccatt  ccaacctgtg
351  ccgcatcgaa  tacgaccgtt  tcggcgagaa  atacctgttc  ttcattaaag
401  gctgggacaa  ccaccaggca  caacgcctgc  ccagcccgct  gtttatcccg
451  ggccgtgcgc  ttgcccgcgt  ttggcacgaa  ttcacatccc  tctccttcac
501  catcattgtc  ggactgctga  tggcatatat  ccttgccggc  aacattgcca
551  aaccatcag  aatcttaggc  aacggcatgg  acaggggtgc  agaacgagaa
601  cttgaagacc  gcgtttgcca  acaggttcgc  gaccgcgacg  acgaattggc
651  cgatgttgcc  atgcaattcg  acacaatggt  ggaaaaactg  gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLFQRIFAT  FCAVIVCAIF  VASFSFWLVQ  NTLAENQFNQ  RRTIETTLMG
51  SIISAFKTRG  DNGAREILTE  WKNSPVSSAV  YVIQDEKKD  ILNRYIDNYT
101  IERARLFAAN  NPHSNLVRIE  YDRFGBEYLF  FIKGWDNHQA  QRLPSPLFIP
151  GLPLAPIWHE  FIILSFIIIV  GLLMAYILAG  NIAKPIRILG  NGMDRVAERE
201  LEDRVCQQR  DRDELADVA  MQFTMVEKL  E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAAACTGT  TCCAACGCAT  TTTGCCACA  TTTTGCGCGG  TTATCGTCTG
51  TGCAATCTTT  GTGGCGAGTT  TTTCTTTCTG  GCTGGTGCAG  AACACCCTTG
101  CCGAAAACCA  GTTCAACCAA  CGCCGCACCA  TCGAAACCAC  TTTGATGGGC
151  AGCATCATTT  CCGCATCCG  GGCACGCGGG  GACGCGGGTG  CGCGCGAAAT
201  CCTGACGGAA  TGGAAAGACA  GCCCCGTCTC  ATCGGGCGTG  TACGTTATAC
251  AGGGCGACGA  GAAAAAGAT  ATCCTGAACC  GGTATATCGA  CAGCTATACC
301  ATCGAACGCG  CCGGCTTTT  CGCCGCCGGA  CACCGGCATT  CCAACCTCGT
351  CCATATCGAA  TACGACCGCT  TCGGCGAAGA  ATACCTGTTC  TTCACCAAAG
401  ACTGGGACAA  ACTCCAAGCC  CGCCGCCTGC  CCAGCCCCCT  GTTGATCCCC
451  GGCCCTGCC  TCGCCCGAT  TTGGCACGAA  CTCATCATAT  TGTCTTCAT
501  CATCATCGTC  GGAATGCTGA  TGGCATATAT  CCTCGCCGGC  AACATTGCCA
551  AACCATCAG  AATCTTAGGC  AACGGCATGG  ACAGGGTGGC  AACGCGAGAA
601  CTTGAAACCC  GTATCTCCCA  ACAGGTCGAC  GACCGCGACG  ACGAATTGTC
651  CCATCTTGCC  ATCCAATTCG  ACAAATGGT  GGAAAACTC  GAAAAACTCG
701  TTGCCAAAGA  ACGCCACCTG  CTCCATCAG  TCTCCCATGA  AATGCGTTCT
751  CCCCTTGCGC  GCATGCAGGC  AATTGTGCGA  CTGATTCAAG  CGCAGCCCCA
801  AAAACAGGAG  CAATATCTCA  AACGGCTGGA  AGGCGAACTG  ACCCGCATGG
851  ATACGCTGGC  CGGGGAACTG  TTAACCTGT  CCGCTCTCGA  AACTTCCAAT
901  ATGGCTTTGG  AAAAAGAAAG  CCTGAAACTC  CTGCCCTTCC  TGGGCAACCT
951  GGTAGAAGAC  AATCAAAGCA  TTGCCAGAA  AAACGGACAA  ACGGTTACCC
1001  TGCTGCGGA  CGGAAAAATC  CCCGAAAACA  CAACATCCT  TGCCAACGAA

```

```

1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CGGTCAACTA
1101 CAGTCCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGA CGAAATGCAG
1201 CTCCCGCACA TCTTACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGBT TCCAAAACAG AAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

m585.pep..

```

1 MKLQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQDEKKD ILNRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPILLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDDELHLA IQFDKMVEKL EKLVAKEHRL LHHVSHMRS
251 PLARMQAIIV LIQAQPKQKE QYLKRLEGEL TRMDTLAGE LTLRLETSN
301 MALEKESLKL LPFLGNLVED NQSIQAQNGQ TVTSLADGKI PENTTILANE
351 SYLYRAFQNV IRNAVNYSPS GSTILINIGQ DHKHWIIDVT DNGPGVDEM
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585 / g585 88.3% identity in 231 aa overlap

	10	20	30	40	50	60
m585.pep	MKLQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFRARG					
g585	MKLQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFKTRG					
	10	20	30	40	50	60
m585.pep	DAGAREILTEWKDSPVSSGVYVIQDEKKDILNRYIDSYTIERARLFAAGHPHNSNLVHIE					
g585	DNGAREILTEWKNSPVSSAVYVIQDEKKDILNRYIDNYTIERARLFAANNPHNSNLVRIE					
	70	80	90	100	110	120
m585.pep	YDRFGEEYLF FTKDWDKLQARRLPSPILLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG					
g585	YDRFGEEYLF FIKGWDNHQAQRLPSPLFIPGLPLAPIWHEFIILSFIIIVGLLMAYILAG					
	130	140	150	160	170	180
m585.pep	NIAKPIRILGNGMDRVANGELETRISQQVDRDDELHLA IQFDKMVEKLEKLVAKEHRL					
g585	NIAKPIRILGNGMDRVAERELEDRVCQQVRDDELADVAMQFDTMVEKLEX					
	190	200	210	220	230	
m585.pep	LHHVSHMRSPLARMQAIIVGLIQAQPKQKEQYLKRLEGELTRMDTLAGE LTLRLETSN					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

a585.seq

```

1 ATGAAACTGT TCCAACGCAT CTTGCCACA TTTGCGCGG TTATCGTCTG
51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAAG AACACCCTTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCGG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAAGACA GCCCCGTCTC ATCGGGCGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCCTGCACC GGTATATCGA CAGCTACACC
301 ATCGAACGCG CCCGGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCCTGC CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCCGAT TTGGCACGAA CTCATCATAT TGTCTTCAT
501 CATCATCGTC GGACTGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
551 AACCCATCAG AATCTTAGGC AACGGCATGG ACAGGTGGC AACCGGAGAA
601 CTTGAAACCC GTATCTCCCA ACAGGTGCAC GACCGCGACG ACGAATTGTC

```

912

```
651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAGA ACGCCACCTG CTCCATCAG TCTCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTGCGA CTGATTCAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAAGT TTAACCCTGT CCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCCGAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGCC CCGGCGTGGG CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAAACAG AAAAAAGTGC
1401 GAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

a585.pep

```
1 MKLFQIRIFAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQDEKDD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSLLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDELSHLA IQFDKMVEKL EKLVAKERHL LHHVSHMERS
251 PLARMQAIVG LIQAQPKQKE QYLRLEGELE TRMDTLAGELE LTLRLETSN
301 MALEKESLKL LPFLGNLVED NQSIQKNGQ TVTSLADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNSPE GSTILINIGQ DHKHIIIDVT DNGPGVDMEQ
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*
```

m585/a585 99.8% identity in 468 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRTIETTLMG	SIISAFRARG				
a585	MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRTIETTLMG	SIISAFRARG				
	70	80	90	100	110	120
m585.pep	DAGAREILTEWKDSPVSSGVYVIQDEKDDILNRYIDSYTIERARLFAAGHPH	SNLVHIE				
a585	DAGAREILTEWKDSPVSSGVYVIQDEKDDILHRYIDSYTIERARLFAAGHPH	SNLVHIE				
	130	140	150	160	170	180
m585.pep	YDRFGEEYLF	FTKDWDKLQARRLPSLLIPGLPLAPIWHELIILSFIIIVG	LLMAYILAG			
a585	YDRFGEEYLF	FTKDWDKLQARRLPSLLIPGLPLAPIWHELIILSFIIIVG	LLMAYILAG			
	190	200	210	220	230	240
m585.pep	NIAKPIRILGNGMDRVANGELETRISQQVDDRDEL	SHLAIQFDKMVEKLEKLVAKERHL				
a585	NIAKPIRILGNGMDRVANGELETRISQQVDDRDEL	SHLAIQFDKMVEKLEKLVAKERHL				
	250	260	270	280	290	300
m585.pep	LHHVSHMERSPLARMQAIVGLIQAQPKQEQYLRLEGELETRMDTLAGELE	LLTLRLETSN				
a585	LHHVSHMERSPLARMQAIVGLIQAQPKQEQYLRLEGELETRMDTLAGELE	LLTLRLETSN				
	310	320	330	340	350	360
m585.pep	MALEKESLKL	LPFLGNLVEDNQSIQKNGQTVTSLADGKIPENTTILANESYLYRAFDNV				
a585	MALEKESLKL	LPFLGNLVEDNQSIQKNGQTVTSLADGKIPENTTILANESYLYRAFDNV				

	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

g586.seq. .

g586.pap.-

m586.seq

m586.pgp

m586 / g586 97.1% identity in 209 aa overlap

```

      10      20      30      40      50      60
m586.pep  MAAHLEEQQEILDNFKYFWKTTGKWL FalliLaALGYLGYTVYQNRRKVSQNQEAAVLANI
          |||||

```

914

```

g586      MAAHLEEQQELDNFKYFWKTTGKWLFAALLILAALGYLGYTVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAE LTKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      VEKAQNKAPOSEINAE LSKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      QKDSLIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           130     140     150     160     170     180

           190     200     210
m586.pep  LKNYGQALEKMPQDSVGR ELVQMKLDSLKX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      LKNYGQALEKMPQDSVGR ELQMKLDSLKX
           190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1  ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAAC TTAATATTT
51  TTGGAAACC ACGGGCAAAT GGCTGTTTGC CGTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTGCGGC TTCCCAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTGGAAAAGG CGCAAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAAGCT
251 ACCCCCATTC CATTTCCGCC GCCCAAGCCA CGCTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT
351 ATTGTCACAC CAAAAGACA GCCTGATCCA GCGGTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAT ACGATGCCGC GCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAAG CCAGGAAGCC TTAATAAAT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1  MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQN
51  QEAAAVLANI VEKAQNKAPO SEINAE LAKL QSYPHSISA AQATLMAAAAT
101 EFDAQRYDVA EGHKLKWVLSN QKDSLIQALA AQLGVVLLQ QKKYDAALAA
151 LDTPEADFAP PLLMETKGDV YAAQGKSQEA LKNYGQALEK MPQDSVGR EL
201 VQMKLDSLK*

```

m586/a586 97.6% identity in 209 aa overlap

```

           10      20      30      40      50      60
m586.pep  MAAHLEEQQELDNFKYFWKTTGKWLFAVLI LAALGYLGYTVYQNRAASQNQEAAAVLANI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      MAAHLEEQQELDNFKYFWKTTGKWLFAVLI LAALGYLGYTVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAE LTKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      VEKAQNKAPOSEINAE LAKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      QKDSLIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           130     140     150     160     170     180

```

915

```

                190      200      210
m586. pep      LKNYGQALEKMPQDSVGRELVMKLDLKLKX
                |||||
a586           LKNYGQALEKMPQDSVGRELVMKLDLKLKX
                190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587. seq..
1   atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101 aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151 gccgcacttg ccgcaccggt ttacattcaa accggcgcaa cctcgtttat
201 cccattccg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251 ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301 ggacagggca gctatctgtg gcacgaagaa cgcaactcg acggcaacgg
351 caaaacccgc acaaacgga tgtccgacat atccgccggc atcagccaca
401 ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501 gctttgcccc tttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587. pep..
1   MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSNSR
51  AALAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLAGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151 TVYEKSRNKA SLIKRGLCP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587. seq..
1   ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCATTCCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGAATAC CGACATTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAACTCG ACGGCAACAG
351 CAAAACCGGC AACAAACGGA TGTCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CGCCCGCCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTTGCTGC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCCGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587. pep..
1   MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
51  AELAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLSDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10

20

30

40

50

60

916

```

m587. pep      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587            MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSITYLNSENSRAELAAPVYIQ
                10      20      30      40      50      60

                70      80      90      100     110     120
m587. pep      TGATSFIPTEIQENGSNNTMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587            TGATSFIPTEIQENGSNNTMLAGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
                70      80      90      100     110     120

                130     140     150     160     170     180
m587. pep      NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587            NKRMSDISAGISHTFLKDGNPALISFLESTVYEKSRNKASLIKRGKLCFPYNLRINYEY
                130     140     150     160     170     180

                190     200     210     220     230     240
m587. pep      LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK
g587            X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1819>:

```

a587. seq
1  ATGAAGCGCA TCTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACGG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCGTCGTC CTCTCATTGA
551 CCGCTGCCCTA CCGTATCAAC GGCAGCAAAA CCCTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCAATATAT CCTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTTCG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCCGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1820; ORF 587.a>:

```

a587. pep
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNRR
51 AELAAPVYIQ TGATSFIPIP TEIQENGSNNT DMLVGTGLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*

```

m587/a587 95.2% identity in 289 aa overlap

```

                10      20      30      40      50      60
m587. pep      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a587            MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                10      20      30      40      50      60

                70      80      90      100     110     120
m587. pep      TGATSFIPTEIQENGSNNTMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a587            TGATSFIPTEIQENGSNNTMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
                70      80      90      100     110     120

```

	130	140	150	160	170	180
m587. pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587. pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587. pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

```

g588.seq
1   atgcttaaac atctcgatt cctactgcc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gcccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaagagac gggcttcctt caggcaaagg catatggcgt
151 tgcgggatg ggcgcgggta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataccg ttgccgcgg cgcggaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaacaag gcttggcaca cggcaggttc gccgcctcgc aaaacggcga
351 aaccctcttt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

```

g588.pep..
1   MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

```

m588.seq..
1   ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCCGTCTGA CTTCCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CCGCAAAGAC GGTAAACCG CCGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTTCG TTTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAAG GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

```

m588.pep..
1   MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAKGKTIWR
51  QDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENMIK EVKLPKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60


```

301 atcggatatgg tagggatgat gctaaaaggg ctgaattgga cacggcacga
351 ttggatgatt ccgcctgtat ggagtttgt actggcaagc atagtgaac
401 tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaagc
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgcgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatgcg gcgcacggta
551 tggcgcatgt gtattttgaa gcgggctgta tgggtatcgg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcaccaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgccgaccca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttatc
751 cgcaccaacc acggcgaacg catcgtgcc gagggcatta tcgaaagcgg
801 cagcggttgg gcggacgaaa gccaccttac cgcgcaatcc aatcccgaag
851 agaaaaaggg gggcggcaaa gtgttggcgg gcgcgctgat gaccgaaggg
901 agcgtgtgtg accgcgcgcg gcagctcggc agccaaaccc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagtaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaactgt cgtgggcac
1051 gcgcttctga cttttatcgt tgcttggctg attaagggcg attggacgg
1101 cgcactgatg cacgccgttg ccgttttggg gattgcctgc ccgtgcgcgc
1151 tcggtctggc gaccctgcc gcgattatgg tcggcatggg caaagcggg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgtatgc gtcgtatttg acaaaaccgg tacgtgacc gaagcgaggc
1301 cgcaggttgc gcgcgttat tacgttccc acagcggctt tgacgaagac
1351 gctttgtacc gcatcgccgc cgccgtcgag caaaacgccg cccaccgcgt
1401 cgcccgccgc atcgtctccg ccgcacaagc gcgcggttg gagattccc
1451 ctgcacaaaa tgcgcaaac gttgtcggag caggcattac cgccgaagt
1501 gaagcggtg gtttgggtga atcaggcaaa gccgaatttg ccgaactgac
1551 cttgccgaag ttttcagacg gcgttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaacg atcggcgcat tcgcactctc cgacgcgttg
1651 aaagccgata ccgcccgaag cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcgcg ataaccaaag tacggtcgaa tacgtcgcca
1751 aacaactggg catcgcacac gccttcggta atatgagtc gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaaaccc tggcgatggt
1851 cggcgacggc atcaacgacg cgcccgcgct tgccgcgcgc aacgtcagct
1901 tcgccatgaa aggcggtgcg gacgttgccg aacacaccgc ctccgcacg
1951 ctgatgcagc attcgggtca tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacgttg gaaaacatca agcaaacct atttttcgcc ttcttctaca
2051 atatatggg cattccgctc gccgcgctcg gctttttaa tcccgtcata
2101 gcaggcgcg caatggcgcg aagctcgggt tcggtattgg gcaatgcctt
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADIAKI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLTINIPFL
101 IGMVGMMLKG LNWTRHDWMI PPVWQFVLAS IVQLWLAI PF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSGW ADESHLTGES NPEKKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVG
351 ALLTFIVAWL IKGDWTVALM HAVAVLVIA C PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRPQVAAYV YVPDSGFDED
451 ALYRIA AAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGA DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA AAATCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCCGCAGC GAAGAGGCGC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGGCTGTGG CTGCTGTTCA CCATCAACGT CCCGTTCTCT

```

```

301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTTACAA AAGCGCGTGG GCGAGCATT AAGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCCGTCTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CGGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTTG TGTCACTGGG TAAATTTTTG
601 GAACACCGTA CCAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGGCGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGGCG AATCCAATCC TGAAGAAAAA AAGGCGGGCG
851 GCAAAGTGTG GCGGGGCGCG TTAATGACCG AAGGCAGTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AAGCCAGCTC GCGGACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TCGCGCGTA GCCGATAAAG
1001 CCGCTGCGGT ATTCGTGCCT GCCGTGCTGG GCATTGCGTT GTTGACTTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTTGCGC TGATGCACGC
1101 CGTCGCCGTT TTGGTGATTG CCTGCCCGTG CCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGGTCGGT ATGGGCAAAG CGGTAAACA CGGTATTGGG
1201 TTTAAAGACG CGGCAGCAAT GGAGGAAGCC GCCCAGTCG ATGCCGTCGT
1251 GTTGGACAAA ACCGGTACGC TGACCGAAGG CAGCCCGCAG GTTGCCGCGG
1301 TTTATTGCGT TCCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCCCGCGCGG TCGAACAAAA CGCCGCCCAT CCGCTCGCCC GTGCCATCGT
1401 CTCCGCGCGC CAAGCGCGCG GTTGGACAT TCCCGCGCA CAAAACGCAC
1451 AAACCGTTGT CGGCGCAGGC ATTACCGCGG AAGTGAAGG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTGT TCGGGTCTCA GTCGATAACA
1601 AACCATCGG CGCATTCGCA CTTGCCGACG CGTTGAAAGC CGATACCGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CGGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACA CTGGGCATCG
1751 CACACGCCTT CGGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAACCAAAG CCGCCGGCAA AACCGTGGCG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TGCCGAACAT ACCGCATCCG CCACGCTGAT GCAGATTTCG
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTTGAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTG
2051 CTCTCGCCGC GCTTGGCTTT TTAAATCCCG TCATCGCTGG CGCGGCAATG
2101 GCGGCAAGCT CGTTTCCGT GTTGAGCAAT GCCTTGCGCC TGAACGGGT
2151 AAAATCGAT TAG

```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

m589.pep..

```

1  MQQKIRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIARI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LFTINVPFL
101 IGMAGMMIGR HDWMIPPLWQ FALASVVQLW LAIPFYKSAW ASIKGGLANM
151 DVLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVEFEVGMV IGFVSLGKFL
201 EHRTKSSLN SLGILLKLTP TQVNVQRNGE WKQLPIDQVQ IGDILIRANH
251 ERIAADGIE SSGSWADESH LTGESNPEEK KAGGKVLAGA LMTESGVVYR
301 ATQLGSQTQL GDMNALSEA QGSKAPIARV ADKAAAVFVP AVVGIALLTE
351 IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
401 FKDAAMEEA AHVDAVVDK TGTLTGSPQ VAAVYCVFDS GFDEDALYRI
451 AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTVVGAG ITAEVEGVGL
501 VKAGKAEFAE LALPKFLDGW WDIASIVAVS VDNKPIGAFA LADALKADTA
551 EAIGRLKKHN IDVYIMSGDN QGTVEYVAKQ LGIAHAFNM SPRDKAAEVQ
601 KLKAAGKTVA MVGDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
651 VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
701 AASSVSVLSN ALRLKRVKID *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

```

               10      20      30      40      50      60
m589.pep      MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIARI
               |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```


921

g589 MQQKIRFQIEAMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVTFDGSKTSVADI AKI
10 20 30 40 50 60

m589.ppe IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
70 80 90 100 1 110
|||||:|||||:|||||:|||||:|||||:|||||

g589 IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLLTINIPFLIGMVGMMMLKGLNWTNRHDWMI
70 80 90 100 110 120

m589.ppe PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
120 130 140 150 160 170
||:|||||:|||||:|||||:|||||:|||||:|||||

g589 PPVWQFVLASIVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA
130 140 150 160 170 180

m589.ppe AYGMAHVYFEVGVVMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
180 190 200 210 220 230
|:|||||:|||||:|||||:|||||:|||||:|||||

g589 AHGMAHVYFEAGVMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
190 200 210 220 230 240

m589.ppe IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLAGALMTEG
240 250 260 270 280 290
|||||:|||||:|||||:|||||:|||||:|||||

g589 IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLAGALMTEG
250 260 270 280 290 300

m589.ppe SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFFIVTWL
300 310 320 330 340 350
|||||:|||||:|||||:|||||:|||||:|||||

g589 SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPTVVGIALLTFFIVAWL
310 320 330 340 350 360

922

	360	370	380	390	400	410
m589 . pep	IKGDWTVVALMHAVAVLVIAACPCALGLATFAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVVALMHAVAVLVIAACPCALGLATFAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589 . pep	VVLDKTGTLTEGSPQVAAYVCPDSEGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
g589	VVLDKTGTLTEGRPQVAAYVVPDSEGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589 . pep	DIPAAQNAQTVVGAGITAEVEGVGLVKAGKAEFAELALPKFLDGVWDIASIVAVSVDNKP					
g589	EIPAAQNAQTVVGAGITAEVEGVGLVKSGKAEFAELTLPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589 . pep	IGAFALADALKADTAEAIIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
g589	IGAFALSALKADTAEAIIGRLKKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589 . pep	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589 . pep	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVSVLGNALRLK					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVSVLGNALRLK					
	670	680	690	700	710	720
	720					
m589 . pep	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

```

a589 . seq
1  ATGCAACAAA AAGTCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCATG
51  TGCTTCGCGC ATTGAAAAAG TGTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCGCCAGC GAAGAGGCTC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GAGGTTGTGG CTTTGTCTGG CCATCAATAT CCCGTTCCCT
301 ATCGGTATGG TAGGGATGAT GCTAAAAGGG CTGAATTGGA CACGGCATGA
351 TTGGATGTTG TCGCCCTTGT TGCACTTTGC ATTGGCGAGT GTGGTGCAGC
401 TTTGGCTGGC GGTGCCATTT TACAAAAGCG CGTGGGCGAG CATTAAAGGC
451 GGGCTGGCGA ATATGGACGT ACTCGTTACC ATCGGCACGG TCTCGATTTA
501 CCTGTATTCC GTCTATATGC TGTTTTTCAG CCCGCACGCG GCGTACGGTA
551 TGGCGCATGT GTATTTTGAA GTAGGCATAA TGGTGATTGG TTTTGTGTCA
601 CTGGGTAAAT TTTTGGAAAC CCGCACCAAA AAATCCAGCC TGAACAGCTT
651 GGGCTTGCTG CTCAAATCA CGCCAACCCA AGTCAACGTG CAACGCGATG
701 GCGAATGGCG GCAGCTACCC ATCGACCAAG TGCAATCGG CGACCTAATC
751 CGCGCCAATC ACGGCGAACG CATTGCCGCC GACGGCATCA TAGAAAGCGG
801 CAGCGGCTGG GCGGACGAAA GCCATCTTAC CGGCGAATCC AATCCGAAG
851 AGAAAAAGGC AGGCGGCAAA GTATTGGCGG GCGCGCTGAT GACTGAAGGC
901 AGCGTGGTGT ACCGCGCCGC GCAGCTCGGC AGCCAAACCC TGCTCGGCGA
951 CATGATGAAC GCGCTCTCCG AAGCGCAAGG CAGTAAAGCA CCGATTGCGC
1001 GTGTGGCGGA CAAGGCGGCG GCGGTATTCC TGCCTGCCGT TGTGGGCATC
1051 GCACTTTTGA CTTTATTCGC TACTTGGCTG ATTAAGGGCG ATTGGACGCT
1101 CGCATTGATG CACGCCGTCG CCGTTTGGT GATTGCCTGC CCGTGTGCAC

```

```

1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTGCG CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAACGCGC CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CCGCCAGGC GCGCGGTTTG GAGATTCCCA
1451 CCGCACAAA TGCCCAAACC ATTGTCGGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTGGTAA AGCAGGCAAA GCCGAATTG CCGAACTGAC
1551 CTTGCCGAAG TTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAA CGGCAAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCGAAGC CATAGCCGT CTGAAAAAAC ACAATATCGA
1701 TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGGTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCGCCGAAG TGCAGAACT CAAAGCCGCC GGCAAAACCG TGGCGATGGT
1851 CGGCGACGGC ATCAACGACG CGCCCGCGCT CGCCGCGGCC AACGTCAGCT
1901 TCGCCATGAA AGGCGGTGCA GACGTGCGG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCGCTC GCGCGCTCG GCTTTTTTAA CCCCCTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCCTGAAA CGGTAATAAA TCGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

```

a589.pep
  1  MQQKVRFOIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
 51  KTSVADIANK IEKTYGAKK KTEDTLPPQE AEHHIGWRLW LLLAINIPFL
101  IGMVGMMLKG LNWTRHDWML SPLLOFALAS VVQLWLAVPF YKSAWASIKG
151  GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201  LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251  RANHERIAA DGIIESGSGW ADESLTGES NPEEKAGGK VLAGALMTEG
301  SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351  ALLTFIATWL IKGDWTLALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401  KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGKQPQAAVY CVPDSGFDED
451  ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501  KGAGLVKAGK AEFAELTLPK FSDGVWEIAS VVAVSUNGKP IGAFALADAL
551  KADTAEAGR LKKHNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601  AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGA DVAEHTASAT
651  LMQHSVNQLA DALSVSRATL KNIKQNLFFA FFYNILGIPL AALGFLNPVI
701  AGAAMAASSV SVLSNALRLK RVKID*

```

m589/a589 94.9% identity in 725 aa overlap

```

              10      20      30      40      50      60
m589.pep      MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANK
              10      20      30      40      50      60
a589           MQQKVRFOIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANK
              10      20      30      40      50      60
              70      80      90      100     110
m589.pep      IEKTYGAKKTEDTLPPQEAHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
              70      80      90      100     110
a589           IEKTYGAKKTEDTLPPQEAHHIGWRLWLLAINIPFLIGMGMMLKGLNWTRHDWML
              70      80      90      100     110     120
              120     130     140     150     160     170
m589.pep      PPLWQFALASVVQLWLAIFFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
              130     140     150     160     170     180
a589           SPLLOFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
              130     140     150     160     170     180
              180     190     200     210     220     230
m589.pep      AYGMHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
              190     200     210     220     230
a589           AYGMHVYFEVGIMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP
              190     200     210     220     230     240

```

924

m589.pep	240	250	260	270	280	290
	IDQVQIGDLIRANHGERIAADGI	IESGSGWADESHLTGESNPEEK	KAGGKVL	L	GAL	MTEG
a589	IDQVQIGDLIRANHGERIAADGI	IESGSGWADESHLTGESNPEEK	KAGGKVL	L	GAL	MTEG
	250	260	270	280	290	300
m589.pep	300	310	320	330	340	350
	SVVYRATQLGSQTQLGDMN	NALSEAQGS	KAPIARVADKAA	AVFVP	PAVVG	IALLTFIVTWL
a589	SVVYRATQLGSQTQLGDMN	NALSEAQGS	KAPIARVADKAA	AVFVP	PAVVG	IALLTFIVTWL
	310	320	330	340	350	360
m589.pep	360	370	380	390	400	410
	IKGDWTVALMHAVAVLV	IACPCALGLATPAA	IMVGMGKAVKHGI	WFKDAAAMEE	AAHVDA	
a589	IKGDWTVALMHAVAVLV	IACPCALGLATPAA	IMVGMGKAVKHGI	WFKDAAAMEE	AAHVDA	
	370	380	390	400	410	420
m589.pep	420	430	440	450	460	470
	VVLDKTGTLTGEGSPQ	VAAVYCV	PD	SGFDE	DALYRIA	AAVEQNAAHPLARAI
a589	VVLDKTGTLTGEGSPQ	VAAVYCV	PD	SGFDE	DALYRIA	AAVEQNAAHPLARAI
	430	440	450	460	470	480
m589.pep	480	490	500	510	520	530
	DI	PAAQNAQT	VVGAGITAE	VEGVGLVKAGKAE	FAELALPKFLD	GVWDIASIVAVSV
a589	DI	PAAQNAQT	VVGAGITAE	VEGVGLVKAGKAE	FAELALPKFLD	GVWDIASIVAVSV
	490	500	510	520	530	540
m589.pep	540	550	560	570	580	590
	IGAFALADALKADTAE	IGRLKKNIDVY	IMSGDNQGTVEY	VAKQLGIAHAF	GNMSPRDK	
a589	IGAFALADALKADTAE	IGRLKKNIDVY	IMSGDNQGTVEY	VAKQLGIAHAF	GNMSPRDK	
	550	560	570	580	590	600
m589.pep	600	610	620	630	640	650
	AAEVQKLKAAGKT	VAMVGDG	INDAPALAAAN	VSFAMKGGAD	VAEHTASAT	IMQHSVNQLA
a589	AAEVQKLKAAGKT	VAMVGDG	INDAPALAAAN	VSFAMKGGAD	VAEHTASAT	IMQHSVNQLA
	610	620	630	640	650	660
m589.pep	660	670	680	690	700	710
	DALLVSQATLKN	IKQNLFFAFFYN	ILGIPLAALGFL	NPVIA	GAMAASSV	SVLSNALRLK
a589	DALLVSQATLKN	IKQNLFFAFFYN	ILGIPLAALGFL	NPVIA	GAMAASSV	SVLSNALRLK
	670	680	690	700	710	720
m589.pep	720					
	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:

g590.seq..

```

1  atgaaaaaac ctttgatttc agttgaggca gtattgctcg gcggtgcttt
51  ggggtacacct tattatttgg gtgtcaaacg agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccag
151 tatgatcgag gctggtttac ctctacggaa acgacggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtggttga acagccggtt acgctggtta accatatcac gcacggccct
301 ttcgcggcgc gattcggcac gcaggcgcac attgaaaccg agttcaataa
351 cgcgctgtaa acggaaaaag ttttggaaac cttttttggg aaacaagttc
401 cggtttcctt tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtggtc cgcgtttoga ttatgaagaa ctgtcgggca tcaggctgca

```

```

501 ctgggaagggc ctgacggggg aaacggttta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttggtca aaatcaagct ggcagacaaa
601 ggcgatgccc cgtttgaaaa agcgcatctc gattcggaat cttcagacgg
651 catcaatccc cttgctttgg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaatg gaaagagggg gtcgattaca acgtcaaatt gaacgaactg
751 gt caacctcg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctgggt ttttcaacca
851 agaccgggga atcgggcccgc tttatcgaca gcgaagggcg gttccggttc
901 gatacgttgg tgtacggcga tgaaaaatac ggcccgttgg acatccatat
951 cgctgcccga cacctcgatg cttctgcctt aacogtattg aaacgcaagt
1001 ttgcacaaa tttctgcaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgcgg cagtcgaaag cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaat atcaaaattt tccgtttcac cctgcctcag ggaataattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggac tgatgtttaa gaaaaccgag gcaaacatca gaatgagtat
1251 tccctcaaaa atgttggaag atttggcggg aagtcaggct ggaataattt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 at taatgaaa cattgcgcct gatggtggac agtacggtcc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccttaaaaa caacgcctg aagttaaacg ggaaaacgct gcaaaatgaa
1501 ccgatccctg attttgacga gggagatatg gtttccggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

g590.pep..

```

1 MKKPLISVAA VLLGVALGTP YYLGVAEES LTQQQKILQK TGFLTVESHQ
51 YDRGWFSTSE TTVIRLKPFL LHNAQKYLDP NLKIVLEQPV TLVNHITHGP
101 FAGGFQTAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAFKAHAF DSETSDGINP LALGSSNLT L EKFSLEWKEG VDVNVLNKL
251 VNLVTDLQIG APINPNISIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTBQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMKKEDLN
401 QLGLMLKKEE ANIRMSIPQK MLEDLAVSQA GNIFSVNAED BAEARASIA
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

m590.seq (partial) ..

```

1 .. TGGTTTACCT CTATGGAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAAATACC TGCCGGATAA CCTGAAACCA GTGTGTGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCCGGCAGC AGCGGTACAT TGAAACCGAG TTCAAATACG CGCCTGAAAC
201 GGAAAAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAAC GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG . CTGCACT GGGAAGGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAAGTTT CAAAGCTAC CCGAACGGCT
401 ATGATGCCCC CTGTGTTTAA ATCAAGCTGG CAGACAAAGG CGATGCCCGC
451 TTTGAAAAAG TGCAATTTCG TCCGAAACT TCAGACGGCA TCAATCOGT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGA AAAATTCTCC CTAGAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAAGTGT CAATCTTGT
601 ACCGATTGTC AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
651 TTCCAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTGA TACACTGGTG
751 TACGGCGATG AAAAAATACG CCGCTGGAC ATCCATATCG CTGCGGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATTT GATTGCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTTACC AACAATCCCG TATTGGACAT
951 TAAAACCTTC CGATTACGCG TGCCATCGGG AAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 TTGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCCAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GCGGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTCTT CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGTT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

m590.pep.. (partial)

```

1  WFTSMETTVI RLKPELLNNA RKYLPDNLKT VLEQPVTLVN HITHGPFAGG
51  FGTQAYIETE FKYAPETEKV LERFFGKQVP ASLANTVYFN GSGKMEVSVF
101 AFDYEEELSGI XLHWEXLTGE TVYQKGFKSY RNYDAPLKF IKLADKGDAA
151 FEKVHFDSET SDGINPLALG SSNLTLEKFS LEWKEGVDYN VKLNELVNLV
201 TDLQIGAFIN PNGSIAPSKI EVGKLAFSTK TGESGAFINS EGQFRFDTLV
251 YGDEKYGPLD IHIAAEHLDA SALTVLKRKF AQISAKKMT EQIRNDLIAA
301 VKGEASGLFT NNPVLDIKTF RFTLPQSKID VGGKIMPKDM KKEDLNQLGL
351 MLKKT EADIR MSIPQKMLED LAVSQAGNIF SVNAEDEAEG RASLDDINET
401 LRLMVDSTVQ SMAREKYLT NGDQIDTAIS LKNNQLKING KTLQNEPEPD
451 FDEGGMVSEP QQ*

```

m590 / g590 93.1% identity in 462 aa overlap

```

                                10      20      30
m590.pep                      WFTSMETTVIRLKPELLNNA RKYLPDNLKT
g590                          VKAESLTQQQKILQKTGFLT VESHQYDRGWFTSTETT
                                30      40      50      60      70      80
m590.pep                      VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
g590                          VLEQPVTLVNHITHGPFAGGFGTQAHIEETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
                                90     100     110     120     130     140
m590.pep                      GSGKMEVSVPAFDYEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLKF IKLADKGDAA
g590                          GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNSYDAPLKF IKLADKGDAA
                                150     160     170     180     190     200
m590.pep                      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
g590                          FEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
                                210     220     230     240     250     260
m590.pep                      PNGSIAPSKIEVGKLAFSTKTGESGAFINSEGGFRFDTLVYGDEKYGPLDIHIAAEHLDA
g590                          PNGSIAPSKIEVGKLAFSTKTGESGAFIDSEGRFRFDTLVYGDEKYGPLDIHIAAEHLDA
                                270     280     290     300     310     320
m590.pep                      SALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPQSKID
g590                          SALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGDASGLFTHDPVLNIIKFRFTLPQSKID
                                330     340     350     360     370     380
m590.pep                      VGGKIMPKDMKKEDLNQLGLMLKKT EADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
g590                          VGGKIMPKDMKKEDLNQLGLMLKKT EANIRMSIPQKMLEDLAVSQAGNIFSVNAEDEARA
                                390     400     410     420     430     440
m590.pep                      RASLDDINETLRLMVDSTVQSMAREKYLTNGDQIDTAISLKNQLKINGKTLQNEPEPD
g590                          RASIADINETLRLMVDSTVQSMAREKYLTLDGNQIDTVISLKNALKLINGKTLQNEPDPP
                                450     460     470     480     490     500
m590.pep                      FDEGGMVS-EPQQX
g590                          FDEGDMVSGQPHX
                                510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCAGCCTT TATTATTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGTTG ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCTT
301 TTTGCCGGCG GATTCCGGAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTTGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAATGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTGGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GCGGATGCCG CGTTTGAAAA AGTGCAATTC GATTGCGAAA CTTCAGACGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACTG
751 GTCAATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAAACTT TCCGATTAC GCTGCCATCG GAAAAATCG
1151 ATGTGGGCGG AAAATCATG TTTAAAGACA TGAAGAAGGA AGATTGAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGCGCA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1  MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE AGFLTVESHO
51  YERGWFTSTE TTVIRLKPEL LHNAQKLPD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLT EKFSLWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDEKY GPLDIHIAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTLLNGDQID TAISLKNNQL KLNGKTLQNE
501 PEPDFDEGGM VSEPQQ*
```

m590/a590 97.8% identity in 462 aa overlap

```

                                     10      20      30
m590.pep                               WFTSMETTIVIRLKPELLNNARKYLPDNLKT
a590      VKAESLTQQQKILQEAGFLTVESHOYERGWFTSTETTIVIRLKPELLHNAQKYPDLNLT
          30      40      50      60      70      80

          40      50      60      70      80      90
m590.pep  VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
a590      VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
          90     100     110     120     130     140

          100     110     120     130     140     150
m590.pep  GSGKMEVSVPAFDYEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
```

928

```

|||||
a590      GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFSYRNGYDAPLFKIKLADKGDAA
          150      160      170      180      190      200

          160      170      180      190      200      210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGV DYNVKLNELVNLVTDLQIGAFIN
a590      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGV DYNVKLNELVNLVTDLQIGAFIN
          210      220      230      240      250      260

          220      230      240      250      260      270
m590.pep  PNGSIAPSKIEVGKLAFFSTKTGESGAFINSEGGFRFDTLVYGDEKYGPLDIHIAAEHLDA
          |||||
a590      PNGSIAPSKIEVGKLAFFSTKTGESGAFIDSEGGFRFGTLVYGDEKYGPLDIHIAAEHLDA
          270      280      290      300      310      320

          280      290      300      310      320      330
m590.pep  SALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPSPGKID
          |||||
a590      SALTVLKRKFARISAKKMTTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPSPGKID
          330      340      350      360      370      380

          340      350      360      370      380      390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
          |||||
a590      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
          390      400      410      420      430      440

          400      410      420      430      440      450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLTLNGDQIDTAISLKNQLKLNKGTTLQNEPEPD
          |||||
a590      RASLDDINETLRLMVDSTVQSMAREKYLTLNGDQIDTAISLKNQLKLNKGTTLQNEPEPD
          450      460      470      480      490      500

          460
m590.pep  FDEGGMVSEPQQX
          |||||
a590      FDEGGMVSEPQQX
          510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```

1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCAGCCTT TATTATTGGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGCTCTGAA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTTGGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301 TTCGCCGCGG GATTGCGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGCTTCCTT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAATGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCGATGCCG CGTTTGAAAA AGTGCAATTC GATTGCGAAA CTTGACGCGG
651 CATCAATCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGTG
751 GTCATCTTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAACTGGCTT TTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTTC
901 GATACACTGG TGTACGGCGA TGAAAAATAC GGCCCGCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGACTGTTCA CCAACAATCC
1101 CGTATTGGAC ATTAAACTT TCCGATTAC GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTAAAGACA TGAAGAAGGA AGATTGAAT
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT

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1251 TC CCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
 1301 TC AGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
 1351 AT CAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
 1401 AA GGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATT
 1451 CT CTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
 1501 CC GGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
 1551 A

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

1 MKKPLISVAA ALLGVALGTP YYLGVKAES LTQOKILOE TGFLTVESHO
 51 YERGWFTSME TTVIRLKP EL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
 101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
 151 VS VPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFRKLADK
 201 GDAAFEKVHF DSETSDGINP LALGSSNLTLEKFSLEWKEG VDYNVKLNEL
 251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
 301 DT LVYGDEKY GPLDIHIAAE HLDASALTVL KRFQAISAK KMTEEQIRND
 351 LI AAVKGEAS GLFTNNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
 401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
 451 INETLRMLVD STVQSMAREK YLTNGDQID TAISLKNQL KLNGKTLQNE
 501 PEPDFDEGGM VSEPQQ*

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAAALLGVALGTPYYLGVKAESLTQOKILOETGFLTVESHOYERGWFTSME					
g590	MKKPLISVAAVLLGVALGTPYYLGVKAESLTQOKILOKTGFLTVESHOYDRGWFTSTE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m590-1.pep	TTVIRLKPPELLNNARKYLPDNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE					
g590	TTVIRLKPPELLHNAQKYLDPNLKIVLEQPVTLVNHITHGPFAGGFGTQAHIEYEFKYAPE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m590-1.pep	TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEE LSGIRLHWEGLTGETVYQKG					
g590	TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEE LSGIRLHWEGLTGETVYQKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
g590	FKSYRNSYDAPLFKIKLADKGDAAFEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m590-1.pep	VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLA FSTKTGESGAFINSEGQFRF					
g590	VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLA FSTKTGESGAFIDSEGRFRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKYGPLDIHIAAEHLASALTVLKRFQAISAKKMTEEQIRNDLIAAVKGEAS					
g590	DTLVYGDEKYGPLDIHIAAEHLASALTVLKRFQAISAKKMTEEQIRNDLIAAVKGDAS					
	310	320	330	340	350	360
	370	380	390	400	410	420
m590-1.pep	GLFTNNPVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK					
g590	GLFTHPVLNLIKIFRFTLPQSKIDVGGKIMFKGMKKEDLNQLGLMLKKTEANIRMSIPQK					
	370	380	390	400	410	420
	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQA GNIFSVNAEDEAEGRASLDDINETLRMLVDSTVQSMAREKYLTLNGDQID					
g590	MLEDLAVSQA GNIFSVNAEDEAEARASIA DINETLRMLVDSTVQSMAREKYLTLNGDQID					
	430	440	450	460	470	480
	490	500	510			
m590-1.pep	TAISLKNQLKLNGKTLQNEPEPDFDEGGMVS-EPQQX					

[illegible]

g591.seq

1	TTGCAAACCC	TTCTAGCTTT	TATCTTCGCC	ATCCTGATT	TGGTCAGCCT
51	GCACGAATT	GGACACATCA	TGCTCGCCAG	GTGTGCGGG	GTCAAGGTTG
101	TGCGTTTTT	CGTCGCGTTC	GCCAAACGTT	TTTTCACCG	AAAGCGCGGC
151	GACACCGAAT	GGTGCTCGC	CCCGATTCCG	TTGGGCGGCT	ACGTCAAAT
201	GGTCGATACG	CGCGAAGGCG	AAGTATCAGA	AGCGATTITA	CCCTACGCTT
251	TTGACAAACA	ACACCCCGC	AAGCGCATCG	CCATCGCTCG	CGCCGGTCCG
301	CTGACCAACC	TCGCActggc	ggTTTtGCTG	TACGGACTGa	gcctTtccct
351	cqccqtaaCC	GAACTCGCGC	CCtatgtcqq	cacaqtcqaA	cccgcacccc

931

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401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtgc ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCAtcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCATCGc ctcaTGCAG
751 GAATGggcaa acctgACccg cCAAAGCCCg ggcAAAAAAA Tcacctgac
801 ctacgAaCGC GCcgacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAAAcagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTCAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCGG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTGGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCCTT CTTCAACGAC GTTACCCGGC TGATCGGTTA G

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This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591. pep..

```

1  LQTLIAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRK
51  DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTVARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTYER AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRSPVVRA FGMWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFLALMM LMMAAFFND VTRLIG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591. seq

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1  TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCTGATTT TGGTCAGCCT
51  GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCTTCGC CCCGATTCCG TTGGCGGGT ACGTCAAAAT
201 GTTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGAATGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 TGGCACACCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCTCAAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTGAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591. pep..

933

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1   TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TGCCTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGCACACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGA AAAAG GCAGCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGACG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAA AACC GTTTC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCGTCAGC
1051 CATATTTCCG GTCGCTGAC CATTGCCGAT ATTGCCGAC AGTCGCGCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTT GGCATGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGCCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTCGCGCT TCGGCTTGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTCAACGAC GTTACCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

a591.pep

```

1   LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRKG
51  DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTIAARAGF QSGDKIQSVN
151 GTPVADWGS A QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQS AELGL QSYLEFLALV SISLGVNLL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMM LMAVAFFND VTRLLG*

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m591/a591 99.6% identity in 446 aa overlap

```

          10      20      30      40      50      60
m591.pep  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRKG DTEWCLAPIP
          |||
a591      LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRKG DTEWCLAPIP
          10      20      30      40      50      60

          70      80      90      100     110     120
m591.pep  LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT
          |||
a591      LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT
          70      80      90      100     110     120

          130     140     150     160     170     180
m591.pep  ELRPYVGTVE PDTIAARAGF QSGDKIQSVNGT PVADWGS A QTEIVLNLEA GKVAVGVQTA
          |||
a591      ELRPYVGTVE PDTIAARAGF QSGDKIQSVNGT PVADWGS A QTEIVLNLEA GKVAVGVQTA
          130     140     150     160     170     180

          190     200     210     220     230     240
m591.pep  SGAQTVRTIDA AGTPEAGKIAKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA
          |||
a591      SGAQTVRTIDA AGTPEAGKIAKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA
          190     200     210     220     230     240

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934

	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFSGMWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFSGMWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVSISLGVNLNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVSISLGVNLNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLLGX					
a591	GLRFGALMMLMMAVAFFNDVTRLLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg acgtgttcgg tcagattttt tcgggcgcgt tcaaattcga
51  cgcggcagca ggcggcttac tcggcggtct gatttcgcaa acgatgatga
101 tgggcatcaa acgcggcctg tattccaacg aggcgggtat gggttccgcg
151 ccgaacgcgc ccgcgcgcgc cgaagtgaac caccctgttt cgcaaggatg
201 gattcaaatg ctgggcgtgt ttgtcgatc catcatcggt tgttcttgca
251 cgcgcttcac catcttgatt taccaacagc cttatggcga tttgagcggg
301 gcggcgctga cgcaggcggc gattgtcagc caagtggggc aatggggcgc
351 gggtttcctc gccgtcatcc tgtttatggt tgccttttcc accggtatcg
401 gcaactatgc ctatgccgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattaccg ccgttttccg tatgctgggt ttggcggtgg tctatttcgg
501 cgcgggttgc aatgtgcctt tggctcggga tatggcggtg atggcgatgg
551 gcatcatggc gtggatcaac ctgcgcgcca tcctgctgct ctgcgcattg
601 gcgtttatgc tgctgcgcga ttacaccgcc aagctgaaaa tgggcaaaaga
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcattcaaat
701 ccgatgtttg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFGQIF SGAFKFDAAA GLLGLGLISQ TMMGIKRL YSNEAGMGS
51  PNAAAAAEVK HPVSQGMQM LGVFVDTIIV CSCTAFIILI YQQPYGDLG
101 AALTQAAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSH
151 LITAVFRMLV LAWVYFGAVA NVPLVDMAD MAMGIMAWIN LVAILLSPL
201 AFMLLRDYTA KLMGKDPEF KLSEHPGLKR RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG ACGTGTTCGG TCAGATTTTTC TCGGGCGCGT TCAAATCGA
51  CGCGGCAGCA GCGCGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
101 TGGGCATCAA ACGCGGCCTG TATTCCAACG AGGCGGTAT GGGTTCGCG
151 CCGAACGCCG CCGCGCGCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAATG CTGGGCGGTG TTGTGATAC CATCATCGTT TGTTCCTGCA
251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
301 CGGCGCGTGA CGCAGGCGGC GATTGTGAGC CAAGTGGGGC AATGGGCGC
351 GGGCTTCCTC GCGTCATCC TGTTCATGTT TGCCTTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATGG
451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTGGG TCTATTTCGG
501 CGCGGTGCCC AATGTGCCCT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGGC GTGGATCAAC CTTGTGCGCA TCCTGCTGCT CTCGCCCTG

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601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCGCGAGTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQPPYGDLSG
 101 AALTQAAIVS QVQWQAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGINAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSAFNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSAFNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQPPYGDLSGAALTQAAIVSQVQWQAGFL					
g592	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQPPYGDLSGAALTQAAIVSQVQWQAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
g592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGINAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVW*					
g592	MAMGINAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVW*					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq
 1 ATGATTCCGG ACGTGTTCCG TCAGATTTTT TCGGGCGCGT TCAAATTCGA
 51 CGCGGCAGCA GCGGGCTTAC TCGGGCGGTCT GATTTCGCAA ACGATGATGA
 101 TGGGCATCAA ACGCGGCTTG TATTCCAACG AGGCGGGTAT GGGTTCGCGG
 151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGCGGA TTGAGCGGT
 301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
 351 GGGCTTCCTC GCCGTCATCC TGTATTGTT TGCTTTTCC ACCGTTATCG
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
 451 CTGATTACCG CCGTTTTCG TATGCTGGTT TTGGCGTGGG TCTATTTCCG
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG
 601 GCCTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCGCGAGTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQPPYGDLSG
 101 AALTQAAIVS QVQWQAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGINAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592/a592 100.0% identity in 237 aa overlap

936

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMIQMLGVFVDTIIVCSCTAFIILIYQQPYGDLGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMIQMLGVFVDTIIVCSCTAFIILIYQQPYGDLGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

g593.seq..

```

1   atgcttgaac tgaacggact ctgcaaatgc ttcggcggca aaacggtcgc
51  cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg
101 ggccggtcggg ctgcgcgcaa tccaccctgc tgaatatgat tgcgggcacac
151 gtccggccggg acggcggcga aattcggctg aacggggaaa acattacctg
201 tatgccgccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301 caaaaaatgc cgaaagccga agccgaacgc ctgccttgtg cggcacttgc
351 cgaagtccggg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacggttg gcaactggcg gcgctttggt tgtccgcctt
451 tccctgctgt tgctggatga atcgttttcc agtttggaca cgcatttgcg
501 cgaccggctg cgccgtatga ccgccgaacg catccgcaag ggcggcatcc
551 tgcgcgtttt ggtaacgcat tcgcccgaa aggcctgcac ggcggcgagc
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcg gtacgcccga
651 aaccttgatt caaacgcctg ccggcgtgca ggtcgccgt ctgatggggc
701 tgcccaatac cgacgatgac cgccatattc cgcaaatgc cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctgctg tccctcgtec gcctgcccga
801 ctgcgtccgg ctttccgcgg tccatcccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacggta tttccggaaa cggtagcggtc
901 cgcattccgg tcgatgaagg gcgtatcgtc cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

g593.pep..

```

1   MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISIMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAEER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSLR LSAVHPEHGE LTLNLTVGQH TDGISGNGTV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

m593.seq

```

1   ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GCGCGGTCGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCCG ACGGCGGGGA AATATGGCTG AACGGAGAAA ACATTACCCG

```



```
m593.pap ..
  1 MLELNLGCKR FGNKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
  51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
  101 QKMPKAAEAE LAMAALAEPV LENEAAHKPE KLSGGEQKRL ALARALVVRP
  151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTVP
  201 EIAVMHKGRI LQYGTPETLV KTPSCVQVAR LMGLPNTDDN RHIPQHAVRF
  251 QDQGMCECRVL SRTCLPESFS LSVLHPHEGI LWNLDMRHA GAVSGKDTVR
  301 IHIEREIVR FR*
```

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m593.pep	MLELNGLCKRFGNKTVD	NICLTVGRGKILAVL	GRSGCGKSTLLNII	AGIVRPDGGEIWL		
g593	MLELNGLCKCFGGKTV	DNICLTVGRGKILAVL	GRSGCGKSTLLNMI	AGIVRPDGGEIRL		
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRIS	LMFQDYALFPHMSA	LENAAFLGKMQKMP	KAEAEERLAMAAL	AEVG	
g593	NGENITCMPPEKRRIS	LMFQDYALFPHMSA	LENTAFGLKMQKMP	KAEAEERLALSAL	AEVG	
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEAHRKEPKLSGGE	KQRLALARALVVRPS	LLLLDESFS	SLDTHLRGTLRRMT	AEIRN	
g593	LENEAHRKEPKLSGGE	KQRLALARALVVRPS	LLLLDESFS	SLDTHLRDLRMRMT	AEIRK	
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSP	EECTTADEIAVMHKG	RILQYGT	PETLVKTPSCVQ	VARLMGLPNTDDN	
g593	GGIPAVLVTHSP	EECTTADEIAVMHEG	KILQCGT	PETLIQT	PAGVQVARLMGLP	NTDDD
	190	200	210	220	230	240

938

	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDQDGMCECRVLSRTCLPESFSLSVLHPEHGILWLNLDLDM-RHAGAVSGKDTV					
	: : : : : : : : : : : : : : : : : :					
g593	RHIPQNAVCLDNHGTCECRLLSLVRLPDSLRLSAVHPEHGELTLNLTVGQHTDGISGNGTV					
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	:: : : :					
g593	RIRVDEGRIVRFRX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1857>:

```

a593.seq
1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCGGCA AAACGGTTGC
51  CGACGATATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GCGCGTCCGG CTGCGGCAAA TCCACCTGCG TGAATATGAT TGCGGGCATC
151 GTCCGGCCCG ACGGCGGGGA AATATGGCTG AATGGGGAAA ACATTACCCG
201 TATGCCGCCC GAAAAACGCC GTATTTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCA TATGAGTGCA CTGGAATATG CGGCATTTCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAAAGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAACACG AGGCGCACCG CAAGCCTGAN AAACTTCCG
401 GAGGCGAAAA GCAACGGTTG GCACTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTCC AGTTTGACA CGCATTGCG
501 CGACCGGCTG CGCCGCATGA CTGCCGAACG TATCCGCAAG GCGGCATCC
551 CTGCCGTTT GTTAACGCAT TCGCCGAAG AGGCCTGCAC GCGGCAGAC
601 GAAATCGCCG TCATGCACGA GGGGAAAATC CTCAATGCG GTACGCCCGA
651 AACCTTGTT CAAACGCCTG CCGGCGTGCA GGTGCGCCAT CTGATGGGCG
701 TGCCCAATAC GCACGATGAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCCGCACGCC GGTGAAATAT CGGGAACGA TACGGTACGC
901 ATCCATATCG AAGACAGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:

```

a593.pep
1  MLELNLCKR FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
101 QKMPKAEAES LAMAALAEVG LENEHRKPEX KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLV QTPAGVQVAH LMGLENTDDD RHIPQHAVRF
251 DQDGMCECRVL SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GEISGNDTVR
301 IHIEDREIVR FR*

```

m593/a593 92.9% identity in 312 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
	: : : : : : : : : : : : : : : : : :					
a593	MLELNLCKRFGGKTVADDICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMOKMPKAEERLAMAALAEVG					
	: : : : : : : : : : : : : : : : : :					
a593	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMOKMPKAEESLAMAALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
	: : : : : : : : : : : : : : : : : :					
a593	LENEHRKPKXKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDRLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTADEIAVMHKGRILQYGTPE TLVKT PSCVQVARLMGLENTDDN					

g594.seq..

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

g594.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

m594.seq

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

m594.pcp

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRLNRTGLVFSILRLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```
a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GGCGGCCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTCGC GAGTGTGAGG AAACGGCGGC
351 GGCCGTTGTT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGAATACCG AGCCATTAAG CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```
a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIHYSVV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*
```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRLNRTGLVFSILRLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```
g595.seq..
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttggggtt
51  gaccgcgtgc cagccgccgg aggcggagaa agccgcgccg gccgcgt ccg
101 gtgagacca atccgccaac gaaggcgggt cggtcggtat cgccgtc aac
```

```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgatgat ggtggtggac gaacgcgaaa atatcgcccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttgaaa aactgcccc accgctcgcc
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgc gtccattacg aacgcacga accgattgcc
601 gagcttttca gcgaactcga ccccgtcac gatgcgtgtg aagacgactt
651 caaagacggt gcgaaagatg ccgggtttac cggcttcac cgtatcgaac
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgcattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaatcagc ggcgaaagaa accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg ccaaaaacaa agccttggtg gaaaaaaccg
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcaccaaa
```

q595.pap

1	MRKFNLTALS	VMLALGLTAC	QPPEAEKAAP	AASGETQSAN	EGGSVGIAVN
51	DNACEEMNLT	VPSGQVVENI	KNNSGRKLEW	EILKQVMVVD	ERENIAPOLS
101	DKMNRNLLPG	EYEMTCGLLT	NPRGKLVVAD	SGFKDTANEA	DLEKLPQPLA
151	DYKAYVQGEV	KEIAAKTKTF	TEAVKAGDIE	GAKSLFAATR	VHYERIEPIA
201	ELFSELPVI	DACEDDFKDG	AKDAGFTGFH	RIEHALWVEK	DVSGVKETAA
251	KLMTDVEALQ	KEIDALAFPP	GKVVGGASEL	IEEAAGSKIS	GEEDRYSHTD
301	LSDFQANADG	SKKIVDLFRP	LIEAKNKKAL	EKTDNTFKQV	NEILAKYRTK
351	DGFETYDKLS	EADRKALQAP	INALAEDLQ	LRGLGLK*	

m595.seq

1	ATGAGAAAT	TCAATTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCGGTGC	CAGCCGCCG	AGCGGAGAA	AGTCGCGCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAT	GAGGGCGGT	CGGTCAAGTAT	CGCGCTCAAC
151	GACAATGCTT	CGCAAGCCAC	GGAACTGACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	CGCGCCGAA	GTCGAATTG	GAATCCTGA
251	AAGGCGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATCGCCCC	CGGACTTTCC
301	GATAAAATGA	CCGTACCCCT	GTTGCCGGGC	GAATACGAAA	TGACTTGCGG
351	TCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAA	AAGTGTCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTACGTTCA	AGCGGAGGTT	AAGAGCTGG	TGGCGAAAAC
501	CAAAACTTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGCGTG	AAGACGACTT
651	CAAAGACGCG	GCGAAAGATG	CCGGATTTAC	CGGCTTTTAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCCG	GCGTGAAAGA	AATTGACGCG
751	AAACTGATGA	CCGATGTCGA	AGCCTGCAA	AAAGAAATCG	ACGCATTGGC
801	GTTTCCTCCG	GGCAAGGTGG	TCGGCGGCCG	GTCGCGAATG	ATTGAAGAAG
851	TGGCGGGCAG	TAAATCAGC	GGCGAAGAGA	ACCGGTACAG	CCACACCGAT
901	TTGAGCGGCT	TCAAAGCCAA	TGTGGACGGA	TCTAAAAAAA	TCGTGATATT
951	GTTCCGTCGG	CTGATCGAGG	CCAAAAACAA	AGCCTTGTTG	GAAAAAACCG
1001	ATACCAACTT	CAAACAGGTC	AACGAAATTC	TGGCGAAATA	CCGACTAAA
1051	GACGTTTTTG	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAGCGTT
1101	ACAGGCTCTT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCCA	CTTCGCGGCA
1151	TACTCGGCTT	GAAATBA			

m595.pap

1	<u>MRKFNLTA</u> <u>LS</u>	<u>VMLALGLTAC</u>	QPPEAEKAAP	AASGEAQTAN	EGGSVSIAVN
51	DNACEEMELT	VPSGQVVFIN	KNNSGRKLEW	EILKGVMVVN	ERENIAPGSL
101	DKMTVTLLPG	EYEMTCGLLT	NPRGKLVVTD	SGFKDTANEV	DLEKLSQPLA
151	DYKAYVQGEV	KELVAKTKTF	TEAVKAGDIE	KAKSLFADTR	VHYERIEPIA
201	ELFSELDPVI	DAREDDFKDG	AKDAGFTGFH	RIEYALWVEK	DVSGVKEIAA
251	KLMTDVEALG	KEIDALAFPP	GKVVGGASEL	IEEVAGSKIS	GEEDRYSHTD
301	LSDFQANVDG	SKKIVDLFRP	LIEAKNKALE	EKTDVTNFKQV	NEILAKYRTRK
351	DGFETYDKLG	EADRKALQAS	INALAEDLAQ	LRGLIGLK*	

Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLTALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	IAVNDNACEPMELT				
g595	MRKFNLTALSVMLALGLTACQPPEAEKAAPASGETQSANEGGSVGI	AVNDNACEPMNLT				
	10	20	30	40	50	60
	70	80	90	100	110	120

943

```

m5 95. pep  VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
              |||||:|||||
g5 95        VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMNRNLLPGEYEMTCGLLT
              70      80      90      100     110     120

              130      140      150      160      170      180
m5 95. pep  NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTTFTEAVKAGDIE
              |||||:|||||
g5 95        NPRGKLVVADSGFKDTANEADLEKLQPLADYKAYVQGEVKELAAKTKTTFTEAVKAGDIE
              130      140      150      160      170      180

              190      200      210      220      230      240
m5 95. pep  KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
              |||||:|||||
g5 95        KAKSLFAATRVHYERIEPIAELFSELDPVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK
              190      200      210      220      230      240

              250      260      270      280      290      300
m5 95. pep  DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD
              |||||:|||||
g5 95        DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEAAGSKISGEEDRYSHTD
              250      260      270      280      290      300

              310      320      330      340      350      360
m5 95. pep  LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG
              |||||:|||||
g5 95        LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLS
              310      320      330      340      350      360

              370      380      389
m5 95. pep  EADRKALQASINALAEDLAQLRGILGLKX
              |||||:|||||
g5 95        EADRKALQAPINALAEDLAQLRGILGLKX
              370      380

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

```

a5 95. seq
1   ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGAATTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGTGG TGGCGAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTCAC CGTATCGAAT
701 ACGCCCTTGG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAA TCGTCGATT
951 GTTCCGTCGG TTGATCGAGA CCAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

```

a5 95. pep
1   MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTN EGGSVSIAVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVVD ERENIAAPGLS

```

```

101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPIV DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKOV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

m595/a595 99.7% identity in 388 aa overlap

```

          10      20      30      40      50      60
m595.pep MRKFNLTALSVMALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT
          |||||
a595      MRKFNLTALSVMALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT
          10      20      30      40      50      60

          70      80      90     100     110     120
m595.pep VPSGQVVFNKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
          |||||
a595      VPSGQVVFNKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
          70      80      90     100     110     120

          130     140     150     160     170     180
m595.pep NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
          |||||
a595      NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
          130     140     150     160     170     180

          190     200     210     220     230     240
m595.pep KAKSLFADTRVHYERIEPIAELFSELDPIV DAREDDFKDGAKDAGFTGFHRIEYALWVEK
          |||||
a595      KAKSLFADTRVHYERIEPIAELFSELDPIV DAREDDFKDGAKDAGFTGFHRIEYALWVEK
          190     200     210     220     230     240

          250     260     270     280     290     300
m595.pep DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD
          |||||
a595      DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD
          250     260     270     280     290     300

          310     320     330     340     350     360
m595.pep LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG
          |||||
a595      LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG
          310     320     330     340     350     360

          370     380     389
m595.pep EADRKALQASINALAEDLAQLRGILGLKX
          |||||
a595      EADRKALQASINALAEDLAQLRGILGLKX
          370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1   ..atgctgctct tggacgagcc gaccaaccac ttggatgcgg aatcggtgga
51  atgctggag caattcctcg tgcgttccc cggcacagt gtcgcggtaa
101 cgcacgaccg ctacttctc gacaacgcc cgaatgatg tttggaactc
151 gaccgcgga acggcattcc gtggaaaggc aattactcgt cttggctgga
201 gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa gccgcgcgcg
251 tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301 cgccaagcca agcccaaagc gcgtttggcg cgttttgaag aatgagcaa
351 ctacgaatac caaaaacgca acgaaactca ggaaatcttt atccctgttg
401 ccgagcggtt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

```



```

451   ttccggcgata aagtgtctgat tgacgggttg agcttcaaag tgccggcgagg
501   cgcgattgtc ggcattcatcg gcccgaaacg cgcgggtaaa tcgacgctgt
551   tcaaaatgat tgcggggcaaa gagcagcccg attcgggcca agtgaaaatc
601   gggcaaaccg tgaaaatgag cttgattgac caaagcccg aaggtttgca
651   aaacgacaaa accgtgttcg acaacattgc cgaaggtcgc gatattttgc
701   aggtcggaca gtttgaaatc cccgcccgcc aatatttggg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcgcgca
801   acgcggccgt ctgcacttgg caaaaacctt gttggcggc ggcaatgtgt
851   tgctgctgga cgaaccgtcc aacgatctcg acgtgaaaac cctgcgcgcg
901   ttggaagacg cattgttga atttgccgcg acgctgatgg tgatttcgca
951   cgaccgctgg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1 001   gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1 051   gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcatcaa
1 101   atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWKG NYSSWLEQKE KRLNEAKSE AARVKAMKQE LEWVRQNAKG
101 RQAKPKARLA RFEEMSNEYE QKRNETQEIF IPVAERLGNE VIEFVNYSKS
151 FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGRFN
251 FKGSQSKIA RQLSGGERGR LHLAKTILGG GNVLLLDEPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351 DKRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCG
51  GCCGCAGAAA ACCATCATTG AAGATATTTT CCTTCTTTT TTCCCGCGCG
101 CGAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTGGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401 CGGCAGGTTT GTCCACGGGC GCGGTTGCGG AACACGAATT GGAATTCGCC
451 GCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
501 CCGCGGTGAA AAACGCCGCG TTGCCTTTGT CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCGGCA CAGTCGTTGC
651 GGTAACGCAC GACCGCTACT TCCTCGACAA CGCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGTTCTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAGAC GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTA AATGTTTCCA
1 001 AATCGTTTCG CGATAAAGTG CTGATTGACG ATTGAGCTT CAAAGTGCCCT
1 051 GCGGGCGCGA TTGTCGGCAT CATCGGCCG AACGGCGCGG GTAAATCTAC
1 101 GCTGTTCAA ATGATTTTCG GCAAAGAGCA GCCTGATTCC GCGGAGGTGA
1 151 AAATCGGACA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1 201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GCCCGGACAT
1 251 TTTGCAGGTT GGTGAGTTTG AAATTCGCG CCGCAATAT TTGGGGCGTT
1 301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
1 351 GCGGAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTGTA GCGGCGGCAA
1 401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCTGCG
1 451 GCGCGTTGGA AGACGCATTG TTGGAATTG CCGGCAGCGT GATGGTGATT
1 501 TCGCACGACC GTTGGTTTCT CGACCGCATC GCCACGCATA TCTTGCGGTG
1 551 TGAAGGCGAC TCTAAATGGG TGTTCTTCGA CGCAACTAT CAGGAATACG
1 601 AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACCG
1 651 ATCAAAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

	160	170	180	190	200	210
m596.pep	LPEWDAKIDNLSGGEKRRVALCKLLLSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTV					
g596	MLLLDEPTNHLDAESVEWLEQFLVRFPGTV					
	10		20		30	
	220	230	240	250	260	270
m596.pep	VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQE					
g596	VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQE					
	40	50	60	70	80	90
	280	290	300	310	320	330
m596.pep	LEWVRQNAKGROAKSKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNIEVIEFVNVS					
g596	LEWVRQNAKGROAKPKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNIEVIEFVNVS					
	100	110	120	130	140	150
	340	350	360	370	380	390
m596.pep	FGDKVLIDDLISFKVPAGAIVGIIGPNGAGKSTLFKMISGKEQPDSDGEVKIGQTVKMSLID					
g596	FGDKVLIDGLISFKVPAGAIVGIIGPNGAGKSTLFKMIAGKEQPDSDGEVKIGQTVKMSLID					
	160	170	180	190	200	210
	400	410	420	430	440	450
m596.pep	QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSQDSKIAGQLSGGERGR					
g596	QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSQDSKIARQLSGGERGR					
	220	230	240	250	260	270

947

	460	470	480	490	500	510
m596.p	LHLAKTLLSGGNVLLLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	:					
g596	LHLAKTLLGGGNVLLLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	280	290	300	310	320	330

	520	530	540	550	559
m596.p	ACEGDSKWVFFDGNVQEYADKKRRLGEEGAKPKRIKYPVTRX				
	:				
g596	ACEGDSKWVFFDGNVQEYADKKRRLGEEGAKPKRIKYPVTRX				
	340	350	360	370	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```

a596.seq
1  ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTA AAGATATTTT CCTTTCTTTC TTCCCGGGCG
101 CGAAATCGG TTTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAAGAATT TGGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
351 GGATTTTGAC GCGTTGGCGG AAGAGCAGGG GCGTTTGGA GCGATTATTG
401 CGGCGGGTTC GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCT
451 GCCGACGCGC TCGCCTGCC GGAATGGGAT GCCAAATCG ATAATTTGTC
501 CGGCGGTGAA AAACGCGCG TCGCTTTGTG CAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCGGTA CAGTCGTTGC
651 CGTAACACAC GACCGTACT TCCTCGACAA CGCCCGCGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGGT ATTCCGTGGA AAGGAAATTA CTCGTCTTGG
751 TTGGAGCAGA AAGAAAAACG TTTGAAAAC GAGGCGAAT CCGAAGCCGC
801 GCGCGTGAAA GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAATGCCA
851 AAGGCCGTCA AGCCAAGTCC AAAGCGCGT TGGCGGTTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGCGTA ACGAAGTGAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTCGG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTGCGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCGTGAAA ATGAGCTTGA TTGACCAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAG GTCGCGATAT
1251 TTTACAGGTC GGGCAGTTG AAATCCCCGC CCGCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGCA GCTTTCCGGC
1351 GGCGAACGCG GACGTTTGCA CTGGCAAAA ACCTTGTTGG GCGGTGGCAA
1401 TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCTGCG
1451 GCGCGTTGGA AGACGATTG CTGGAATTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GCTGGTTCCT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGGCGAC TCCAAATGGG TGTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAAATACA AACCAGTAAC GCGTTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```

a596.p
1  MSQQYVYSML RVSKVVPQK TIIKDISLSF FPGAKIGLLG INGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEP LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADFD ALAEQGRLE AIIAAGSSTG GGAHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEARVK AMQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEKVP
351 AGAIVGIIGP NGAGKSTLFK MIAGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKITGQLSG
451 GERGRHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGTEKPR
551 IKYKPVTR*
  
```

m596/a596 99.3% identity in 558 aa overlap

948

	10	20	30	40	50	60
m596.pep	MSQQYVYSMLRVSKVVPQKTI IKDISLSFFPGAKIGLLGNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVVPQKTI IKDISLSFFPGAKIGLLGNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m596.pep	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m596.pep	ALAEEOGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEEOGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m596.pep	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m596.pep	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQLEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQLEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m596.pep	SNYEYQKRNETQEIFIPVAERLGNIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
a596	SNYEYQKRNETQEIFIPVAERLGNIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
	310	320	330	340	350	360
	370	380	390	400	410	420
m596.pep	NGAGKSTLFRKMSISGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTLFRKMIAGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m596.pep	GQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGRHLAKTLLSGGNVLLDEPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSDQSKITGQLSGGERGRHLAKTLLSGGNVLLDEPSNDLDV					
	430	440	450	460	470	480
	490	500	510	520	530	540
m596.pep	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFDGNYQEYADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFDGNYQEYADKKRR					
	490	500	510	520	530	540
	550	559				
m596.pep	LGEEGAKPKRIKYPVTRX					
a596	LGEEGAKPKRIKYPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAAA CAGCGCGAGG CTGGGACAA ATTCCAAAAA

```

```

151 CTTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCC CGTTTCGTAT CGGGGAACCTA TAAAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCTTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGGAG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATTGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGCGCGGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaaaaagcc
601 gaaacaccgCA TTCaggAtgc ggAagcaaaa agaAAATTGG CTGAagCaa
651 aCtGgcggca gccgAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCGCGACG TCGGGAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 GGCAGAACCG GAGCGGcgGc GATGTTTGA AAGCGGTGTT CTATTCCACT
901 CGCGCTGCAA CGGTTGAAAG CATTGCGCcg gGAACggtaa GCTATGCCGA
951 cgaGTTGGAC GGCTACGGCA AAGTGGTCGT GATCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCCGT TTGAGCGAAA TTTCCGCGCG CAAGGGTTAT
1051 ACGGTCGCGG CAGGAAGCAA AATCGGCACg AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 CTTCCGGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

g597.pep

```

1 MLLHVSNSLK QLQEEIRIOE RIRQERIROA RGNLASVNRK QREAWDKFOK
51 LNTLNLRLKT EVAATKAQIS RFVSGNYKNS RPNALFLK NAEPGQKNRF
101 LRYTRVYNAS NREVVKDLEK QOKALAVQEQ KINNELARLK KIQANVSLL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAQ OKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISYIAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLQIRYRQ VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

m597.seq

```

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAACACAGC CGAGGCTTGG GACAAGTTCC AAAAACTCAA TACCGAGCTG
151 AACCCTTTGA AAACGGAAAGT CGCCGCTACG AAAGCGCAGA TTTCCCGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTC
251 TGAAGAACCG CGAACCGGGT CAGAAAAACC GCTTTTTCG TTATACGCGT
301 TATGTAAACG CCTCCAATCG GGAAGTTGTC AAGGATTGG AAAAACAGCA
351 GAAGGCTTTG GCGGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCCGTT
401 TGAAGAAAAT TCAGGCAAAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAGCCCGC AGACAGAAAT CCAAAATCGC
501 CAAAGATGCC CGAAAACTGC TGAACAGAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTG GAGAAGAAAA AGGCCGAACA CCGCATTGAG
601 GATGCCGGAAG CAAAAAGAAA ATTGGCTGAA GCCAGACTGG CGGCAGCCGA
651 AAAAGCCAGA AAAGAAGCGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
701 AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCGGGCAG AACCGGAGCG
851 GCGGCATAT TTGAAAAGGC GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAACTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAAGT GTCTGTGTCG ATCAGCGCGA GAACTACATC AGCATCTATG
1001 CCGGTTTGA GCGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GCTCGAGCGG GTCGCTGCCG GACGGGGGAG AGGGGCTTTA
1101 CCTGCAAATA CGTTATCAAG GTCAGGTATT GAACCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

m597.pep

```

1 MLLHVSNSLK QLQEEIRIOE RIRQARGNLA SVNRKOREAW DKFQKLNTL
51 NRLKTEVAAT KAQISRFVSG NYKNSQPNV ALFLKNAEPG QKNRFLRYTR
101 YVNASNREVV KDLEKQOKAL AVQEQKINNE LARLKKIQAN VQSLKKQGV
151 TDAEQTESR RONAKIAKDA RKLLEQKGNE QQLNKLNSL EKKKAHRIQ
201 DAEAKRLAE ARLAAAEKAR KEAAQOKAEA RRAEMSNLTA EDRNIQAPSV
251 MGIGSADGFS RMQGRLLKPV DGVPTGLFGQ NRSGGDIWKV VFYSTAPATV
301 ESIAPGTVSY ADELGYGKV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEGLYLQI RYQGQVLNPS SWIR*

```

950

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

	10	20	30	40	50	60
g597.pep	MLLHVSNSLKQLQEERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRKLT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNRKLT					
	10	20	30	40	50	
	70	80	90	100	110	120
g597.pep	EVAATKAQISRFVSGNYKNSRPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
g597.pep	QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
m597	QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
g597.pep	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
g597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
g597.pep	APATVESIAPGTVSYADELDGYGKVVVIDHGENYISYIYAGLSEISAGKGYTVAAGSKIGT					
m597	APATVESIAPGTVSYADELDGYGKVVVIDHGENYISYIYAGLSEISVGRGYMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
g597.pep	SGSLPDGEEGLYLQIRYRQGVLPNSGWIRX					
m597	SGSLPDGEEGLYLQIRYRQGVLPNSGWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

a597.seq

1	ATGCTGCTTC	ATGTCAGCAA	TTCCCTCAAG	CAGCTTCAGG	AAGAGCGTAT
51	CCGCCAAGAA	CGTATCCGCC	AAGAGCGTAT	CCGTGAGGCG	CGCGGCAACC
101	TTGCTTCCGT	CAACCGCAAA	CAGCGCGAGG	CTTGGGACAA	GTTCCAAAAA
151	CTCAATACCG	AGCTGAACCG	TTTGAACACG	GAAGTCGCCG	CTACGAAAGC
201	GCAGATTCC	CGTTTCGTAT	CGGGGAAC	TAAAAACAGC	CAGCCGAATG
251	CGGTTGCCCT	GTTCTGAAA	AACGCCGAAC	CGGGTCAGAA	AAACCGCTTT
301	TTGCGTTATA	CGCGTTATGT	AAACGCCCTC	AATCGGGAAG	TTGTCAAGGA
351	TTTGGAAAAA	CAGCAGAAGG	CTTGGCGGTT	ACAAGAGCAG	AAAATCAACA
401	ATGAGCTTGC	CGGTTTGAAG	AAAATTCAGG	CAAACGTGCA	ATCCCTGCTG
451	AAAAAACAGG	GTGTAACCGA	TGCGGCGGAA	CAGACGGAAA	GCCGCAGACA
501	GAATGCCAAA	ATCGCCAAAG	ATGCCCGAAA	ACTGCTGGAA	CAGAAAGGGA
551	ACGAGCAGCA	GCTGAACAAG	CTCTTGAGCA	ATTGAGGAAA	GAAAAAGGCC
601	GAAACCCGCA	TTCAAGGATG	GGAAGCAAAA	AGAAAATTGG	CTGAAGCCAG
651	ACTGGCGGCA	GCCGAAAAAG	CCAGAAAAAG	AGCGGCGCAG	CAGAAGGCTC
701	AAGCACGACG	TGCGGAAATG	TCCAACCTGA	CCGCCGAGAA	CAGGAACATC
751	CAAGCGCCTT	CGGTTATGGG	TATCGGCAGT	GCCGACGGTT	TCAGCCGCAT
801	GCAAGGACCT	TTGAAAAAAC	CGGTTGACGG	TGTGCCGACC	GGACTTTTCG
851	GCCAGAACCG	GAGCGGCGGC	GATGTTTGGG	AAGGCGGTGT	CTATTCCACT
901	GCACCGGCAA	CGGTTGAAAG	CATTGCGCCG	GGAACGGTAA	GCTATGCGGA

951

```

951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGTCGG CAAGGGTTAT
1051 ATGGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTTCGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

```

a597.pep
1  MLLHVSNSLK QLQEEIRQE RIRQERIROA RGNLASVNRK QREAWDKFQK
51  LNTLNLRLKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QOKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGG VLPSSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

a597.pep	10	20	30	40	50	60
m597	10	20	30	40	50	
a597.pep	70	80	90	100	110	120
m597	60	70	80	90	100	110
a597.pep	130	140	150	160	170	180
m597	120	130	140	150	160	170
a597.pep	190	200	210	220	230	240
m597	180	190	200	210	220	230
a597.pep	250	260	270	280	290	300
m597	240	250	260	270	280	290
a597.pep	310	320	330	340	350	360
m597	300	310	320	330	340	350
a597.pep	370	380	390			
m597	360	370	380			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

```
g601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGACGAA ATTGATGTGC CGAATATAGG
51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ACGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151 AACGATGCCG CCGCGCTGGA AAAATTTGAA ACCATCCGCG CATATGGCGC
201 GCTGAAAATG GGTTCGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251 GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTCGCGG TACGCGCCCT
351 GAGCATGGGC AAATGCAACC ACGCTATGAT GGGCATCGCC TCGGTGCGCA
401 TCGCGCGCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451 AC'GCGTAAAG AAGTGCCTT CGGGCATCCG TCAGGTACGC TCGGTGTCGG
501 TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGCGCGCc aaagcgtca
551 tgaGCCGCAG CGCACgcggtg attatggaaa gttgGGTGCg cgttcccgat
601 gattGTTTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

```
g601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101 SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
151 TRKEVRFGHP SGTLRVGAAA ECQDQQTAA KAVMSRSARV IMESWVRVPD
201 DCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

```
m601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTTCGCTG TACGCGCCCT
351 GAGCATGGGC AAATGCAACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCGCCGTA CCCGGTACGC TGGTCAACCT TGCCGAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCGG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTCATGAG CCGTAGCGCA CGCGTGATGA TGGAAGGTTG GGTCAGGGTG
601 CCTGAGGATT GTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

```
m601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFG HPSGTLRVGA AAECQDQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

	10	20	30	40	50	60
m601.pep	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
g601	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m601.pep	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					

953

```

g601      |||||
          TIRAYGALKMGLISDVSEAAARATPKPAFVAPAADYTASSGKTVNAADIDLPVRALSMG
          70      80      90      100     110     120

          130     140     150     160     170     180
m601.pep  KLHHAMMGTSVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
          |||||
g601      KLHHAMMGTSVAI--AAAVLGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
          130     140     150     160     170

          190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
          |:|||||:|:|||||:|
g601      AAKAVMSRSARVIMESWVRVPDDCFX
          180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51 CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
1 01 ATGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
1 51 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
2 01 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
2 51 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
3 01 AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTGCTGG TACGCGCCCT
3 51 GAGCATGGGC AAATTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
4 01 TTGCGACCGC CGCCGCCGTG CCCGGTACGC TGGTCAACCT TGCCGCAGGC
4 51 GCGGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
5 01 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
5 51 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGAAGGTTG GGTGAGGGTG
6 01 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51 NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
1 01 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
1 51 GGTRKEVRFH HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
2 01 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

          10      20      30      40      50      60
m601.pep  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          |||||
a601       MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          10      20      30      40      50      60

          70      80      90      100     110     120
m601.pep  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
          |||||
a601       KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
          70      80      90      100     110     120

          130     140     150     160     170     180
m601.pep  KLHHAMMGTSVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
          |||||
a601       KLHHAMMGTSVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
          130     140     150     160     170     180

          190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
          |||||
a601       ATKAVMSRSARVMMEGWVRVPEDCFX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTTCTGCT
51  CGGCAGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTCAT GCGTTGTTTG TCCTTAATAT TCAGATAATT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCCTGCAAA Tgcgagatta TATCACTGTC TTTtggcgcg TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
1  MLLHQCDKAR HMRPFLGGQ INRHRQASNR GLCSFGGFQG NREAQVFNAD
51  LIDRQIAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLsAA
101 CLQMRDYITC FWRHL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
1  ATGTTGCTCC ATCAATGCGA CAAACGCGA CATATGCGTC CCCTTCTGCT
51  CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTCAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
1  MLLHQCDKTR HMRPLLSRQ VNRHGQTGNG GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVs AGEYTVNLQM
101 RDYITRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPFLLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	: : : :: : : : : :					
g602	MLLHQCDKARHMRPFLGGQINRHRQASNRGLCSFGGFQGNREAQVFNADLIDRQVAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHVIIVEMCAWYGVSA-GEYTVN---LQMRDYITRF*QLHX					
	: : : : : : : : :					
g602	AGLHVCNGVHALFVLNIQIIEMCVLYGRQMPSEKTLsAACLQMRDYITCFWRHLX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
51  CGGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTCAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
1  MLLHQCDKAR HMRTLLGRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVs TGEYTVNLQM
101 RDYITRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

955

	10	20	30	40	50	60
m602. Pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNGLDAFCSLQGNRKAQVFDLIDRQIAQIS					
a602	MLLHQCDKARHMRPLLLGRQVNRHGQTGNGLDAFCSLQGNRKAQVFDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602. Pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSAEYTVNLQMRDYITRFQQLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFQQLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603. seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTTT
101 CAGACGCCCC CGCACCAAAA AAACAACCAC AACTACAAG GAGAAACATC
151 ATGTCGACCC AACTATTCTT TGTCCTGAAC TCGGTCAGTT CATCGCTCAA
201 AGGCGCGGTT ATCGACCGCA AAAGCGGCAG CGTCGTCTTA AGTGCCTCG
251 GGGAAACGCT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCCTT GAGCGCGCGC AACTGCCACG CCGCGCGGTT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCAGGCGC GCGAAAAATA TCACGAGTCC
451 GTCCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCGCTG CACAACCCCG CCAACATCAG CGGCATCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTGCGCG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCGCG GCGAATTGCG
651 CAAAAAATAC GCCTTCCGCC GCTACGGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
751 CGCATGATTA TTGCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTACGCGCG ATCGAAGGTT
851 TGGTAATGGG TACACGTTGC GGCAGACCCG ATCCGGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GTTTCCCGG GTATTTCCga actTCCCAAC GACTGCCGCA
1001 CCTCGAAAT CGCCGCGGAC GAAGGCCGCG AAGGCGCGCG CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCTT CGCAAATAC ATCGCTTGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTCAC CGGCGGTATC GGCGAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCCT ATCTTGATT CTGGGCTCTG
1201 CACATCGACA CCAAAGCCAA TATGGAAAAA CGTACGGCA ATTCGGGCAT
1251 TATCAGCCCG ACCGATCTT CTCGGCTGT TTTGGTCGTC CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCG CATCTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603. pep

```

1  MDSRLRGND RYKIRFAQR GRLKHTPPNA HPFSDGPAPK KQPQTRRNI
51  MSDQILILVN CVSSSLKGAV IDRKSGSVVL SCLGERLTPP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPANISGIL AAQEHFPGLP NVGVMDSFHF
201 QTMPEAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLGNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISSELPN DCRTLEIAAD EGREGARLAL
351 EVMTCLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDPLGL
401 HDTKANMEK RYGNISGIISP TDSSPAVLVV PTNEELMIAC DTAELAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603. seq

```

1  CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACCT TCGCCTGAT GTCTGC.CTT
101 TTTGAGACGA CCCACACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGCGGCC GTTATCGACC GAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCACG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```

m603.ppt

```

1  LSSRRRGRNN DRKCGIRFAQ RGRLKHLAPD VCXFSDDPTL KKQPQTTRRN
51  IMSDQILILVL NCGSSSLKGA VIDRXSGSVV LSLCLGERLTT PEAVITFNKO
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHGL HDRIKAIGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHNPAINTSGI LAAQEHFPGL PNVGVMDTSF
201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ARILGKPLED
251 IRMIIAHLGN GASITAKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
301 YLTSHAGMDV AQVDEMLNKK SGLLGISES NDCRTLLEIAA DEBGEGARLA
351 LEVMTYRLAK YIASMAVCGC GVDALVFTEG IGENSNRIRA KTVSYGLDFLG
401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELAGIL
451 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 603 shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng) from *N. gonorrhoeae*:

m603/g603

	10	20	30	40	50	60
m603.pep	LSSRRRG	RNRDKCGIR	FAQGRGLKHL	APDVCFSD	DDPTLKKQ	PQPTRRNIMSDQLILVL
	:	:	:	:	:	:
g603	MDSRLRG	-NDARKYGIR	FAQGRGLKHT	PPNAHPFSD	GDPAPKKQ	PQPTRRNIMSDQLILVL
	10	20	30	40	50	
	70	80	90	100	110	120
m603.pep	NCGSSSLK	GAVIDRXSGSV	VLSC	LGRLTTPEAV	ITFNKDG	NKRQVPLSGRNCHAGAVGM
	:	:	:	:	:	:
g603	NCVSSSLK	GAVIDRXSGSV	VLSC	LGRLTTPEAV	ITFNKDG	NKRQVPLSGRNCHAGAVGM
	60	70	80	90	100	110
	130	140	150	160	170	180
m603.pep	LLNELEKH	GLHDRIKAIGH	RIAHGGEKY	SESVLIDQAV	MDLNA	CIPPLPHNPANISGI
	:	:	:	:	:	:
g603	LLNELEKH	GLHDRIKAIGH	RRIAHGGEKY	SESVLIDQD	VLDELKACIP	PFAPLPHNPANISGI
	120	130	140	150	160	170
	190	200	210	220	230	240
m603.pep	LAAQEHF	PGLPNVGVM	DTSFHQ	TMPERAYT	YAVPREL	RKKYAFRRYGFGHTSMRYVAEPA
	:	:	:	:	:	:

957

```

g603      LA AQEHFPPLNVGVMDTSFHQTMPERAYTVAPRELKKYAFRRYGFGHTGMRMYVAPEA
          180           190           200           210           220           230

                250           260           270           280           290           300
m603.pep   ARILGKPLEDIRMIIAHLGN GASITAIKN GKSVDS TSMGF TP I EGLVMGTRCGDIDPGVYS
            |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g603       ARILGKPLEDIRMIIAHLGN GASITAVKN GKSVDT GMGF TP I EGLVMGTRCGDIDTPGVYS
          240           250           260           270           280           290

                310           320           330           340           350           360
m603.pep   YLTSHAGMDVAQVDEMLNKKSGLLGIS EL SNDCRTLEIAADEGHEGARLALAEVMTYRLAK
            |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g603       YPTFFHAGMDVAQVDEMLNEKSGFPGIS EL PNDCRTLEIAADEGREGARLALAEVMTCLRAK
          300           310           320           330           340           350

                370           380           390           400           410           420
m603.pep   YIASMAVGCCGVDALVFTGGIGENS RNIRAK TVSYLD FLGLH IDTKANMEKRYGNSGIIS
            |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g603       YIASMAVACGSVDALVFTGGIGENS RNIRAK TVSYLD FLGLH IDTKANMEKRYGNSGIIS
          360           370           380           390           400           410

                430           440           450
m603.pep   PTDSSPAVLVVPTNEELMIACDTAELAGILX
            |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g603       PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420           430           440           450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```
a603.seq
1 CTGTCTCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51 CTTTGGCCCAA AGAGGCCGTC TGAAACACAC TCCGCCCAAC GCCCATCCTT
101 TTTCAGACGA CCCACACCC. AAAAAACAAC CACAAACTAC AAGGAGAAAT
151 ATCATGTCCG ACCAACTCAT TCTTGTCTGT AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAAGC CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAACG GCCAAGTTCC CCTGAGCGGC CGGAACCTGCC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGAAAA ACACGAACCTG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG CGCGCGAAAA ATACACGCGAG
451 TCTGTTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATTT CCCCGGTCTG CCCAATGTCG GCGTGATGGA TACTTCGTTT
601 CACCAAAACCA TGCCGAGCG TGCCTACACT TATGCCGTGCA CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCGCGTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GCGCATCCA TTACGCCCAT
801 CAAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGGTACGCGC TCGCGCGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTT CGAACTCTCC AACGACTGCC
1001 GCACCTTCGA AATCGCCGCG GACGAAGGCC ACGAAGGCCG GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGCGTCGCGC GGCCTTGACG CACTCGTGTT CACCGCGGCT ATCGGCGAAT
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGCG TGTTTTGTTT GTCCCGACCA
1301 ATGAAGAAGT GATGATTGCC TGCACACTG CCGAACTTGT CGGCATCTTG
1351 TAG
```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

a603.pep

1	LSSRRRGRNN	DRKCGIRFAQ	RGRLKHTPPN	AHPFSDDPXTX	KKQPQTTRRN
51	IMSDQLLVL	NCGSSSLKGA	VIDRKSGSVV	LSCIGLERLTT	PEAVITFSKD
101	GNKRQVPLSG	RNCHAGAVGM	LLNELEKHEL	HDRIQAVGHR	IAHGGEKYDE
151	SVLIDQAVMD	ELNACIPLAP	LHNPNANISGI	LAAQEHFPGL	PNVGVMDSF

958

201 HQTMPERAYT YAVPRELRKK YAFRRYGFGH TSMRYVAPEA ACILGKPLED
 251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
 301 YLTSHAGLDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA
 351 LEVMTYRLAK YIASMAVGCG GVDALVFTGG IGENS RNIRA KTVSYLDFLG
 401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELVGIL
 451 *

m603/a603 96.7% identity in 450 aa overlap

	10	20	30	40	50	60
m603.pep	LSSRRRGRNDRKCGIRFAQRGRKLHAPDVCKFSDDPTLKKQPQTRRNIMSDQLILVL					
a603	LSSRRRGRNDRKCGIRFAQRGRKLHAPDVCKFSDDPTLKKQPQTRRNIMSDQLILVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m603.pep	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGNGKRVPLSGRNC HAGAVGM					
a603	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFSKDGNGKRVPLSGRNC HAGAVGM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m603.pep	LLNELEKHGLHDRIKAIGHRIA HGGEKYESVLIDQAVMDELNACIPLAPLHN PANISGI					
a603	LLNELEKHGLHDRIKAIGHRIA HGGEKYESVLIDQAVMDELNACIPLAPLHN PANISGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m603.pep	LAAQEHFPGLPNVGVM DTSFHQTMPERAYTYAVPRELRKKYAFRRYGFGH TSMRYVAPEA					
a603	LAAQEHFPGLPNVGVM DTSFHQTMPERAYTYAVPRELRKKYAFRRYGFGH TSMRYVAPEA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m603.pep	ARILGKPLEDIRMIIAHLGN GASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
a603	ACILGKPLEDIRMIIAHLGN GASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m603.pep	YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAA DEGHEGARLA LEVMTYRLAK					
a603	YLTSHAGLDVAQVDEMLNKKSGLLGISELSNDCRTLEIAA DEGHEGARLA LEVMTYRLAK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m603.pep	YIASMAVGCGGVDALVFTGGIGENS RNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
a603	YIASMAVGCGGVDALVFTGGIGENS RNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
	370	380	390	400	410	420
	430	440	450			
m603.pep	PTDSSPAVLVVPTNEELMIACDTAELAGILX					
a603	PTDSSPAVLVVPTNEELMIACDTAELVGILX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:

g604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
 51 CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCATC
 101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT
 151 GTCGGCGGCG TTTACGGTTT TGCCGCTGGA GGCGGTGTAA TCGGCGGCGG
 201 GCGCGACGAA GGCGGGTTTC GCGGTGCGCG CGCGGGCGGC GGCTTCGGAT

959

251 ACCTCGCTGA TCAAACCCAT TTTCAGCGCG CCATATGCGC GGATGGTTTC
 301 AAATTTTCC AGCGCGGCGG CATCGTTGTT GATGTCGTCC TGCAACTCTT
 351 TGCCCGTGTA GCCCAAGTCG GCGGCGTTCA GGAAAACGGT CGGAATGCCC
 401 GCGTTGATGA GCGTGCTTT CAGACGACCT ATATTGGCA CATCAATTTC
 451 GTCGACCAA TTGCCGTTG GGAACATACT GCCTTcgCG TCGGCTGGAT
 501 CTA

This corresponds to the amino acid sequence <SEQ ID 1902; ORF 604.ng>:

g604.pep

1 MPEAHFFTRS AACGKVDQRT EHGGGDGDRG DAHHSVVQFA HAQAYRQID
 51 VGGVYGFAG GVGIGGRDE GGFRRARAGG GFGYVADQTH FQRAICADGF
 101 KFFQGGIVV DVVLQLFARV AQVGVQENG RNARVDERGF QTTYIRHINF
 151 VDQIAGWEHT AFAVGWI*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1903>:

m604.seq

1 ATGCCCCAAG CGCACTTCTT TACGCGTTCC GCCGCTGCG GCAAGGTTGA
 51 CCAGCGTACC GGTACGCGG GCGGCGGTCG CAATGGCAAC AGAGGCGGTA
 101 CCATCATCG CGTGGTGCA TTTGCCCATG CTCAGGGCGC GTACCAGCAA
 151 ATCGATGTCG GCGGCGTTCA CGGTTTGGC ACTGGAGGCG GTGTAATCGG
 201 CGGCGGGCGC GACGAAGCG ACTTTCGGCG TGTGCGCGC AGCGGCAGCT
 251 TCGGATACGT CGCTGATCAG ACCCATTTT AGCGCACCGT AAGCGCGGAT
 301 TTTCTCGAAT TTTCCAAAG CCGCGGCATC GTTGTGATG TCGTCTTGCA
 351 ACTCTTTGCC TGTGTAGCC AAGTCGGCG CATTCAAGAA AACGGTCGGA
 401 ATGCCCCGCT TGATGAGCGT GGCTTTCAA CGGCCTATAT TCGGCACATC
 451 AATTTTCATG ACCAAATTGC CGTTTGGGAA CATACTGCCT TCGCGTCGG
 501 CTGGATC

This corresponds to the amino acid sequence <SEQ ID 1904; ORF 604>:

m604.pep

1 MPEAHFFTRS AACGKVDQRT GYGGGGRNGN RGGTHHRVQ FAHAQAYQQ
 51 IDVGGVHGFA TGGVIGGGR DEGDFFRVRA SGSFGYVADQ THFORTVSAD
 101 FLEFFQSRGI VDVVLQLFA CVAQVGGIQE NGRNARVDER GFQYAIRHI
 151 NFIDQIAGWE HTAFAVGWI

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng) from *N. gonorrhoeae*:

m604/g604

	10	20	30	40	50	60
m604.pep	MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVQFAHAQAYQQIDVGGVHGFA					
g604	MPEAHFFTRSAACGKVDQRTTEHGG--DGDGDAHHSVVQFAHAQAYRQIDVGGVYGF					
	10	20	30	40	50	
	70	80	90	100	110	120
m604.pep	TGGGVIGGRDEGDFFRRVRASGSFGYVADQTHFORTVSADFLEFFQSRGIVDVVLQLFA					
g604	AGGGVIGGRDEGGFRRARAGGFGYVADQTHFQRAICADGFKFFQRGIVDVVLQLFA					
	60	70	80	90	100	110
	130	140	150	160	169	
m604.pep	CVAQVGGIQENGRNARVDERGFQYAIRHINFIDQIAGWEHTAFAVGWI					
g604	RVAQVGGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAFAVGWIX					
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1905>:

a604.seq

1 ATGCCCCAAG CGCACTTCTT TACGCGTTCC GCCGCTGCG GCAAGGTTGA
 51 CCAGCGTACC GGGCACGGCG GCGGCGGTCG CAATGGCAAC AGAGGCGGTA
 101 CCCATCATCG CGTGGTGCAA TTTGCCCATG CTCAGGGCGC GTACCAGCAA
 151 ATCGATGTCG GCGGCATTCA CGGTTTGGC ACTGGAGGCG GTGTAATCGG

960

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201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GCGGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGATG TCGTCTTGCA
351 ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTGAGGAA AACGGTCGGA
401 ATGCCCAGCGT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
451 AATTTTCATCG ACCAAATTGC CGGTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATCAAG AAATTTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551 TCGAGCTCAA AATCGCCTGT TTCCAAACT GCGCCGTTT GCATCGGTAC
601 ATGGGCAATA ATGGTTTTGC CGATGTTTT CTGCCAGATT TTGACTGTGC
651 AGATGCCGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
1 MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51 IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFORTVSAD
101 FLEFFQSCGI VVDVVLQLEA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFVGVWIK KFDLYFGCRE RYAVELKIAC FQNCVLRHY
201 MGNGFADVF LPDFDCADAV *

```

m604/a604 97.0% identity in 169 aa overlap

	10	20	30	40	50	60
m604.pep	MPEAHFFTRS AACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA					
a604	MPEAHFFTRS AACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA					
	10	20	30	40	50	60
m604.pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFORTVSADFLEFFQSRGIVVDVVLQLEA					
a604	TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFORTVSADFLEFFQSCGIVVDVVLQLEA					
	70	80	90	100	110	120
m604.pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFORTVSADFLEFFQSRGIVVDVVLQLEA					
a604	TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFORTVSADFLEFFQSCGIVVDVVLQLEA					
	70	80	90	100	110	120
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIK					
a604	RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIKKFDLYFGCRE					
	130	140	150	160	169	
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIK					
a604	RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIKKFDLYFGCRE					
	130	140	150	160	170	180
a604	RYAVELKIACFQNCVLRHYMGNGFADVF LPDFDCADAVX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATCtacCc cgGCCAGCTT TTTTgcaata ttgccgccga agcCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGaa atCTTTACCG CGATTGAAAG
351 CTCCGCTCC GGCTAcccgT CCGAACAAGG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAC
451 AAACGCCTTG CCGCCGTCCT TAAAGGCGTG GCGGAACTCG ATTTTCGGCAA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTTCCAATA CGCgcCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTCAAC AAAATCTACG ACCCCGCCTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACACAC CACCTACAAC CTCGCCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GCGGACACGC
851 TGACCAACCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT

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951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCGCGCTA TCGTCTCATT CCCCGGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCGCA AATCGTCAAA CTCTTCGCGG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCGGTCAGC AGCTATGTG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQORAO LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNNTKLKE IFTAIESSAS GYPSEQGIKG LFDDEFDTTSS RLGSTVADKN
151 KRLA AVLKGV AELDFGNFED HRIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIIIEGFF
251 GQEIHNHTTYN LARMNMFHVN VNYNKFHIEL GDTLTNPKLK DSKPFDVVVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPFI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTCAIVNI
401 LVL SKHKDNT DIQFIDASGF FKKETNNNVL TEEHIAEIVK LFPADKADVP
451 IAQNAAQQT V KDN GYNLA VS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTCACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCGGCTA TGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCGCA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACC GATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACGTGTCG CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGGCGTG GCGGAACTCG ATTTCGGCAA
501 TTTTGAAAAA CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAAC TA CGCTGCCAAC GCAGGCAAAT CCGCGGCGCA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GGCAGACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCGGCCA TCGTCTCATT CCCCGGCATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCGG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCGGTCAGC AGCTATGTG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQORAO LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

```

101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
 151 KRLA AVLKGV AELDFGNFEN HHIDLFGBAY EYLISNYAAN AGKSGGEFFT
 201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLQAKKQF DEHIEEGFF
 251 GQEIHTTYN LARMNMFHN VNYNQFHIEL GDTLTNPCLK DSKPFDAIVS
 301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAL HALNYLSGRG
 351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
 401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL IEEHIAEIVK LFADKADVP
 451 IAQNAAQQT V KONGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER
 501 LRREIDEVIA EIEA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng)

from *N. gonorrhoeae*:

m605/g605

	10	20	30	40	50	60
m605.pep	MMTEMQRAQLHRQIWKIADEVIRGAVDGVDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
g605	MMTEMQRAQLHRQIWKIADEVIRGAVDGVDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVGKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
g605	YAAMPDSIITPEIKDDAVKVGKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKKNKRLA AVLKGV AELDFGNFENHHIDLFGBAY					
g605	GYPSEQDIKGLFDDFDTTSSRLGSTVADKKNKRLA AVLKGV AELDFGNFEDHRIDLFGBAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m605.pep	EYLISNYAANAGKSGGEFFT PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF					
g605	EYLISNYAANAGKSGGEFFT PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m605.pep	DEHIEEGFFGQEIHTTYN LARMNMFHN VNYNQFHIELGDTLTNPCLKDSKPFDAIVS					
g605	DEHIEEGFFGQEIHTTYN LARMNMFHN VNYNQFHIELGDTLTNPCLKDSKPFDAIVS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAL HALNYLSGRGRAAIVSFPGI					
g605	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAL HALNYLSGRGRAAIVSFPGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNL FYGTGIAVNI LVLSKHKDNTDIQFIDASGF					
g605	FYRGGAEQKIRQYLVEGNYVETVIALAPNL FYGTGIAVNI LVLSKHKDNTDIQFIDASGF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m605.pep	FKKETNNNVLEEHIAEIVKLFADKADVP HIAQNAAQQT VKONGYNLAVSSYVEAEDTRE					
g605	FKKETNNNVLEEHIAEIVKLFADKADVP HIAQNAAQQT VKONGYNLAVSSYVEAEDTRE					

	430	440	450	460	470	480
	490	500	510			
m605.pep	I I D I K Q L N A E I G E T V A K I E R L R R E I D E V I A E I E A X					
	: : : :					
g605	V I D I R Q L N A E I S E T V A K I E R L R R E I D E V I A E I E T X					
	490	500	510			

a605.s eq

This corresponds to the amino acid sequence <SEQ ID 1912: ORF 605.a>:

a605.pcp

1	MMTEIQRAQ	LHRQIWKIAD	EVRGAVDGDW	FKQYVLGTLF	YRFISENFTD
51	YMQAGDSSID	YAAMPDSIIT	PEIKDDAVKV	KGFYIYPGQL	FCNIAAEAHQ
101	NEELNTKLKE	IFTAIESSAS	GYPSEQDIKG	LFDDFDTTSS	RLGSTVADKN
151	KRLAALVKGV	AELDGFSGED	HHIDLFGDAY	EYLLISNYAAN	AGKSGGEFFT
201	PQSUVKLIAR	LAVHGOKEVN	KIYDPACGSG	SLLLQAKKQF	DEHIIIEGGF
251	GQEIHNHTYIN	LARMNMFLHN	VYNNKFHIEL	GDTLTNPKLK	DSKPFDAVVS
301	NPPYSINWIG	SGDPTLINDD	RFAPAGVLAP	KSKADFAFIL	HALNYLSGRG
351	RAAIVSFPGI	FYRGGAEQKI	RQYLVEGNYV	ETVIALAPNL	FYGTGIAVNI
401	LVLSKHKDNT	DIQFIDAGGF	FKKETNNNVL	TEEHIAEIVK	LFADKADVPH
451	IAQNAAQQTQ	KDNGYNLAVS	SYVEPEDTRE	IIDIKQLNAE	ISSETVAKIER
501	LRREIDEVIA	EIEA*			

m605/a605 98.1% identity in 514 aa overlap

```

      10          20          30          40          50          60
m605.pep    MMTEMQQR AQLHRQIWKIAD EVRGAVD GWD F KQYVLGT L FYRFI S ENFTDYMQAGDSSID
             |||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a605        MMTEIQQR AQLHRQIWKIAD EVRGAVD GWD F KQYVLGT L FYRFI S ENFTDYMQAGDSSID
             10          20          30          40          50          60

              70          80          90         100         110         120
m605.pep    YAAMPDSIITPEIKDDAVKVKGYFIYPGOLF C NIAAEAH QNEELNTKLKEIFTAIESSAS

```

a605	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS	70	80	90	100	110	120
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEALDFGNFENHHIDLFGDAY	130	140	150	160	170	180
a605	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEALDFGSFEDHHIDLFGDAY	130	140	150	160	170	180
m605.pep	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF	190	200	210	220	230	240
a605	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF	190	200	210	220	230	240
m605.pep	DEHIIIEGFFGQEIINHHTYNLARMNMFHLNVNYNQHFIELGDTLTNPKLKDSKPFDAIVS	250	260	270	280	290	300
a605	DEHIIIEGFFGQEIINHHTYNLARMNMFHLNVNYNKFHIELGDTLTNPKLKDSKPFDAVVS	250	260	270	280	290	300
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI	310	320	330	340	350	360
a605	NPPYSINWIGSGDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI	310	320	330	340	350	360
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF	370	380	390	400	410	420
a605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDAGGF	370	380	390	400	410	420
m605.pep	FKKETNNNVLIEEHIAEIVKLFADKADVPHIAQNAAQQTVKDNGYNLAVSSYVEAEDTRE	430	440	450	460	470	480
a605	FKKETNNNVLTEEHIAEIVKLFADKADVPHIAQNAAQQTVKDNGYNLAVSSYVEPEDTRE	430	440	450	460	470	480
m605.pep	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX	490	500	510			
a605	IIDIKQLNAEISSETVAKIERLRREIDEVIAEIEAX	490	500	510			

g606.seq

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNFATGAS RNSSLIAVST GLLDHMTRE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKS*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGCGGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTGCGGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCCT GGTCAGCATG GTATTCCAAA TCCTGTTCGG CTTCCTTGCC
451 AGCTTAATG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
501 GGGCGCGGCA AAACCTGGTC GCGCGCGGAA AATGATTTCC GCCCTGCAAA
551 GGCTCAAAGG CAACCCGGTC GATTGCCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCACC CTTCGCTGGA
651 CAACCGTATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNFATGAS RNSSLIAVST GLLDHMTRE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

m606.pep	10	20	30	40	50	60
	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPPEVAIYHSPEPNFATGAS					
g606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPPEVAIYHSPEPNFATGAS					
	10	20	30	40	50	60
m606.pep	70	80	90	100	110	120
	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTLTLIQGVNTFVVFLSRIIAN					
g606	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTLTLIQGVNTFVVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	130	140	150	160	170	180
	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	190	200	210	220		
	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSIX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSIX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```

1   ATGTCCAAAT TCATCGCCAA ACAATCGGTC GGCGCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTGTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTGAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGACGC
501 GGGCGCGGCA AAACCTGGTC GCGCGCCGAA AATGATTTCG GCCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCACC CTTCGCTGGA
651 CAACCGAATC GCCGCGCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1   MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTI
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

m606/a606 100.0% identity in 226 aa overlap

	10	20	30	40	50	60
m606.pep	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPPEVAIYHSPPEFNAFATGAS					
a606	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPPEVAIYHSPPEFNAFATGAS					
	10	20	30	40	50	60
m606.pep	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTITLIQGVVNTFVFLSRIIAN					
a606	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTITLIQGVVNTFVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTITLIQGVVNTFVFLSRIIAN					
a606	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTITLIQGVVNTFVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
a606	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
a606	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
a606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```

g607.seq
1   ATGCTGCTCG accTgaCCG CTTTTCCTtt tccGTCTTCC TGAAAGAAAT
51  CCGCCTGCTG ACCGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTGCGCG
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGATTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGCTGATTTT GGGGATTTTC GGATGATTT TGATGTGGGC
351 GGCGATTACG CCGTTCGCGA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG
401 gcacAAtggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCGCGG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGTGCGGCA

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601 GGTTCGCGCG TGGCGACAAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
 651 GTGGATTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGACTGACAG
 701 CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
 751 gGcgcgCCCA TCGGGCTGTC TTATTTTTTG GAAGccaGcg cGTTTTCGTT
 801 TATCGTGTtT TTGATTGCGC CtttcggCGA GGATTATGTG GCGGCGCAGC
 851 AGGTCGGCAT CAGTTTGTG GGGATTCTCT ATATGATTCC GCAAAGCGTC
 901 GGCTCGGCAG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
 951 TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTG GGCTGGGTGC
 1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTT CCGCTGGCA
 1051 AGCATGTACA ACGATGaTCC GGCAGTTTA AGCATCGCCT CCACCGTCTT
 1101 GCTGTTTCGCC GGCCTGTtcc aACCGGCAGA CTTCAACCAA TGTATCGCGT
 1151 CCTATGCCCT GCGCGGCTAC AAAGTACCA AGGTGCCGAT GTTCATCCAC
 1201 GCGCGCGCCT TCTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
 1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
 1301 TCACCATCGC AGCCGTCGCC TTGGTGTGGT GCTTGGAAAA ATACAGTATG
 1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

1 ML^{LDLDRFSF} SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTMAGGAGK
 51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
 101 IWFGILIGIF GMILMWAAT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
 151 MVHRAHLHAYA SSLNRPRILIM LVSPFAFVLN VPLNYIFVYG KFGMPALGGA
 201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
 251 GAPIGLSYFL EASAFSIFV LIAPFGEDYV AAQQVGISLS GILYMPIQSV
 301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFERSPLA
 351 SMYNDPAVL SIASVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
 401 AA^{AFWGCGLL} PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
 451 ELVKSHKAV*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

1 ATGCTGCTCG ACCTCAACCG CTTTTCTTTT CCGTCTTCC TGAAAGAAGT
 51 CCGCCTGCTG ACCACTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTGCGCG
 101 AGGTGGGCAT CGGTTTTGTC GATACTGTGA TGGCGGGCGG TCGGGGCAAG
 151 GAAGACTTGG CCGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
 201 TATTACCTTT ATGGGCATTA TGGCGCGCT GAACCCGATG ATTGCCCAGC
 251 TTTACGGCGC GGTA^{AAACC} GACGAAGTGG GCGAAACGGG GCGGCAGGGG
 301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTC GGCATGGTCT TGATGTGGGC
 351 GCGGATTACG CGGTTCCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
 401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT GCCGGCGGCA
 451 ATGGTACACC GCGCGCTGCA CGCCTACACT TCCAGCCTGA ACCGCCCGCG
 501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
 551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
 601 GGCTGCGGAC TGGCGACGAT GGC^{GTGTTT} TGGTTCAGCG CGCTGGCATT
 651 GTGGATTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGACTGACCG
 701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAAAATC
 751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCGTT
 801 TATCGTGTtT TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
 851 AGGTCGGCAT CAGTTTGTG GGGATTCTCT ATATGATTCC GCAAAGCGTC
 901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
 951 TTCGCGGGCG CGTTATATTT CCGGCGTGTC ACTGGTGTTA GGATGGATGC
 1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTT CCGCTGGTA
 1051 AGTATGTACA ACAATGATCC GCGGTTTTTA AGCATCGCGG CCACCGTCTT
 1101 ACTGTTTCGCC GGCTTGTTC AACC^{GGCAGA} CTTCAACCAA TGTATCGCCT
 1151 CCTACGCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
 1201 GCCCGCGCCT TTTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
 1251 CCGTTTCAAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
 1301 TCACCATCGC CGCATCGCC TTGGTGTGGT GCTTGGAAATT GTGCAGTAGG
 1351 GAGATGGTCA GATCGCATAA GGCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

1 ML^{LDLNRFSF} PVFLKEVRLT TTLALPMLLA QVAQVGIGFV DTMAGGAGK
 51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

968

101 IWFGFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
 151 MVHRLHAYT SSLNRPRIM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
 201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
 251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIQSV
 301 GSAGTVRIGF SLGRREFSRA RYISGVSLVL GWMLAVITVL SLVLFPSPLV
 351 SMYNNDFAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMTIH
 401 AAAPWGCGLL PGYLLAYRFN MGIYGFWTAL IASLTIAAIA LVWCLELCSR
 451 EMVRSHKAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng) from *N. gonorrhoeae*:

m607/g607

m607.pep	10	20	30	40	50	60
	MLLDLNRFSFPVFLKEVRLLTTLALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
g607	MLLDLDRFSFSVFLKEIRLLTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	70	80	90	100	110	120
	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGLFLGVFGMVLWMAAIT					
g607	SAFATVYITFMGIMAALNPMIAQLYGAGKTGEAGETGRQGIWFGLILGIFGMILWMAAIT					
	70	80	90	100	110	120
m607.pep	130	140	150	160	170	180
	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAMVHRLHAYTSSLNRPRIMLVSFAAFVLN					
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAMVHRLHAYASSLNRPRIMLVSFAAFVLN					
	130	140	150	160	170	180
m607.pep	190	200	210	220	230	240
	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD					
g607	VPLNYIFVYGKFGMPALGGAGCGVATMAVFWFSALALWIYIAKEKFFRPFGLTAKFGKPD					
	190	200	210	220	230	240
m607.pep	250	260	270	280	290	300
	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIQSV					
g607	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIQSV					
	250	260	270	280	290	300
m607.pep	310	320	330	340	350	360
	GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMLAVITVLSLVLFPSPLVSMYNNDFAVL					
g607	GSAGTVRIGFSLGRREFSRARYISGVSLVSGWVLAVITVLSLVLFPSPLASMYNNDFAVL					
	310	320	330	340	350	360
m607.pep	370	380	390	400	410	420
	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMTIHAAAPWGCGLLPGYLLAYRFN					
g607	SIASVLLFAGLFQPADFTQCIASYALRGYKVTKVPMTIHAAAPWGCGLLPGYLLAYRFD					
	370	380	390	400	410	420
m607.pep	430	440	450	460		
	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX					
g607	MGIYGFWTALIASLTIAAVALVWCLEKYSMELVKSHKAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GACGAAGTGG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTT GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCGA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCCA GCTTGCGCAT GCCGGCGGCA
451 ATGTTACACC GCGCACTGCA CGCCTACGCC TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTCTT CCGCCCATTC GGACTGACCG
701 CGAATTCGG CAAACCGAT TGGGCGGTGT TCAAACAGAT TTGAAAAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCTGT
801 TATCGTGTTC TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTGCGGCG GGACGGTGCG CATCGGCTTT TCGCTGGGCG GCGCGCAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTCG GGATGGATGC
1001 TCGCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGTA
1051 AGTATGTACA ACAATGATCC GGCGGTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTCCGC GGCTTGTTCC AACCGGCAGA CTTACCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCGCCGCCT TTTGGGCTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCCG
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1  MLLDLNRFSE SVFLKEVRLL TALALPMLLA QVAQVGIGFV DTVMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFLFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRAHAYA SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSEIVF LIAPFGEDYV AAQQVGISLS GILYMIPQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFSPILV
351 SMYNDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFMFIH
401 AAFFWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCRS
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSPFVFLKEVRLLTTALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
a607	MLLDLNRFSPFVFLKEVRLLTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFLFLGVFGMVLMWAAIT					
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFLFLGVFGMVLMWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRAHAYTSSLNRPRILMLVSFAAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRAHAYASSLNRPRILMLVSFAAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240

970

```

m607.pep      VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
a607          VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
              190      200      210      220      230      240

              250      260      270      280      290      300
m607.pep      WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPOSV
a607          WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPOSV
              250      260      270      280      290      300

              310      320      330      340      350      360
m607.pep      GSAGTVRIGFSLGRREFSRARYISGVSLVGLWMLAVITVLSLVLFRSPLVSMYNNDPAVL
a607          GSAGTVRIGFSLGRREFSRARYISGVSLVSGWMLAVITVLSLVLFRSPLVSMYNNDPAVL
              310      320      330      340      350      360

              370      380      390      400      410      420
m607.pep      SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPFIHAAAFWGCGLLPGYLLAYRFN
a607          SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPFIHAAAFWGCGLLPGYLLAYRFD
              370      380      390      400      410      420

              430      440      450      460
m607.pep      MGIYGEFTALIASLTIAAIALVWCLELCSREMVRSHKAVX
a607          MGIYGEFTALIASLTIAAIALVWCLELCSREMVRSHKAVX
              430      440      450      460

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

```

g608.seq
1   ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCGCA ACAGCGCGAT
201 ACGGAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACgA ATTGGCACGG ATTTTCGGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCATcaaa cAAATCGGCA
401 GGAACATCGC CGAACAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
551 ACATTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

```

g608.pep
1   MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LQGGEPEGAGD IRLEGDLILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

```

m608.seq
1   ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGCAG CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAATC GGCGGATTTT CCCGCGAATC CGAGTCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

```

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGLLIG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRS ELAAFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
g608	MSALLPIINRLILQSPDSRSELT SFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEPEGAGDIGLEGLLIGIAVLSLLGSLRSRASDELARIFGTQADIGS					
g608	TFRNSAIRKILQGGEPEGAGDIRLEGLLIGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADC LDEISRLRDGVERLNERLDR					
g608	RATDIGHGIKQIGRNIAEQIGGFSREPESANTGNEALADC LDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq

1 ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51 CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGTT GAACTTGCGG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATC ACCTTCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGCG GCGAACCCGG GCGGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCGCGCG CATCGGACGA ATTGGCACGG ATTTTCGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCGG ACATCGGACA CGGCATCAA CAAATCGGCA
401 GGAACATCGC CGAACAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGLLIG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

972

```

m608.pep    MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
a608        MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
              10      20      30      40      50      60

              70      80      90     100     110     120
m608.pep    TFRNSAVQKILQGGEPPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
a608        TFRNSAVQKILQGGEPPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
              70      80      90     100     110     120

              130     140     150     160     170     180
m608.pep    RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR
a608        RAADIGHGIKQIGRNIAEQIGRFSREPESANIGNEALADCLDEISRLRDGVERLNERLDR
              130     140     150     160     170     180

              189
m608.pep    LERDIWIDX
a608        LERDIWIDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1931>:

```

g609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTTTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGTT TCCACATAAT
201 CGATAACTTC CTCGATACCG ACTTCGGCAT CGGAAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGATTATG CGCGCCATAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTG TGGCCGTATG
351 CCCCCTCTTT CATTTACCC GTGAGGCTGA CATCATAATC CAGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1932; ORF 609.ng>:

```

g609.pep
1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRVFV GLFGNVFFIG
51 AFEQAVELAA RLRFHIIIDNF LDTDFGIGSQ ADGNVRTLM RAILGNFFGT
101 RAKRGYGNHD LHTVAVCPVF HFTREADIII Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1933>:

```

m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTTTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGCGCCGTAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTG TGGCCGTATG
351 CCCCCTCTTT GATTTCGCCC GTGAGACAGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1934; ORF 609>:

```

m609.pep
1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRVFV GFFGNVFFIG
51 AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAVCPVF DFAETDIII Q*

```

m609/g609 93.1% identity in 131 aa overlap

```

              10      20      30      40      50      60
m609.pep    MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFVGFVGNVFFIGAFEQAVELAA
a609        MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFVGLFGNVFFIGAFEQAVELAA
              10      20      30      40      50      60

              70      80      90     100     110     120
m609.pep    RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF
a609        RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF

```


801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
 851 CCTATCAGGT TTCGGGCGAA TATGCGATGT TGCAGGCGGC GGTGCGCAAC
 901 GGC TGGCTGG ACGGCGGCAA AGTGGTTTG GAAAGCCTGC TGGCATTCAA
 951 ACGTGGCGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
 1001 AGA TGCTGAA GCGTTGA

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

g610.pep
 1 MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
 51 AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA
 101 QEA YNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHVG DGLTDENGIV
 151 MND ETVELV KQALCHAEAG QVVPASDMM DGRIGAIRES LEDAGHIHTR
 201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTQMDPAN TDEALHEVAL
 251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAVAN
 301 GWLDGGKVVL ESLLAFFKRA ADGILTYAI EAAKMLKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

m610.seq
 1 ATGATTGGAG GGCTTATGCA GTTCTCTTAC CGCAATGTTC CGGCTTCGCG
 51 TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCGT ATGCGCGAAC
 101 ACACGCTGAC CGCCGATGAT TTGATTATC CGGTGTTCTG ATTGGAGGGG
 151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG
 201 TTTGGACAGG CTGCTGTTTA CGCGGGAAGA GCGGTAAAG CTCGGTATTG
 251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
 301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
 351 GCGCGAGAGG TTTCCGGAAC TGGGCATTAT GACGGATGTC CGGCTCGATC
 401 CTTATACGGT TCACGGTCAG GACGGGCTGA CGGACGAAAA CGGTTATGTG
 451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGCCACGC
 501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTC CGATATGATG GACGGGCGTA
 551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
 601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
 651 TGATGCGGTA GGCAGTTCGG GCAATTGGG CAAGGCAGAT AAAAGACCT
 701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
 751 GACATTACAG AAGGTGCGGA TATGTAATG GTCAAGCCCG GTTTGCCGTA
 801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
 851 CCTATCAGGT TTCGGGAGAA TACCGATGT TGCAGGCAGC GATTGCGAAC
 901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTG GAAAGCCTGC TGGCATTCAA
 951 ACGTGGCGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
 1001 AGATGTTGAA GCGTTGA

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

m610.pep
 1 MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
 51 SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
 101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHVG DGLTDENGIV
 151 MND ETVELV KQALCHAEAG QVVPASDMM DGRIGAIRES LEDAGHIHTR
 201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTQMDPAN TDEALHEVAL
 251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAIAN
 301 GWLDGGKVVL ESLLAFFKRA ADGILTYAI EAAKMLKR*

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM					
g610	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGAAREEDVPSM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTGRAQEAYNPEGLVPSTVRALRER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m610.pep	FPELGIMTDVALDPYTVHVGQDGLTDENGIVMND ETVELVKQALCHAEAGA QVVPASDMM					
g610	FPELGIMTDVALDPYTVHVGQDGLTDENGIVMND ETVELVKQALCHAEAGTQVVPASDMM					
	130	140	150	160	170	180
	190	200	210	220	230	240
m610.pep	DGRIGAIRESLEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTQMDPAN					

975

```
g610      DGRIGAIREALDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLKGADKKTYQMDPAN
           190      200      210      220      230      240
           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
           ||||||||||||||||||||||||||||||||||||||||||||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300
           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           ||||||||||||||||||||||||||||||||||||||||
g610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```
a610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTTATC CGGTGTTCTG ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTAAG CTGCGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CGGACGAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAAG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCGCGG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTGCCAAC
901 GGCTGGCTGG ACGCGGCAA AGTGGTTTGG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```
a610.pep
1  MIGGLMQFFY RNVSASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPGLGIMTDV ALDPYTVHQQ DGLTDENGIV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KKTQYMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLOAAVAN
301 GWLDGGKVVV ELLAFKRAG ADGILTYAI EAAKMLKR*
```

m610/a610 99.4% identity in 338 aa overlap

```
           10      20      30      40      50      60
m610.pep  MIGGLMQFFYRNVPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
a610      MIGGLMQFFYRNVSASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60
           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120
           130     140     150     160     170     180
```

976

```

m610.pep    FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
a610        FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
              130      140      150      160      170      180

              190      200      210      220      230      240
m610.pep    DGRIGAIRESALEDAGHIHTRIMAYSAKYASAFYGFPRDAVGSSGNLKGADKKTYQMDPAN
a610        DGRIGAIRESALEDAGHIHTRIMAYSAKYASAFYGFPRDAVGSSGNLKGADKKTYQMDPAN
              190      200      210      220      230      240

              250      260      270      280      290      300
m610.pep    TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
a610        TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
              250      260      270      280      290      300

              310      320      330      339
m610.pep    GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
a610        GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
              310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGTCCTG AAAACGGGAT GGGAAAACGG CAGCTTCCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCGAG
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TTTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT Ctcgcgcagg ttgtGGCtgt
201 tatcctTGGG CGGGCTGggt tgtttgcccg ccataaTtTc cagtacctga
251 TcgcgGTCTa tggtttCCa ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTcatcga ggaTTTGTa ggaacCTGA TACTgctcgt
351 ccaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTTCTCGGAA
401 ATGTTTTCGG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc gCTCATgcCG TAGCGCGTTA
501 CCATTTCCGG TGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIAYVGFP FHQGFARHNF
101 LVAVFIEDFV GNLLLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAFV AHAVARYHFA CHLGCAFKV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGTCCTG AAAACGGGAT GGGAAAACGG CAGCTTCCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTGCA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTGCGCG TTTTCATCGA GGATTTTGTa GGCAACCTGA TATTGCTCGT
351 CCAAAATCCG GCGGATTTC GCGTCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCGG AACGGGTtac GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc GCTCATGCCG TAGCGCGTTA
501 CCATTTCCGG CGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF FHQGFARHNF
101 LVAVFIEDFV GNLLLVQNP ADFRVDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAFV AHAVARYHFA RHLGCAFKV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

977

```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
g611          MPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHREHLVAVFIEDFVGNLILLVQNP
g611          LAQVVAVILGRAGLFARHNFQYLIADVGFPHQGFARHREHLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
g611          ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAHFVAHAVARYHFACHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X
               |
g611          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1  ATGCCGCTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCGA TGGTTTCCCA TTCCATCAGG GCTTGCACA TCGTTTCCAT
301 CTTGTCGCGG TTTTCATCGA GGATTGTGTA GGCAACCTGA TACTGCTCGT
351 CCAAATCCG GCGGATTTCC GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTAC GTCGCTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTG GTCATGCCG TAGCGCGTTA
501 CCATTTGCGC CGCATTGTT GTTGCCTGT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1  MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51 RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF FHQGFARHREH
101 LVAVFIEDFV GNLILLVQNP ADFRIDVLLG FLGNVLRGTGY AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/a611 98.9% identity in 180 aa overlap

```

              10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
a611          MPSENRMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHREHLVAVFIEDFVGNLILLVQNP
a611          LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHREHLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
a611          ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
              130     140     150     160     170     180

m611.pep      X

```

a611

|
X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

```
g612.seq
1  ATGGGcttcg gcggcaatat tgcAAAAAAG CTGGCcgGg taGATGAAAT
51  AGCCTttgac ttgacggcA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CCGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCGATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTAC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

```
g612.pep
1  MGFGGNIAKK LAGVDEIAFD FDGIVDFGR DDAVRHSGVI NAAVAGLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRFFY GHSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

```
m612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTAAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CCGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA .AAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTAC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

```
m612.pep
1  MGFGGNIAKK LAGVDEIAFN FDGIVDFGR DDAVRHSGVI NTAVACLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXKLNKSK SPDIFRFFY GHSN*
```

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIAKKLAGVDEIAFNFDGIVDFGRDDAVRHSGVINTAVACLHIVGEVFADKAVE					
g612	MGFGGNIAKKLAGVDEIAFDGIVDFGRDDAVRHSGVINAAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
m612.pep	KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRFFY					
g612	KCAENVLFKVP AIHRAAYFVGDFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRFFY					
	70	80	90	100	110	120
m612.pep	KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRFFY					
g612	KCAENVLFKVP AIHRAAYFVGDFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX 					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

```
a612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CCGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGTATTTCGG TCATCATCGA
301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTT.AC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
1  MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
51  GKVFADKAVE KCAENLVFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101 NPYXKLNKSK SPDIFRRFFX GHSN*

m612/a 612    96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep      MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
a612           MGFGGNIAKKLAGVDEIAFDGIVDFDGRDDAVRHSGVINTAVACLHIVGKVFADKAVE
              10      20      30      40      50      60

              70      80      90     100     110     120
m612.pep      KCAENLVFKVPAIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY
a612           KCAENLVFEVPAIHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRRFFX
              70      80      90     100     110     120

m612.pep      GHSNX
a612           GHSNX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101 tgtttGcgGA CTCGGGTTTCG CGGGAAAATC CGCCGATTTC TTCGGCGATG
151 TTCCTGCCGA TTTgtttGat GCCGTGTCCG ATGTCGGTGG CACGgtgccc
201 gatgcCTGCC TGCCTGCCGA AAATCCGTGC CAATTCgtCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCG
301 CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCCTT GGAGGATTTT
351 CCGTATCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501 GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551 ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTTGCT GTTGCCGCTT
601 ATTTTACAGG CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101 PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFFAESKPS SVMRPASFSP
151 AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
201 ILQA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
1  ATGTCGCGTT CGAGCCGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101 TGTTTGGCGA CTCGGATTTCG CGGGAAAATC CGCCGATTTC TTCGGCGATG
151 TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGCTGCC
201 GATGTCTGCC TGCCTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
301 CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351 CTGTACCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
501 GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551 ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTTGCT GTTGCCGCTT

```

980

601 ATTTTACAGG CTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

```

m613.pep
  1  MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSDS RENPPICSAM
 51  FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFFAESKPS SVMRPASFSP
151  AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
201  ILQA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
g613	MSRSSLRRSLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVVKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRICTA					
	:					
g613	MSVARLPMPACVVKIRANSSDARERRLPSRDSTAMPRMRSPSSLMSPAPGSPPWRICTA					
	70	80	90	100	110	120

981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPKAASSERLSGLCRIRRLMMG					
g613	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPKAKEVSSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
1  ATGTGCGCGTT  CGAGCCGGTC  GAGGCGTTCG  TTGAGGCGTT  CCACGCCGTC
51  GCGCAGTCTG  CTTATTTCGT  CGAGGCAGTC  GGCAAGGGCT  TCGTTGCCGA
101  TGTTCGCGGA  CTCGGGTTTCG  CGGGAATAATC  TGCCGATTTC  TTCGGCGATG
151  TTCCTGCCGA  TTTGTTTGAT  GCCGTGTCCG  ATGTCGGCGG  CACGGCTGCC
201  GATGCTCTGC  TCGGTGCCGA  AAATCCGTGC  CAATTCGTCC  GATGCGCGGG
251  AACGCAGGCT  GCCGAGCAGG  GACAGTACCG  CGATGCCGAG  GATGAGGTCG
301  CCTTCGAGCC  CGATGTCGCC  CGCCCCGGGT  TCGCCGCCTT  GGAGGATTTT
351  CTGTACCGCG  CTGTTGCCGA  AGGTGATTTC  GGTGTCTGCA  AAGCCGTTTC
401  CCGCCGAGAG  CAAACCGTCT  TCCGTGATGC  GTCCCGCCAG  TTTCAACCCG
451  GCAATGTTCA  GGGTCAGTGT  TTTGCCTGCG  AAGCGGCAA  GTTCCGAGCG
501  GCTGTCCGGG  CTTTGCAGAA  TCAGGCGGTT  GATGATGGGG  AGGAGGGCGG
551  ACATATTTTC  TGATCGGGGC  GGAGAATGCC  TGTGTTGCT  GTTGACGCTT
601  ATTTTACAGG  CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```

a613.pep
1  MSRSSRSRRS  LRRSTPSRSL  LISSRQSARA  SLPMFADSGS  RENLPICSAM
51  FLPICLMPCP  MSAARLPSA  CVPKIRANSS  DARERRLPSR  DSTAMPRMRS
101  PSSPMSPAPG  SPPWRIFCTA  LLRKVISVSA  KPFFAESKPS  SVMRPASFNP
151  AMFRVSVLPA  KAASSERLSG  LCRIRRLMMG  RRADIFSDRG  GECLLLLLTL
201  ILQA*

```

m613/a613 98.0% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
a613	MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSGSRENLPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPPWRIFCTA					
a613	MSAARLPSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPPWRIFCTA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPKAASSERLSGLCRIRRLMMG					
a613	LLRKVISVSAKPFPAESKPSSVMRPASFNPAMFRVSVLPKAASSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
a613	RRADIFSDRGGECLLLLLTLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

g614.seq

```

1   AtggcTgcgt tcAacgcttt ggacggcaaa aaagaagaca acgggcaaat
51  cgaaTATTCT CAGTTCATCC GACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGTT ACCTGATTAA AGGCGAGCGC
151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCCTTGGATG ACAACCTGAT
201 TCAAACCTTT TTGAACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCGAGCGC GCTGACTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGGCGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCCT TCGGCAAAAG CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCAC CGAACCGCta
501 tcaAAGcctc ggcggccgtg ttcCGCGCGG CATCctgCtg gcgGgcagcc
551 CGGGAaccgg taaAACACTC TTGGCGAAAG CCATTGCAGG CGAGGCCGGC
601 GTGCCGTTCT TCAGCATTTT CGGTTCCGAT TTTGTGAAA TGTTCGTGCG
651 TGTCCGTTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCA AAGAAAAACG
701 CCCCATGCAT TATCTTTATC GACGAGATTG ACGCGGTAGG CCGCCAACGC
751 GCGCGAGgTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTATTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACGCCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GCGCGCTTCG ACCGCCAAGT CGTCGTCCCC CTGCCGACA TCCGGGGGCG
951 CGAACAGatn ttGAACGTCC ATTCTaaaAAA AGTGCcttTG gacgaATCTg
1001 tggatTTTATT GTCCCTCGCG CGCGGCACGC ccggtttTtc cggcgcggat
1051 tTggcgaaac tgytcaacga agccccctg tttgccggcc gccgcaacaa
1101 agtgaaagtc gatcaaagcg attTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

g614.pep

```

1   MAAFNALDGK KEDNGQIEYS QFIRQVNNGE VSGVNIIEGSV VSGYLIKGER
51  TDKSTFFFTNA PLDDNLIQTL LNKNVVRVKVT PEEKPSALTA LFYSLLPVLL
101 LIGAWFYFMR MQAGGGGKGG AFSFGKSRAR LLDKDKANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
201 VPFFSISGSD FVEMFVGUGA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQX LNVHSKKVPL DESVDLLSLA RGTGPFSGAD
351 LAKLVNEAPL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

m614.seq

```

1   ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
51  CGAATACTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTGGACG ACAACCTAAT
201 TAAACACTG CTGACAAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCGAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGTAAAAG CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTGACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TACAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCG
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTT AGGTTCCGAC TTTGTGAAA TGTTCGTGCG
651 TGTCCGTTGCG AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGTCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GCGCGAGGTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACGCCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GCGCGTTTCG ACCGCCAAGT GGTGTGCCCC CTGCCGACA TCCGAGGGCG
951 CGAACAGATT TTGAACGTCC ATTCTAAAAA AGTGCCTTTG GACGAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGGCGGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

983

m614.pep
 1 MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER
 51 TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
 101 LIGAWFYFMR MQTGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
 151 KEEVQEIYDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAEAG
 201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
 251 GAGLGGGND REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
 301 GRFDRQVVPLPDIRGREQI LNVHSHKKVPL DESVDLLSLA RGTPGFSGAD
 351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

m614.pep	10	20	30	40	50	60
	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA					
g614	10	20	30	40	50	60
	MAAFNALDGKKEDNGQIEYSQFIRQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA					
m614.pep	70	80	90	100	110	120
	PLDDNLIKTLDDKNVRVKVTPPEEKPSALAAFYSLLPVLLLIGAWFYFMRMQTGGGKGG					
g614	70	80	90	100	110	120
	PLDDNLIQTLLNKNVRVKVTPPEEKPSALTALFYSLLPVLLLIGAWFYFMRMQAGGGKGG					
m614.pep	130	140	150	160	170	180
	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIYDY LKAPNRYQSLGGRVPRGILL					
g614	130	140	150	160	170	180
	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIYDY LKAPNRYQSLGGRVPRGILL					
m614.pep	190	200	210	220	230	240
	AGSPGTGKTL LAKAIAEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
g614	190	200	210	220	230	240
	AGSPGTGKTL LAKAIAEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
m614.pep	250	260	270	280	290	300
	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQT VIVIAATNRP DVLDPALQRP					
g614	250	260	270	280	290	300
	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQT VIVIAATNRP DVLDPALQRP					
m614.pep	310	320	330	340	350	360
	GRFDRQVVVPLPDIRGREQILNVHSHKKVPLDESVDLLSLARGTPGFSGADLANLVNEAAL					
g614	310	320	330	340	350	360
	GRFDRQVVVPLPDIRGREQXNVHSHKKVPLDESVDLLSLARGTPGFSGADLAKLVNEAPL					
m614.pep	370	380	390			
	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
g614	370	380	390			
	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

a614.seq
 1 ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
 51 CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
 101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
 151 ACCGACAAA GCACCTTCTT CACCAACGCG CCTTTGGACG ACAACCTGAT
 201 TAAACACTG CTCGACAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
 251 AACCAGAGCG GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCTGCTG

984

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301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTACTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCCTGA
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTT AGGTTCGGAC TTTGTGAAA TGTTCGTCGG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGTCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GCGCGAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATGTTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGTTTCG ACCGCCAAGT GGTTGTCCCC CTGCCGGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAA AGTGCCCTTTG GACAAATCTG
1001 TGGATTATTT GTCCCTCGCG CGCGGCACGC CGGGTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```

a614.pep
  1 MAAFNALDGK KEDNGQIEYS QFIQVNNGE VSGVNIIEGVS VSGYLIKGER
 51 TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIYDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGND EQLNLQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHSHKVP LDKSVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

m614/a614 99.7% identity in 391 aa overlap

          10      20      30      40      50      60
m614.pep  MAAFNALDGKKEDNGQIEYSQFIQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFTNA
          |||
a614       MAAFNALDGKKEDNGQIEYSQFIQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFTNA
          10      20      30      40      50      60

          70      80      90      100     110     120
m614.pep  PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG
          |||
a614       PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG
          70      80      90      100     110     120

          130     140     150     160     170     180
m614.pep  AFSFGKSRARLLDKDANKVT FADVAGCDEAKEEVQEIYDY LKAPNRYQSL GGRVPRGILL
          |||
a614       AFSFGKSRARLLDKDANKVT FADVAGCDEAKEEVQEIYDY LKAPNRYQSL GGRVPRGILL
          130     140     150     160     170     180

          190     200     210     220     230     240
m614.pep  AGSPGTGKTL LAKAIAEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI
          |||
a614       AGSPGTGKTL LAKAIAEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI
          190     200     210     220     230     240

          250     260     270     280     290     300
m614.pep  DEIDAVGRQRGAGLGGGNDEREQLNLQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          |||
a614       DEIDAVGRQRGAGLGGGNDEREQLNLQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          250     260     270     280     290     300

          310     320     330     340     350     360
m614.pep  GRFDRQVVVPLPDIRGREQILNVHSHKVP LDKSVDLLSLARGT GPGFSGADLANLVNEAAL
          |||
a614       GRFDRQVVVPLPDIRGREQILNVHSHKVP LDKSVDLLSLARGT GPGFSGADLANLVNEAAL

```


985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAAC GCGCGCGCGC CGGTGtcggc AGCTTtgaag agcagcGaAT
51  agatgCCGCC GGCAAACCAC AATGCGGAAa gcaggCtgaa gcGGTTgcgC
101 GGCagcTTca tGCCCGCTCC TcGTCCaGCC ACGtttGgca gattttggac
151 aggcgcAGga ATTTGCGcCc gcgtgcggCA agtatgtcgc gcCattgtgc
201 cacttcttcg gcggacggTG cttegtcgaT gctgCATTcG TACagcagga
251 aatcgagggt ttcttcgatg acggGgatgg AttccgTTTG GataAgCTgc
301 ttgagttcgt tcatgactGt TCgGATAcgg aaatcgggaa aatgccgtct
351 gAaagggttt CAGACGGCat tggATTATTT GCTGTGCAGG AAgcgcggtt
401 cctcttccca tttgcCGGAA AtgATGTCGg gtacggcctg cAGGGATTtg
451 gCGACGGcat cgtcgatttg ccgGcggtgc ttCcgcgctc ggtttGTTca
501 agacgtagcc gaCGACGagg ttgcggtcGC CGGGtgggcC GATGCCGAGG
551 CGCAGGCGGt aatagtcctgC CGTGCCGAGT TTTGcctgAA TGTCTTTCAA
601 GCCGTTGTGT CcgCGttgc cgcCGCCGAG TTTGAATTTg ATCCGTCCGC
651 AAGGGATGTC GAGTTCGTCG TGGACGACGA GGATTCTTC GGGTTTGATT
701 TTGTAGAAct GTGCAAGCGC GGCAACCGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGCGGGT TTGAGCAGCC AAACATCGCC GTCGGGCAGG GCGGCGCGGG
801 CAACTTCGCC GAAGAATTTT TTTCTTCTT TAAACGAAGC CTTCCATTTC
851 CAGCCAGTT CGTCGAGGAA CCAAAGCCC GCATTGTGGC GGGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGtctg
951 acatgataTT TtccgtgTTT CTgTCGaag cggcCtgaAG GCTTCAGacg
1001 gcatggTtaT TCTTCTTgat TTtgaACgcg tgtgcggCGC GCTTCTTTGG
1051 GGTCGATCAA CAGCGGCGG TACACTTCGA TGCGGTGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMRHRCATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSFMTVRIK KSGKRLKGL QTALDYLLCR KRVASSHLPE MMSGTACRDL
151 ATASSICRRC FRARFVDVA DDEVAVAGVA DAEQAIVIVC RAEFCLNVFO
201 AVVSAVAAAE FEFDPSARDV EFVVDDEFF GFDFVELCKR GNRLSGTVHE
251 RGRFEQPNIA VGQGGAGNFA EEEEEFFKRS LPFPRQFVEE PKARIVAGLF
301 VFARVAQAD NHFDCVRHDI FRVSVECGLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq Length: 1116
1  ATGCGGAAAA GCGGTGGCG CGGTTTCGGC AGCTTTGAAA AGCAGTGAGT
51  AAATGCTGCC TGCAAACCAC AATGCCGAGA GCAGGATAAA GCGGTTGCGT
101 GGCAGATTCA TGCTTGTTCC TCTCAAGCC ATGCTGGCA TAGTTTGAT
151 AGGCGCAGGA ATTTCCGCC GCGTGCGGCC AGCATATCGC GCCAAACGGC
201 AATTTCTTCG GCGGAGGGGG CATCGTCTAT GCTGCATTcG TAGAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTcATT GCTGTGCAGG AAGCGGTTG
401 CTCTTTCCCA TTGCGCGCA AGGATGTCGG GTATGGCTTG CAGGGATTTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTGT .TCCGTACTG GGTTTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTTCAA
601 GCCGTTGTGT CCGCGGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCCGC
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTCTTC GGGTTTGATT
701 TTGTAGAAct GTGCAAGCGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGCAGGT TTGAGCAGCC AAACGTGCC GTCGGGCAGG GCGGCACGGG

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986

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801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTCGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTCGATCAA CAGCGGCGG TACACTTCGA TCGGGTCGCC GTCGCGCAGC
1101 GGCGTGTCTG CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SFEKQXVNA CKPQCREQDK AVAWQIHACS SSSHVWHS LD
51 RRRNFPPRAA SISRQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAVAAAE FEFDP SAGNV EFVVDDEDF GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTG DFA EEEFFFKXS LPFPQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVX HDI FRVSVECLK ASDGMVILL DFERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

m615.pep	10	20	30	40	50	60
	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHS LDRRRNFPPRAA					
g615	MWKRRRRGVGSFEEQRIDAAGKPQCGKQAEAVARQLHAASSSSHVWQILDRRRNLPPRAA					
	10	20	30	40	50	60
m615.pep	70	80	90	100	110	120
	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
g615	SMSRHCATSSADGASSMLHSYSRKSRSVSSMTGMDSVWISCLSSFM TVRIKSGKCR LKGL					
	70	80	90	100	110	120
m615.pep	130	140	150	160	170	180
	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRCXRTGFVQDIADDEVAVARVA					
g615	QTALDYLLCRKRVASSHLPEMMSGTACRDLATASSICRRCFRARFVQDVADDEVAVAGVA					
	130	140	150	160	170	180
m615.pep	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDP SAGNV EFVVDDEDF GFDFVELCKR					
g615	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDP SARDVEFVVDDEDF GFDFVELCKR					
	190	200	210	220	230	240
m615.pep	250	260	270	280	290	300
	GNCLSGTVHERGRFEQPNVAVGQGGTG DFAEEFFFKXSLPFPQFVEE PKTRIVACLF					
g615	GNRLSGTVHERGRFEQPNIAVGQGGAGNFAEEFFFKRSLPFPQFVEE PKARIVAGLF					
	250	260	270	280	290	300
m615.pep	310	320	330	340	350	360
	VFFARVAQADNHDFCVX HDI FRVSVECLK ASDGMVILL DFERVCGALLWGRSTAGGTLR					
g615	VFFARVAQADNHDFCVRHDI FRVSVECLK ASDGMVILL DFERVCGALLWGRSTAGGTLR					
	310	320	330	340	350	360
m615.pep	370					
	CGRRRAAACRLX					
g615	CGRRRAAACRLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1   ATGCGGAAAC GCGGCGCGCG CGGTGTCGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAAACCAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCTCC TCGTCCAGCC ACCTTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTGC GGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTTC TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCAATT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG TTCCGTA CTG GGTTTGTTC
501 GGACATAGCC GACGACGAGG TTGCGGTGCG CCGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCGAGT TTTGCTGAA TGTCTTTCAA
601 GCCGTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCCGC
651 AGGGAATGTC GAGTTCGTGC TGGACGACGA GGATTCTTC GGGTTTGATT
701 TTATAAACT GCGCAAGGGC GGCAACTGCC TGTCGGGAAC GGTTCATGAA
751 CGTGGTCGGC TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCACGGG
801 CGACTTCGCC GAAGAATTTT TTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTGTC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGGCGCGC GCTTCTTTGG
1051 GGTCGATCAA CAGCGGGCGG TACACTTCGA TGGCGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1   MRKRRRRGVG SFEEQRIDAA GKPCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDPAGNV EFVVDDEDFE GFDFIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQSTGDEA EEEFFFFK*S LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECRLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSF EKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHSIDRRRNFPRAA					
a615	MRKRRRRGVGSFEEQRIDAA GKPCGKQAEAVARQLHAASSSSHVWQILDRRRNLPRAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m615.pep	SISROTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
a615	SMSRHCATSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m615.pep	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA					
a615	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m615.pep	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPAGNV EFVVDDEDFE GFDFIKLRKG					
a615	DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPAGNV EFVVDDEDFE GFDFIKLRKG					
	190	200	210	220	230	240
	250	260	270	280	290	300

988

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m615.pep  GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEFFFKXSLPFPQFVEEPKTRIVACLF
a615      GNCLSGTVHERGRLEQPDIAVGQGSTGDFAEFFFKXSLPFPQFVEEPKTRIVACLF
           250      260      270      280      290      300

           310      320      330      340      350      360
m615.pep  VFFARVAQADNHDFCVXHDIFRVSVECCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
a615      VFFARVAQADNHDFCVXHDIFRVSAECLLKASDGMVILLDFERVCGALLWGRSTAGGTLR
           310      320      330      340      350      360

           370
m615.pep  CGRRRAAACRLX
a615      CGRRRAAACRLX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaca CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACTGG
101 CGTGGAATG GAAGGCTTCG TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CCGCCCTGCC CGACGGCGAT GTTGGCTGCG TCAACCGGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGCGGAC GGATCAAATT CAAACTCGGC GgcggcaacG gcgGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGCagac tattaCCGCC
401 TCGCCTCGG CATCGgccaC CCCGGCgacc gcaacctCGT CGtcggctac
451 gtcttgAAca aaccgagcgc gGaagcaccg Ccggaatc gacgatgCCG
501 TCGccaaATC CCTgcaggcc gtaccCGACA TcaTTTCCGg caaatgggaa
551 gaggcaacgc gCTTCTGCA CAGCAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgg cattttcccg atttccgTAT CcGAaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaaTccatcc ccgtcatcga agaaacctc
701 gatttcctgc tGTACGAATG cagcAtcgac gaagCaccgt ccgccaaga
751 agtggcacaa TGgcgcgaca tactTGccgc acgcgGcgGC AAATtCCTgc
801 gctgtccaa aatctgcCaa aCGTGGctGG ACgAGGAGG GGCatgAAgc
851 tGCCGcgcaA CCgcttcaGc ctgctTTCCG CATTGTGGTT TGCCGGCGGc
901 atctATtCgc tgctcttcaA AGCTGccgaC ACCGCGCCGC CGCCGTTTCC
951 ACATTTcgac AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAaatCTTgt
1001 tTctGGCCAA AGCATTCAAA ACCGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGCCGTC GGCAGCGAAT GCGCGCAGG
1101 ATGGTTTACC GCAACGCGAA CCGCAGTTT GGGCGATGTC CTTGCCgACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTGCCG CGCGTTCTGC CTGCCGccc
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51  VARAALPDGD VWLLKPATFM NRSQAVAAAL AQFYKIKPEE ILVHDELDI
101 PCGRIFKFLG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVGY
151 VLNKPSAEAP PANRRCRROI FAGRTRHHFR QMGRGNALPA QQIIQCRLKP
201 FQTAFSRFPY PMSHERTOAA YPNGIHPRHR RNPRFPAVRM QHRRSTVRRR
251 SGTMARHTCR TRQIPAPVQ NLPNVAGRG GMLPRNRF LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QILFLAKAFK TGKLPPIYRS
351 LIAFAFCFAV GSECAQAWFT ATRTGS LGDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACTGG
101 CGTGGAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCGTG CCGCCCTGCC CGACGGCGAC GTTGGCTGCG TCAACCTGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGAT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCTTGCGGAC GGATCAAATT CAAACTCGGC GCGGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 TGCTTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCCG CAAATGGGAA

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551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTT CAGACGG CATGTTCCCG ATTTCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAACCCCTC
701 GATTTCCTGC TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGGCCGA AAATTCCTGC
801 GCC TATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATT TACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCA TTTTGAC AAAGTGCGC ACCTCGCCT GTTTTCGCA CAAATCTGGC
1001 TTC TGACCAA AGCATTGAGA ACCGACAACC GCCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCCGCCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

```

m616.pep
  1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
 51 VARAALPDGD VWLLKPATFM NRSQGAAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIFKFLG GNGGHNGLK DIQAKLGTD YRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTDXRRCRQI PASHTRHPCR QMGRSNPLPA QMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPALRM QHRRCPRLRR
251 NCRLLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPFPFHD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGS LGDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

m616.pep	10	20	30	40	50	60
	MSNTIKMVVGLNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
g616	10	20	30	40	50	60
	MSNTIKMVVGLNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
m616.pep	70	80	90	100	110	120
	VWLLKPATFMNRSQGAAVALAQFYKIKPEEILVVHDELDIPCGRIKFLGGGNGGHNGLK					
g616	70	80	90	100	110	120
	VWLLKPATFMNRSQGAAVALAQFYKIKPEEILVVHDELDIPCGRIKFLGGGNGGHNGLK					
m616.pep	130	140	150	160	170	180
	DIQAKLGTDYYRLRLGIGHPGDRNLVVGIVLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
g616	130	140	150	160	170	180
	DIQAKLGTDYYRLRLGIGHPGDRNLVVGIVLNKPSAEAPPANRRCRRQIPAGRTRHHFR					
m616.pep	190	200	210	220	230	240
	QMGRSNPLPAQMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRNPRFPALRM					
g616	190	200	210	220	230	240
	QMGRGNALPAQQIIQCRLKPFQTAFSRFPYPNSHRTQAAAYPNRIHPRHRNPRFPALRM					
m616.pep	250	260	270	280	290	300
	QHRRCPRLRRNCRLLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPRNRFILLSALWFAGS					
g616	250	260	270	280	290	300
	QHRSTVRRRSGMTARHTCTRTRQIPAPVQNLPNVAGRGGMKLPNRNRESLLSALWFAGG					
m616.pep	310	320	330	340	350	360
	IYSLLFKAAETAPPPFPFHDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL					
g616	310	320	330	340	350	360
	IYSLLFKAAETAPPPFPFHDKAAHLALFFAQILFLAKAFKGLPIPYRSLIAFAFCFAV					
m616.pep	370	380	390	400		
	FSECAQAWFTATRTGSLGDVLAADLTGAALALFTARAACRPDX					
g616	370	380	390	400		
	GSECAQAWFTATRTGSLGDVLAADLTGAALALFAARSACRPDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

990

a616.seq
 1 ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
 51 ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAAGTGG
 101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
 151 GTCGCCCGTG CTACCTGCCG CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
 201 CACGTTTCATG AACCGTTCGG GACAGGCAGT TGCCGCCCTT GCGCAGTTTT
 251 ATAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
 301 CCCTGCCGAC GGATCAAATT CAAACTCGGC GCGGCAACG GTGGACACAA
 351 CGGCTTGAAA GACATTCAGG CAAACTCGG CACGGCAGAC TATTACCGCC
 401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
 451 GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
 501 TCGCCAAATC CCGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGTGAA
 551 GAGGCAACCC GCTTCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
 601 TTTTCAGACG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
 651 TCAAGCAGCT TATCAAACC GAATCCATCC CCGTCATCGA AGAAACCCTC
 701 GATTTCTGCG TGTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAAGA
 751 AGTGGCACA TGGCGCGACA TACTTGCCGC ACGCGCGGCG AAATTCTGCG
 801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
 851 TGCCGCGCAA CCGCTTCAGC CTGCTTCCG CATTGTGGTT TGCCGCGGCG
 901 ATCTATTGCG TGCTCTTCAA AGCTGCCGAC ACCGCGCCGC CGCCGTTTCC
 951 GCATTTTCGAC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAAATCTGGC
 1001 TTTTGACCAA AGCATTCAA ACCGGAAC TTCCCATCCC CTACCGCAGC
 1051 CTGATGGTCT TTGCCCTCTG TTTGCCCTC TTCAGCGAAT GCGCGCAGGC
 1101 ATGATTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTGCGCGATA
 1151 TGGCAGGTAC GGTCTCGCA CTCTTGCCG CCGCGCCGC CGACCGCCGC
 1201 GACTGA

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep
 1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
 51 VARATLPDGD VWLLKPTTFM NRSQQAVAL AQFYKIPKEE ILVVHDELDI
 101 PCGRIKFKLG GNGGHHGLK DIQAKLTAD YYRLRLGIGH PGDRNLVVG
 151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QMTRCRLKP
 201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPAVRM QHRRRTIRRR
 251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMLPRNRF LLSALWFAGG
 301 IYSLLFKAAD TAPPPPHFD KAAHLALFFA QIWLTKAFK TGKLPPIYRS
 351 LMFALCFAL FSECAQA*FT ATRTGLGDV LADMAGTVLA LFAARAADRP
 401 D*

m616/a616 90.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
a616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARATLPDGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m616.pep	VWLLKPATFMNRSQQAVALAQFYKIPKEEILVVHDELDIPCGRIKFKLGGNGGHHGLK					
a616	VWLLKPTTFMNRSGQAVALAQFYKIPKEEILVVHDELDIPCGRIKFKLGGNGGHHGLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m616.pep	DIQAKLTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
a616	DIQAKLTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m616.pep	QMGRSNPLPAQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPALRM					
a616	QMXRGNPLPAQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPVRM					
	190	200	210	220	230	240
	250	260	270	280	290	300

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g619.seq
1  ATGCCGCTCTG  AAAAAAATAT  CGGTTTTATG  GCAGGAAGCA  GCCGTCCGTT
51  GCGAGGTCGCC  TTTGCGCTGT  TGCTGGTTTC  TGCACTCTCG  TTTATGACGC
101  TCAACGCTCAA  AAGAGATTGG  GAGCTGTGCT  CTCACCTGCG  CTTGACCAAC
151  CTTGCCCGCG  TGCTGATGGT  GCCTATGCG  GTCGGCGTGT  CCACTCAACT
201  CTTCCAACG  CTGACCAACA  ACCCGATTCT  GACCCCTFCG  ATTTTGGGTT
251  TCGATTCTGT  GTATTGTGTT  TGCAGACCT  TGGTgttGTT  TACGttcgCG
301  GCGGTGGGCT  ATAcateccct  gccgttgacy  gGCAAAATTG  GCttTGAACT
351  GGTtGTtTATG  ATGGCGCGCT  CGCTGCTGCT  GTtTTACAGC  CTCATCCGTC
401  AGGCGGGGCG  CGATTtGCCG  CACATGATT  TAATCGGCGT  GAtTTTCGGG
451  AtTTtGTtTCC  GCGACTtTTC  TCGCTGCT  TCGCGCATGA  TAGACCCCGA
501  AGAAtTTACC  GCCGCGCAGG  CGAATATGTT  TGCCGGATT  AATACCGTCC
551  GCAGCGAGCT  TTAGGCATA  GCGCGCGCTG  TTCTGCTCT  CAGCGCGCGG
601  GTCGtTTGGC  ACGAACGCTA  CCGTCTGGAG  GTACACCTTT  TGGGGCGCGA
651  CCAAGCCGTC  AATTtGGGCA  TCAGCTACAC  GCGCAACACC  TtATGGATAC
701  TGCTtTTGGAT  TCGCGCATTG  GTGGCGCAGC  CGACCGCCAT  TGTCGGCCCG
751  gtGAGCTTTT  TCGGGCTTCT  CGCCGCTCG  CTTGCCAAC  actTTTCCCC
801  gtCCGTGCTC  CATTCGCTCC  CGCTCGcat  gacggtttGC  gctcgGcggtCA
851  TCCTCTTgt  cggCggacaA  ACCGTATTG  AACACTTCT  GGGCATGAag
901  gCggtATTAA  GCGTGtGGT  cgAATTGCG  ggcggactcg  TTTTCTCTA
951  TCTCGtTTTA  AAACACAAAA  ATAGA

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g619.pap

1	MPSEKNIGFM	AGSSRPLRVA	FALLVSCIL	FMTLNVKGDW	DFVLHLRLTK
51	LAALLMVAYA	VGVSTQLFQT	LTNNPILTPS	ILGFDLSLYVE	QLTLVLVFTFG
101	GVGYTSLPLT	GKFGFELVVM	MGGSLLLFYT	LIRQGGRDLP	HMLILGVIFG
151	ILFRSLSSLL	SRMIDPEEFT	AAQANMFAGF	NTRVSELLGI	GALVLLVSAA
201	VVWHERYRSD	VHLGRDQAV	NLGISYTRNT	LWILLWIAAL	VATATAVVG
251	VSFFGLLAAS	LANHFSPSVR	HSVRLEPMTVC	VGGILLVGGQ	TVFEHFLGMK
301	AVLSVVVEFA	GGLVFLYLVL	KHKK*		

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m619.seq
1 ATGCCGCTCG AAAAAATAT CGGTTTATG GCAGGAAGCA GCCGCCGGTT
51 TCGGCTCGCC TTTCGCGTGT TGTTGGTTTC CTGCGCTCGT TTTATGACGC
101 GTAACGTCAA AGGCGATTGG GATTTGTGTT TGCAACTGCG CGTGACCAAA
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACGCAACT
201 CTTCCAAACG CTGACCAATA ATCCGATTCT GACCCCTTCA ATTTTGGGTT
251 TCGATTCTGT GTATGTGTTT TTGCAGACCT TGCTGGTGTG TACGTTCCGG
301 GCGCTGGGCT ATGCTTCCCT GCGGTTGACG GCGAAATTCT CGTTTGAAC
351 GGTCTGTCATG ATGGCGCGCT CGCTGCTGCT GTTCTACACG CTCATCAAAC
401 AGGCGCGGACG CGATTTGTCT CGCATGATT TAATCGCGCT TCGTTCCGG
451 ATTTTGTTC GCAGCCTGTC GTCCGTGCTT TGCGCATGA TCGATCCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 ACAGCGAGCT TTTGGGCATA CGCGCGCTGA TTCTGCTCTG CAGCGCGCGG
601 CTCGTTTGCG CGGAACGCTA CCGCTTGGAC GTTTACCTTT TGGGCGGTGA
651 CCAAGCCGCT AATTGGGCA TCAGCTACAC GCGCAACACC TTATGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT GGTTCGGCCC
751 GTAAGCTTTT TCGGGCTTCT CGCGCGCTCG CTTGCCAAAC ACTTTCCCC
801 GTCGGTCAAA CATCCGTC CCCTCGCCGT GACGGTTTGT ATTCGGCGGA
851 TCTCTTGGT CGCGCGACG ACCGTGTTCT AACACCTGCT CGGTATGCAG
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901 GCAGTGTGTA GCGTAGTAGT AGAATTGCC GCGGACTCG TTTCTCTCTA
 951 TCTCGTTTAA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep
 1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNVKGDW DFVLQRLTK
 51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLVFTFG
 101 GVGYSASPLT GKFGFELVVM MGGSLLLFYT LIQGGGRDLS RMILIGVIFG
 151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
 201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMQ
 301 AVLSVVVEFA GGLVFLYVL KHKK*

m619/g619 95.1% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLWVAFALLLVSCVL FMTLNVKGDWDFVLQRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
m619.pep	70	80	90	100	110	120
	VGVSTQLFQTLTNNPILTPSILGFDSLTVF LQTLVFTFGGVGYASPLTGKFGFELVVM					
g619	VGVSTQLFQTLTNNPILTPSILGFDSLTVF LQTLVFTFGGVGYTSLPLTGKFGFELVVM					
	70	80	90	100	110	120
m619.pep	130	140	150	160	170	180
	MGGSLLLFYTLIQGGGRDLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
g619	MGGSLLLFYTLIRQGGGRDLPMLIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
m619.pep	190	200	210	220	230	240
	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVHSELLGIGALVLLVSAAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
m619.pep	250	260	270	280	290	300
	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
g619	VATATAVVGVPVSFFGLLAASLANHFSPSVRHSLPMTVCVGGILLVGGQTVFEHLLGMK					
	250	260	270	280	290	300
m619.pep	310	320				
	AVLSVVVEFAGGLVFLYVLKHKKX					
g619	AVLSVVVEFAGGLVFLYVLKHKKX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq
 1 ATGCCGCTCTG AAAAAAATAT CGGTTTATG GCAGGAAGCA GCCGTCCGTT
 51 GTGGGTGCTT TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
 101 TCAACGTCAA AGCGGATTGG GATTTTGTTT TGCACCTGCG CCTGACCAAG
 151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGCGGTTT CGACCCAGCT
 201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTTCG ATTTTGGGTT
 251 TCGATTCTGT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCCGC
 301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT
 351 GGTCGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAC
 401 AGGGCGGGCG CGATTGCGG CGTATGATTT TAATCGGCGT GATTTTCGGG
 451 ATTTTGTTCG GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCCGA
 501 AGAATTTACG GCGGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
 551 ACAGCGAGCT TTTAGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
 601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTACACCTTT TGGGCGCGCA
 651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
 701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTGGCCCG

993

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7 51 GTAAGCTTTT TCGGGCTTCT CGCCGCTCG CTTGCCAACC ACTTTTCCCC
8 01 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
8 51 TCCTCTTGGT CGGCGGACAG ACCGTATTCTG AACACTTCTT GGGCATGAAG
9 01 GCGGTATTAA GCGTGGTGGT CGAATTGCG GCGGACTCG TTTCTCTCTA
9 51 TCTCGTTTTA AGACACAAAA AATGA

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This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

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a619.pep
1  MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLVNKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLYVF LQTLVFTFG
1 01 GVGYASLPLT GKFGFELVVM MGSLLLLFYT LIKQGRDLR RMILIGVIFG
1 51 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
2 01 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
2 51 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
3 01 AVLSVVVEFA GGLVFLYLVL RHKK*

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m619/a619 97.2% identity in 324 aa overlap

	10	20	30	40	50	60
m619.pep	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLVNKGDWDFVLQRLTKLAALLMVAYA					
a619	MPSEKNIGFMAGSSRPLWVAFALLLVSCILFMTLVNKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m619.pep	VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLVFTFGGVGYASLPLTGKFGFELVVM					
a619	VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLVFTFGGVGYASLPLTGKFGFELVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m619.pep	MGSLLLLFYTLIKQGRDLRSMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
a619	MGSLLLLFYTLIKQGRDLRPMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m619.pep	NTVHSELLGIGALILLVSAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
a619	NTVHSELLGIGALILLVSAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m619.pep	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
a619	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
	250	260	270	280	290	300
	310	320				
m619.pep	AVLSVVVEFAGGLVFLYLVLKHKXX					
a619	AVLSVVVEFAGGLVFLYLVLKHKXX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gttttcgCCT TAAGTCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCGGCAG AtTAGCGacc
101 gttegggtcgg aCACTAttgc Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAACCC GATCAGCCG TTTGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAG CCTTTACGT
351 CATCGACAGC GCCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCGATGCT TACATTTCA AGTAA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

m620/g620 97.0% identity in 164 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

```
a620.pep
1  MKKTLAIVA VSALSACROA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGK DQPWFSTIK QMFGYTKLFE EPKGRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGMGMAED ALFPNGKEQA EKFAKDGGK
151 VVGFDMPDT YIFK*
```

995

m620/a 620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.p.ep	MKKTL LAIVAVSALSACRQAE EGPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a620	MKKTL LAIVAVSALSACRQAE EGPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.p.ep	DQPVWFSTIKQMFYTKLP EEPKGI RVIYVTD MGNVTDW TNP NADTEWMDAKKAFYVIDS					
a620	DQPVWFSTIKQMFYTKLP EEPKGI RVIYVTD MGNVTDW TNP NADTEWMDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.p.ep	GFIGGMGAEDALPFGNKEQAEKFAKDKGKGVVGFDDMPDITYIFKX					
a620	GFIGGMGAEDALPFGNKEQAEKFAKDKGKGVVGFDDMPDITYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta ccgctgtcgg ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAaag ctggCGTTTG CCGCCGCCGC CCTGCCAGAA gccgTccgCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGCGAT TCGGAaagaa TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACA CGCTGGA TATGCAGGAA ACCGTGCGCC ACGCCTTCCG CGTTGCCTGC
301 GGC TTGGATT CGATGGTTT GGGCGAGCCG CAGATTTTGG GGCAGATTAA
351 AGATGCGGTG CGTGCGGCTC AAGAACAGGA AAGTATGGGG GCAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAGAAGT CCGTACCGAT
451 ACCGCTGTG GCGAAAATTC GGTTCGATG GCTTCCGCGT CCGTCAAGTT
501 GGC GGAACAG ATTTTCCCG ACATCGGCGA TTGAACGTA TGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGTTGCCA CTTATTTTGC CGCCAAAAAT
601 CCCCGGTGTA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTTA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTGGTGG TTTCTTCAAC GGCGAGCCAG
751 CTTCCGATAG TCGGCAAAAG CATGGTCGAA CGCGCATTGA AACAGCGTCA
801 GAGTATGCCG TTGTTATGCG TTGACTTGGC CGTGCCGCGC GATATTGAAG
851 CGGAAGTCGG CGATTGAAC GATGCGTATC TTTATACGGT GGACGATATG
901 GTC AACATCG TCCAAAGCGg caaggaggca aggcagaaag ccgccgcCgc
951 cgc cgaacg ctggtGTCCG AAAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GagcgttcCG CTGATTAAGG CCTTGCGGGA CGAGGCGGAG
1051 AAAGCGCGCA AGCAGGTGTT GGAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGcaacGCGG GAAGaggttt TGgaacggt gtccgtcCAA CTGACCAACA
1151 AGCTGTGCA TTCGCCAACT CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAA GatttGG TTCATGCCgt cGCGCAGAtt tatcatttGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.p.ep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAALPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYTLDME TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RAAQEESMG AKLNALFORT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKN
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAIHDY DVVVSSTASQ
251 LPIVVGKME RALKRQSMP LFMLDLAVPR DIEAEVVDLN DAYLYTVDDM
301 VNI VQSKEA RQAAAAAET LVSEKVAEFV RQQQGRQSV LKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAQAQI YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA CCGCTGTGCG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAaag CTGGCGTTTG CCGCCGCCGC CCTGCCATAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGTGAT TCGGAAGAAA TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACGCGCTGGA TATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC

```

```

301 GGGCTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTCCGTTG CTAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTCATG GCTTCGCTT CCGTCAAATT
501 GGC GGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACACG CTCGGTGTCA ACGCCGAACC GTGCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTTG TCGGCAAAGG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTCATG TTAGTTTGGC AGTGCCCGCT GACATTGAAG
851 CGGAAGTCGG CGATTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAACAG CTGGTGTCCG AGAAAGTTGC CGAATTGTC AGGCAGCAGC
1001 AGGCAGGCGA GAGTGTCCCC TTGATTAAGG CGTTGCGGGA CGAGGCGGAG
1051 AAAGCGCGCA AACAGGTGTT GGAATGACC ATGAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGAACGGCT GTCCGTCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGCGGG GGAAGAAGAT
1201 AAAGATTGTTG TTCATGCCGT CGCGCAGATT TATCATTGG ACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

```

m622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLRNSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMPL FMLDLAVPRD IEAEVGDNDL DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPL IKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

m622/g622 98.8% identity in 415 aa overlap

m622.pep	10	20	30	40	50	60
	MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLRNSNAATEAVILSTCNRTELYCVGD					
g622	MQLTAVGLNHQTAPLSIREKLAFAAAAALPEAVRNLRNSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
m622.pep	70	80	90	100	110	120
	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEEIRPYLYTLDQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
m622.pep	130	140	150	160	170	180
	RVAQEESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	RAAQEESMGAKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180
m622.pep	190	200	210	220	230	240
	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	LFIGAGEMIELVATYFAAKNPRMLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
	190	200	210	220	230	240
m622.pep	250	260	270	280	290	300
	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDLNDAYLYTVDDM					
g622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDLNDAYLYTVDDM					
	250	260	270	280	290	300
m622.pep	310	320	330	340	350	360
	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
	310	320	330	340	350	360
m622.pep	370	380	390	400	410	
	MKQLAKGATAEEVLERLSVOLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622	MKQLAKGATAEEVLERLSVOLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

370

380

390

400

410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

a622.s eq

```

1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
1 01 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
1 51 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
2 01 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
2 51 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
3 01 GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
3 51 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
4 01 ATGCCCTGTT CCAAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT
4 51 ACTGCCGTCG GCGAAAAC TC GGTTCCTG GCTTCCGCTT CCGTCAAGTT
5 01 GGCAGAGCAG ATTTTCCCGG ACATCGGCGA TTTGAATGTC TTGTTTATCG
5 51 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
6 01 CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
6 51 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
7 01 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
7 51 TTGCCCATTT TCGGCAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
8 01 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
8 51 CGGAAGTCGG AGATTGAAAC GATGCCTATC TTTATACGGT GGACGATATG
9 01 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
9 51 CGCCGAAACG CTGGTGTCCG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
10 01 AGGCGAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
10 51 AAAGCGCGCA AACAGGTCTT GGAAATGCG ATGAAACAGC TTGCCAAAGG
11 01 CGCAACGGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
11 51 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
12 01 AAAGATTGGT TTCACGCCGT CGCGCAGATT TATCATTGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

a622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
1 01 GLDSMVLGEP QILGQIKDAV RVAQEESMG KKLNALFQKT FSVAKEVRTD
1 51 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
2 01 PRIMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
2 51 LPIVGKGMVE RALKQRQSMF LFMLDLAVPR DIEAEVGD LN DAYLYTVDDM
3 01 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV LIRALRDEGE
3 51 KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLHSPT QTLNKAGEED
4 01 KDLVHVAQI YHLDK*

```

m622/a622 98.1% identity in 415 aa overlap

```

              10      20      30      40      50      60
m622.pep      MQLTAVGLNHQTAPLSIREKLAFAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a622           MQLTAVGLNHQTAPLSIREKLAFAAACLPEAVRNLARSNAATEAVILSTCNRTELYCVGD
              10      20      30      40      50      60

              70      80      90      100     110     120
m622.pep      SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a622           SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
              70      80      90      100     110     120

              130     140     150     160     170     180
m622.pep      RVAQEESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a622           RVAQEESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
              130     140     150     160     170     180

```

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq
 1 ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
 51 GATAATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTACTAC
 101 TCTCCGCCGC CTGCTGGGCA AAGGCATccc cgcgcTTTCa ccgCTGGCTG
 151 CACcgcGacc gCTATTTCGG CCCGATGGT CATAACTGGG AACAAAACGG
 201 CGCAGTGCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt
 251 cctgcctcat gatctTTtgg CattTTCccc aacnctgggtg ggctGGGGCG
 301 GTTTCATCGG TTTTTGTTC CCTTGTcacc ATacggatgt gGcacAGacc
 351 cgaatCTTGA

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep
 1 MIRYLLIACG GISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
 51 HRRHYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPOXWWVGA
 101 VSSVFCSLVT IRMWRHPES*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq
 1 ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTCTCC TACTGTTGGG
 51 TATCATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTACTGC
 101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
 151 CACCGGCACC GCTATTTCGG CCCGATGGT CATAACTGGG AACAAAACGG
 201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
 251 CCTGCCTGAT AATGTTTGG CAGTTTCCCC AACGCTGGTG GGTGCGGGCG
 301 GTTTCATCGG TTTTTGTTC CCTTGTGCGC ATATGGATGT GCGCAGGCC
 351 CGAATCTTGA

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep
 1 MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFYRWL
 51 HRRHYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMEW QFPQRWWVGA
 101 VSSVFCSLVA IWMWRHPES*

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRRHYFGPMV					
g624	MIRYLLIACGGISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRRHYFGPMV					
	10	20	30	40	50	60

999

```

              70      80      90      100     110     120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              |||||
g624           HNWEQNGAVPRKAKIFAISMITASCLMIFWHFPQXWWVGAVSSVFCSLVTIRMWHRPESX
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```

a624.seq
1  ATGATACGTT ATCTTTTAAT TGCTGCGGC TGCATTCC C TGCTGTTGGG
51 TATCATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTA CTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCGG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTTCG CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTTGG CAGTTTCCCC AACCTGGTG GGTCCGGGCG
301 GTTTCATCGG TTTTTTGTTC CCTTGTCGCC ATATGGATGT GCGCAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```

a624.pep
1  MIRYLLIACG CISLLGLIIG IFLELLPTTP FVLLSAACWA KASPRFHRWL
51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*

```

m624/a624 99.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
m624.pep      MIRYLLIACGCISLLGLIIGIFLPLPTTFVLLSAACWAKASPRFYRWLHRHRYFGPMV
              |||||
a624           MIRYLLIACGCISLLGLIIGIFLPLPTTFVLLSAACWAKASPRFHRWLHRHRYFGPMV
              10      20      30      40      50      60

              70      80      90      100     110     120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              |||||
a624           HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```

a625.seq
1  ATGTTTGCAA CCAGGAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTCCTTG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCCG
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```

g625.seq
1  atGTTTGCAA CCAGGAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTCCTTG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttGCCGCC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351 gTAA

```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```

g625.pep
1  MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPmie ASAVPTASRA

```

1000

51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq
1 ATGTTTGCAA CCAGGAAAT GAAGAAGATG ACGATGTGCA CGCGCGGGT
51 ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGCGGGACGC GCCAAAACC
301 AAACGAAACG GGATGAGGAA GAGCAATGTC CAAAGGCGG TAATTTTGCC
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPME ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMEASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKGMYSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
g625	PQTMPPEMVYRASSSRMKGMYSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPME ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMEASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKGMYSTSACATVWIPADAPKTKLNGMRKSNVQKAVILEX					
a625	PQTMPPEMVYRASSSRMKGMYSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq
1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTCATCCTG ATTACATTGA
101 CGCCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
201 CATCACCATC TTCCCGTCC TGAGATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GCGGGGCGGC GATGCCCAAG
401 CCTTAATGAC GGGTCCCTG TTTCAATcgc TGCTGGCGGT TTCTAtgggT
451 tCGGTATTCA TGGGCGCACT GaccTACATc gGCAAcgcac cgaactTCAT

1001

501 GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGCcg actTTCTTcc
 551 ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CATcgTACAT
 601 ACCCTcgtCT TTTTcgTTtt cAAACTACTg taa

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

g627.pep
 1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
 101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
 201 TLVFFVFKLL *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

m627.seq
 1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
 51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
 101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
 151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
 201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
 251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
 301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
 351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
 401 CCTTGATGAC GGGTACCCTG TTTTCATTCG TGCTGGCGGT TTCTATGGGT
 451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
 501 GGTCAAGGCC ATTGCCGAAC AGCGCGCGCT ACCGATGCCG ACTTCTTTCG
 551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
 601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

m627.pep
 1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
 101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
 201 TLIFFVFKLL *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	:					
g627	MSGLWKPEHPGFEILGSRYALQNLVRDVILITLTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m627 . pep	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
g627	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINTMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627 . pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
g627	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
	130	140	150	160	170	180
	190	200	210			
m627 . pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627 . seq
1  ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AACTCTTCC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTTCCCTG TTTCATTGCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTC AAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```

a627 . pep
1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FVLSILKAG EAGALGGVVS LVHDTAGHP
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGSL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627 . pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m627 . pep	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
a627	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627 . pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
	130	140	150	160	170	180
	190	200	210			
m627 . pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					

1003

a627 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX
 190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq
 1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT
 51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTTAC
 101 ACACATGGAT TTTACGTTTCG GTCAGGCGGC TCAATACCAA CAGGCCGCGT
 151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GCGGAACGGC TCGGCATCTA
 251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT
 301 GATTGAATCA GGTGCGGCG CACTTTTTCG CTGCTCAATT TTGCCAGCGC
 351 TTCAGGTacg TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep
 1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRLNTNRP
 51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
 101 D*IRLRRTFS LLNFASASGT *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq
 1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT
 51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
 101 AAACATGGAT TTTGCGTTTCG GTCAAACGGC TCAATACCAA CAGGCCGCGT
 151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GCGGAACGGC TCGGCATCGA
 251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG
 301 GATTGGATCA GGTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAGCGC
 351 TTCAGGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep
 1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQTWILRS VKRLNTNRP
 51 LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
 101 DWIRLRRTSS PLKFASASGA *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m628/g628 93.3% identity in 119 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS					
g628	MCVPLKPAGCGPPNSCVSILAAFS					
	10	20	30	40	50	60
	TVGSAASGLVSI					
m628.pep	TVGSAASGLVSI					
g628	TVGSAASGLVSI					
	70	80	90	100	110	120
	TVGSAASGLVSI					
m628.pep	TVGSAASGLVSI					
g628	TVGSAASGLVSI					
	70	80	90	100	110	120
	TVGSAASGLVSI					
m628.pep	TVGSAASGLVSI					
g628	TVGSAASGLVSI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

1004

```

a628.seq
1   ATGTGCGTGC CACTCAAACC GGCCGGATGC GGGCCGCCGA ATTCATGTGT
51  TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
101 ACACATGGAT TTTACGCTCG GTCAAACGGC TCAATACCAG CAAACCTCGT
151 CTGAAATCCT CGGCGGCTTC TTTGATCACA ACCACAGGGT CTGCCGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
251 CGGCAGGGAT TTTGCTGAAC GGACGGGTAC GCAGCGCAGT CCACAAACCG
301 GATTGGATCA GATTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAACGC
351 TTCGGGCGCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

```

a628.pep
1   MCVPLKPAGC GPNSCVSM LAAFSDGTSAP AALHTWILRS VKRLNTSKPR
51  LKSSAASLIT TTGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHVKP
101 DWIRLRRTSS PLKFANASGA *

```

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPNSCVSM LAAFSDGTSAP AALHTWILRSVKRLNTNRPR LKSSAASLIM					
a628	MCVPLKPAGCGPNSCVSM LAAFSDGTSAP AALHTWILRSVKRLNTSKPR LKSSAASLIT					
	10	20	30	40	50	60
m628.pep	TVGSAASGLV SIALTKMANGSASTAGILLN GRVRSVHVKPDWIRLRRTSS PLKFASASGA					
a628	TTGSAASGLV SIALTKMANGSASTAGILLN GRVRSVHVKPDWIRLRRTSS PLKFANASGA					
	70	80	90	100	110	120

```

m628.pep    X
             |
a628        X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

```

g629.seq
1   ATGACTGCca aacCTTTTTC CCTCAACCTG GCcaaCCTCC TGCTGCCggc
51  ggtatTGTTT GCCGTCAGcc tGtcggtTCGG cattgccgat TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCC GACAGCCAGC AAGTGATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGcgaT TGTGTTGACG GGCgcgtcga tagcgGtggc
201 gGGGAtgatt atgcagATTc TGATGCGCAA CcgtTTTGTC GAGCCTtcta
251 tggcgGGTGC GGGCCAAAGt gcgGCTTTGG GTttgcttct gAtgtccctg
301 ctgctgcctg CcgGcccgct gccggtcaAA ATGTCGGtag Ccgccgttgc
351 CGCGCTGATC GGGATGTTGG tctTtatgct gctaaccgC Cgcctgccac
401 cgacggcgca gctgatgGTg ccgCTGGTGG Gg.ttATTTT CGGCGGCGTG
451 GttgaGGCGG TGGCGACGTT TGTCGCGTAT GAGTTTGAGA TGCTGCAAAAT
501 GTTGGGCGTG TGGCAGCAGG GCGACTTTTC AAGCGTGCTG CTGGGGCGGT
551 ACGAGCTGCT TTGGATTACG GCGGTTTGG CGGTGTGTC CTACCTGATT
601 GCCGACCGGC TGACGATTTT GGGGTGCGG GAGACGTGA GCGTGAATT
651 GGGTTTGAAC CCGACGGCGG TGTGTTGGTC GGGTTTGATT ATTGTGGCAC
701 TGATTACATC GCTGGTCATT GTAACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAATATCGT CAGCCGCTG ATGGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGCGCC TCTTGGGCG GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGCATGATT GTGTTTCCGT TTGAAATTCC GGTCTCCACG
901 GTTTTGGTG TGTTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
951 ACCCGCTAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

```

g629.pep
1   MTAKPFSLNL ANLLLPAVL AVLSVGIAD FRWSDVFSLS DSQQVMFISR
51  LPRTFIAVLT GASIAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLLMSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGXIFGGV

```



```

g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
          190      200      210      220      230      240

          250      260      270      280      290      300
m629 .pep VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPEIPVST
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g629      VTVGNIPFIGLVVPNIVSRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFPEIPVST
          250      260      270      280      290      300

          310      320
m629 .pep VFGVLGTALFLWLLLRKPAYAVX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g629      VFGVLGTALFLWLLLRKPAYAVX
          310      320

```

```
a629.seq
1 ATGACTGCCA AACCTTTTTT CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51 GGTGTTGTTT GCCGTACAGC TGTCCGTGGG CGTTAGCCGAT TTCCGCTGGT
101 CGGATGCGTT TTCGTGTGCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCGAT TGTGTTGACG GGC CGCTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTC TGATGCGTAA CCGTTTTTGC GAGCCTTCTA
251 TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTTGCTTCT GATGTCCCTG
301 CTGCTGCCTG CCGCGCCGCT GCCCGTCAA ATGTCGGTTG CCGCCGTTGC
351 CGCGTTAATC GGGATGTTGG TGTTTTATGAT GCTTATCCGC CGCTGCCGC
401 CGACGGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGCGTG
451 GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAAT
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGCGGTGTTG CTCGGACGGT
551 ATGAACTGTT GTGGGCAACG GGGATTTTGG CTTTGTGTTG CTATTTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA CGGTGAACCT
651 GGGGCTGAAC CGGACGGCGA TTCGTGTGTC GGGGCTGATT ATTGTGGCTT
701 TGATTACGTC GCTGTTATAT GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCTTG ATAGGCGACA GGCTCGCCCA
801 AAGCCTGCCT GCGGTGCGTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTTCCGT TTGAAATTCC TGTATCGACG
901 GTCTTCGGCG TATTGGGTAC GCGGTTGTTT TTA TGCTTTT TGTAAAGGAA
951 ACCTGCTCAT GCGGCTCGA
```

```
a629.pep
1  MTAKPFSNLN TNLLLLAVLF AVSLSVGVD FRWSDVFSLS DSQQVMFISR
51 LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMAGAGQS AALGILLMSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMLLR RLPPTAQLMV PLVGIIFGGV
151 VEAVATFIAY ENEMLQMLGV WQOGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251 LVPVNIISRL IGDRLRQSLV AVALLGASLV LLCDITGRVI VFPFEIPVST
301 VFGVLGTALF LGWLLRKPAA AV*
```

[illegible]

1007

```

a629      GMLVFMMLIRRLPPTAQLMVPLVGIIFGGVVEAVATFIAYENEMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180
           190      200      210      220      230      240
m629 - pep  LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           |||||  ||  ||:|||||:|||||:|||||:|||||:|||||:|||||
a629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
           190      200      210      220      230      240
           250      260      270      280      290      300
m629 - pep  VTVGNIPFFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFFFEIPVST
           |||||  |||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      VTVGNIPFFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFFFEIPVST
           250      260      270      280      290      300
           310      320
m629 - pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||  |||||:|||||
a629      VFGVLGTALFLWLLLRKPAHAVX
           310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATTT TGGTGTGGCT ggctttgttt cccccatgt tttacggcat
51  g tacaacgtc GGCACACAGG CATTGGGTGC CTTAACGCCC GAttgtctgc
101 a acaaaqcat cgccacacgac ggcaattacg ccctcgccaa cgctttgggc
151 a tcaatatgt cccccgaaGc gggcgtgtTg ggcaaaatgc tgttcgGCGC
201 GATTtacttc ctgccgattt acgcgaccgt aTTTATTGTG GGcggtctct
251 g gGaagtCTT GTTCGCATCc gtACGCAAAc ACGAAATCAa CGAAGGTTTC
301 T TCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTGCGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCCG
451 GCCTTCCTGT TCTTCGCCTA CCCCGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGACG CGTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTT GCCCGCATCG
701 CTtcttgGCG CATTATTGCC ggCGTGATGA TCGGTatGat tGcgtatTCT
751 t cgctgatta acttcatCGg ttctgacacc aaagctatgt ttgctatgca
801 c ttggtacat ggcacttggT GGAaagatGa ttAtcactca ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF PPMFYGMYNV GAQAFGALT P DLLOQSIADH GNYALANALG
51  I NMSPAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAS VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 A FLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAGHADGL KNAVGTQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLINFIGSDT KAMFAMHLVH GTWKKDDYHS LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51  GTACAACGTC GGCACACAGG CATTGGGTGC GTTAACGCCCT GATTTGCTGC
101 AACAAAACAT CGCCAACGAC TGGCATTACG CCTTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GACAAAATGC TGTTTGGCGC
201 GATTTACTTC CTGCCGATTT ACGCGACTGT ATTTGTTGTG GCGGTTTCT
251 GGGAAGTTT GTTCGCCACC GTGCGCAAAc ACGAAATCAa CGAAGGTTTC
301 T TCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTGCGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCCTTCCTGT TCTTCGCCTA CCTGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCACTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGACG CGTTATCGG CAAACTGCCC GGCTCCATG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTT GCCCGCATCG
701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TCGGTATGCT
751 TCGTGTTCa ACTTCATCG TTCGGACACC AACGTATGT TTGCTATGCC

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1008

801 T TGGTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
 851 T GCGGACCGA CCCTGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
 901 T ACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
 951 G GCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTGCC AACCTGTTG
 1001 C CCCGATTTT CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
 1051 GCGCGCAGCA ATGGCTAA

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

m630.pep
 1 MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQONIAND WHYAFANALG
 51 I NMSSEAGVS DKMLFGAIYF LPIYATVFVV GGFWEVLFAT VRKHEINEGF
 101 F VTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
 151 A FLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVGTQTIT
 201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
 251 S LFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
 301 Y GALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
 351 ARSNG*

m630/g630 93.5% identity in 275 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIANDWHYAFANALGINMSSEAGVS					
g630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQSIADHGNALANALGINMSPEAGVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m630.pep	DKMLFGAIYF LPIYATVFVVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
g630	GKMLFGAIYF LPIYATVFIVGGFWEVLFASVRKHEINEGFFVTSILFALIVPPTLPLWQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m630.pep	ALGISFGVVVAKEVFGGTGKNFMN PALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
g630	ALGISFGVVVAKEVFGGTGKNFMN PALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m630.pep	QWAAHGADGLKNAVGTQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
g630	QWAAHGADGLKNAVGTQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m630.pep	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW					
g630	GVMIGMIAMSSLFNFIGSDTKAMFAM----HLVHGTWKKDDYHSLYIK.					
	250	260	270	280		
	310	320	330	340	350	
m630.pep	YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

a630.seq
 1 ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
 51 GTACAACGTC GCGGCACAGG CATTGCGTGC GTTAACGCCC GATTGCTGTC
 101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
 151 ATCAATATGT CGTCTGAAGC GGGCGTGTTG GGCAAATGC TGTTGCGCGC
 201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATTGTC GGCGGTTTCT
 251 GGAAGTTTT GTTCGCCACC GTGCGCAAC ATGAAATCAA CGAAGGTTTC
 301 TTTGTTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
 351 GTGGCAGGCA GCTTTGGGTA TTTCTTTTCG CGTTGTGGTT GCGAAAGAAG
 401 TATTCGCGCG TACAGGTAAG AACTTCATGA ACCCTGCGCT GGCAGGCCGT
 451 GCCTTCCTGT TCTTCGCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
 501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG
 551 CACACGGTGC AGACGGCCTG AAAACGCCA TAACCGGTCA AACCATCACT
 601 TGGATGATG CGTTTATCGG CAAACTGCCG GGCTCCATCG GCGAAGTCTC
 651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG

1009

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701 CTTCTTGGCG CATTATTGCC GGCCTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGGTTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGGC AACCTGTTTG
1 001 CCCGATTTC CGACTATTTT GTCGCACAAG CGAACATCAA ACGCAGAAAG
1 051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

a630.pep

```

1  MMILVWLALF PAMFYGMYNV GAQAFGALT P DLLQOSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFI V GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIDYF VAQANIKRRK
351 ARSNG*

```

m630/a630 98.3% identity in 355 aa overlap

m630.pep	10	20	30	40	50	60
a630	10	20	30	40	50	60
m630.pep	70	80	90	100	110	120
a630	70	80	90	100	110	120
m630.pep	130	140	150	160	170	180
a630	130	140	150	160	170	180
m630.pep	190	200	210	220	230	240
a630	190	200	210	220	230	240
m630.pep	250	260	270	280	290	300
a630	250	260	270	280	290	300
m630.pep	310	320	330	340	350	
a630	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

g635.seq

```

1  ATGACCCGGC GACGGGTCGG CAAGCAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTGGCGT ATTTAGATA CACGATGACG
101 GGGATTTCCT ACTGCGCGAG CTGTTGAAA GACAGGCGAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCG CATATCCTCA AACGACGCGC
201 GCATCTGTTC CTTACCCAGT TTTTCCAACA CTTCTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAGCCG CCCCAGGA

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1010

301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCGCGCGC GCTTTCCAAC
 351 TCTGCAATTT GATTTTCCG TAAACAACAG GATTATCGTT AACATCGGT
 401 GCAGCATTCA AACGATAAGA CAAGGGTCTG TACCAGATTA G

This corresponds to the amino acid sequence <SEQ ID 2034; ORF 635.ng>:

m635.pep
 1 MTRRRVGKQN RIAIHSAYR KMVFAVFQI HDDGDFQLRE LFERQGIAR
 51 LKTQIGHNAP HILKRRALHF LTQFFQHFFF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IPPREPTLQF DFSVNNRIIV KHRCSTQIR QGSVPD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2035>:

m635.seq
 1 ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG
 101 GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCCG
 151 TTCAAAACCC AAATCAGGCA TAATGCGCCG CATATCCTCA AACGACGCGG
 201 GCATCTGCTC CTTATCCAGT TTTTAAACA CGTCTCTTC CGTCAGCTTT
 251 TGCCCGTAAA AATTGTTCAA AAGCGTCACC ACCGAAGCCG CCCCAGGAG
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACCTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2036; ORF 635>:

m635.pep
 1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIAR
 51 EKTQIRHNAP HILKRRGHLH LIQFF*HVLV RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/g635 80.0% identity in 130 aa overlap

	10	20	30	40	50	60
m635.pep	MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHNAP					
g635	MTRRRVGKQNRIAIHSAYRKMVFAVFQIHDDGDFQLRELFERQGIARFKTQIGHNAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m635.pep	HILKRRGHLHLLIQFFXHVLFRLLPVKIVQKRRHRSRPAGKIQILLYNIEIAPFFPTLHF					
g635	HILKRRALHFLTQFFQHFFFRLLPVKIVQKRRHRSRPAGKIQILLYNIEIPPREPTLQF					
	70	80	90	100	110	120
	130					
m635.pep	DFSISNRIIVDX					
g635	DFSVNNRIIVKHRCSTQIRQGSVPDX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2037>:

a635.seq
 1 ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG
 101 GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCCG
 151 CTCAAAACCC AAATCAGGCA TGATGCGCCG CATATCCTCA AACGACGCGC
 201 GCATCTGCTC CTTATCCAGC TTTTCAACA CGTCTCTTC CGTCAGCTTT
 251 TGCCCGTGAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGAG
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACCTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2038; ORF 635.a>:

a635.pep
 1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIAR
 51 LKTQIRHDAP HILKRRALHL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/a635 95.4% identity in 131 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

1011

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m635 - pep      MTQRRVGKQNR IAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHNAP
                  |||
a635            MTQRRVGKQNR IAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHDAP
                  |||
                  10      20      30      40      50      60

                  70      80      90      100     110     120
m635 - pep      HILKRRGHLLLIQFFXHVLF RQLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
                  |||
a635            HILKRRGHLLLIQFFXHVLF RQLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
                  |||
                  70      80      90      100     110     120

                  130
m635 - pep      DFSISNRIIVDX
                  |||
a635            DFSISNRIIVDX
                  |||
                  130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  A TGATTGGCG GACAGTTTAT CGTAGTtgGc attGTAGGCA AAAACGCACT
51  T GCCCGCTTT GTTGATAATA ttgtcGTGAA TatcGGAATA GTTGACATAG
101 T TGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
151 T TTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgCCACGG
201 A AATATTGCC GCTGacttcg ctgtcgtTGG TGTACATATA GTGGACGGCG
251 A AACGCAGGT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
301 A TTGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 G CGCgcccgg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTACAG
401 C GCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 A GAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 C AACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 G CTGGCAGGC TCATACCGGA ACGGTAACG GTCAGGTTGC GGAGCGTTAC
601 G TCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCC CCTTCGATGG
651 T TGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATATAA
701 A GTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 G CGCGCGGCA AAAATTTCGG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 C GGTGCGCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCACG
851 G CCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 C GTTCGGTAT GGCCGAACAA AATAAGCAT CATTCAAATG TGCCTGTTTT
951 T ATAGCGAAA CCGCTGAAA CCGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGNALARF VDNIVVNIGI VDIVEHDAI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVRAG
101 I GKNAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 R TMKVYAERI IKNIVVFNQ ARGGFFEINT GIHCWQAHTG TGNGQVAERY
201 V RRVYGYGTP ALVPFDGCGT VGRPFNRNRF VDIKFLIYA GSQFDRIAR
251 G AGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 R SVWPNKIKH HSNVPVFIAR PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTGGC ATTATAGGCA AATACGCACT
51  TGCCCTGCCCT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 T TGAGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
151 T TTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACGG
201 A AATATTGCC GCTGATTTTC GTGTCGTTGG TGTACATATA GTGGACGGCG
251 A AACGCAAAAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
301 A TTGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 G CGCACCAGG TGCGTTCCAA ACGGTAACGC CGTGGCCGCG CTCGTTACAG
401 C GCAAGATCG CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 A GAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTTGTGTT
501 C AATCAGGGC GCGCGGGGCA GTTCTTCGA GATAAATACC GGCATCCATT
551 G CGGCGCAGG TCATACCGGA ACGGTAACG GTCAGGTTGC GGAGCGTTAC
601 G TCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCG CCTTCGATGG
651 T TGCGGAACG GTCGGCAGG CCTTCAATCG TAATCGGTTT GTCATGTGA
701 A GTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 G CGCGGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```

1012

This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

m638.pep
 1 MIGEKFIVVG IIGKYALACL VDNVVVNIIGI VDIVEHNALI AAADGDIVEY
 51 FEPLGKHQHI AHIVAHGNIA ADFAVVGVIH VDGETQIAEA VVFGVVRAG
 101 IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
 151 RTMQIYADRI IQNIVVFNOG ARGSSFEINT GIHCGQAHTG TGNQQAERY
 201 VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
 251 GAGKCGIPIS IIGS*

m638/g638 88.2% identity in 254 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVG	IIGKYALACL	VDNVVVNIIGI	VDIVEHNALI	AAADGDIVEY	FEPLGKHQHI
g638	MIGGQFIVVG	IVGKNALARE	VDNVVVNIIGI	VDIVEHDALV	AAADGDIVEH	FEPLGKHQHI
	10	20	30	40	50	60
	70	80	90	100	110	120
m638.pep	AHIVAHGNIA	ADFAVVGVIH	VDGETQIAEA	AVVFGVVRAG	IGKNAVPPFG	NVVADDLRTG
g638	AHIVAHGNIA	ADFAVVGVIH	VDGETQVAAE	AVVFGVVRAG	IGKNAVPPFG	NVVADDLRAG
	70	80	90	100	110	120
	130	140	150	160	170	180
m638.pep	CVPNGNAVAL	LVHAQSRVAD	DFILAHHRIG	RTMQIYADRI	IQNIVVFNOG	ARGSSFEINT
g638	RVPNGNAIAA	LVHAQSRVAD	DFILAHHRIG	RTMKVYAEIR	IQNIVVFNOG	ARGSGFFEINT
	130	140	150	160	170	180
	190	200	210	220	230	240
m638.pep	GIHCGQAHTG	TGNQQAERY	VRRVYGYGTP	APVAFDGCCT	VGRPFNRNRF	VNVKFGFIYA
g638	GIHCWQAHTG	TGNQQAERY	VRRVYGYGTP	ALVPFDGCCT	VGRPFNRNRF	VDIKFGLIYA
	190	200	210	220	230	240
	250	260				
m638.pep	GSQFERIARP	GAGKCGIPIS	IIGSX			
g638	GSQFDRIARP	GAGKCNFGKV	VLRGNVDDGC	RCRLKNAAGG	KYQHLQPYTER	GCVHSVPLF
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

a638.seq
 1 ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
 51 TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
 101 TTGAGCATGA TGCCTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
 151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCGG
 201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
 251 AAACGCAAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGTCTGGT
 301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
 351 GCGCGCCGGG CGCGTTCCAA ACGGTAACGC CATTGCCCGC CTCGTTACAG
 401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
 451 AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
 501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
 551 GCGGGCAGGC TCATACCGGA ACGGTAACG GTCAGGTTGC GGAGCGTTAC
 601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCCTGTCT CCTTCGATGG
 651 TTGCAGAACG GTCGGCAGGC CCTCAATCG TAATCGGTTT GTCGATGTGA
 701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCGCCCGG
 751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

a638.pep
 1 MIGGQFIVVG IVGKNALARE VDNVVVNIIGI VDIVEHDALV AAADGDIVKH
 51 FEPLGKHQHI AHIVAHGNIA ADFAVVGVIH VDGETQIAEA VVFIGVVRAG
 101 IGKNAVPPFG NIVADDLRAG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
 151 RTMQIDADRI IQNIVVFNOG ARGSSFEINT GIHCGQAHTG TGNQQAERY
 201 VRRVYGYGTP APVSFDGCRV VGRPFNRNRF VDVKFGLIYA GSQFERIARP

1013

251 GAGKCGIPIS IIDSW*

m638 /a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638 .pep	MIGEKFIVVGIIGKYALACLVNVDVNVNIGIVDIVEHNLIAAADGDIVEYFEPLGKHQHI					
a638	MIGGQFIVVGIVGKNALARFVDNVVNIGIVDIVEHDALVAAADGDIVKHFEPLGKHQHI					
	10	20	30	40	50	60
m638 .pep	AHIVAHGNIAADFVAVGVHIVDGETQIAEAVVFGVVVRAGIGKNAVPPFGNVVADDLRTG					
a638	AHIVAHGNIAADFVAVGVHIVDGETQIAEAVVFGVVVRAGIGKNAVPPFGNIVADDLRTG					
	70	80	90	100	110	120
m638 .pep	CVPNGNAVALVHAQSRVADDFILAHHRIGRTMQIYADRIIQNIIVFNQARGSFEEINT					
a638	RVPNGNAIALVHAQSRVADDFILPHHRIGRTMQIDADRIIQNIIVFNQARGSFEEINT					
	130	140	150	160	170	180
m638 .pep	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCRTVGRPFNRNRFVNVKFGFIYA					
a638	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVSFDGRTVGRPFNRNRFVNVKFGFIYA					
	190	200	210	220	230	240
m638 .pep	GSQFERIARPGAGKCGIPISIIGSX					
a638	GSQFERIARPGAGKCGIPISIISWX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTTC TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACA CCTATAAATA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTCACG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAAATGGG GCAGGCGCAG TTTCCCGCGG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGCGAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVAVHYM YTNDSEVSGN ISVGNMNGYV LMFSERLKVF DNIIVGSRD*
151 GIMLVVNVYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201 AIEGTSLHDN SFINNGSQVK YVSTRFLDWS EGGHGNYSWD NSPFDLNGDG
251 FGDSAYRPDG IIDQIWRAP VSRLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEKET RQSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1014

m639-1.seq

```

1   ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AACTGCCCC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGAA
201 CGCACCCTGG GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAAAC CCTACAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCC GATATTACAG ACAACATTAT
501 CAACAAGGCA GGCAAGTGCG TATTGCTTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAA TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTCAGCA CGCGCTTCT CGATTGGAGC GAGGCGGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG CCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAAATGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CGGCAGTCGG
1001 AATGGGCGAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

m639-1.pep

```

1   MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEISGN ISVGNNMGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLNYYNYS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLDN SFINNESQVK YVSTRFLDWS EGGHGNYSW SDNSAFDLNGDG
251 FGDSAYRPNG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIOTRYQAM KDELLEKETV RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

g639-1.pep	10	20	30	40	50	60
m639-1	10	20	30	40	50	60
g639-1.pep	70	80	90	100	110	120
m639-1	70	80	90	100	110	120
g639-1.pep	130	140	150	160	170	180
m639-1	130	140	150	160	170	180
g639-1.pep	190	200	210	220	230	240
m639-1	190	200	210	220	230	240
g639-1.pep	250	260	270	280	290	300
m639-1	250	260	270	280	290	300
g639-1.pep	310	320	330	340		
m639-1	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

a639-1.seq

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```

1  ATGAGCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AACTGCCCC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTCG GTCGGCGTCT
101 A.TCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGAA
201 CCGCGCCGGC GCGCAGGTCG TCGGCAACGA TATTTCCAAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACAACA CCTATAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAACATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTCAGCA CGCGCTTCT CCACTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCACCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATGGGC GCAGGCGCAA TTTCCGCGC TTTGCGCTGG CGGCGTGGTG
901 GACAGCAAA CCGTGATGAA GCCTTATGCC CCAAAATTC AAACCGTTA
951 TCAGGCGATG AAGGACGGC TGCTCAAAA AGTCGAAAC GGCAGTTGG
1001 AATGGGCGAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 S.DLRFVHYM YTNDSEISGN ISVGNMGGYV LMFSERLKVF DNIIVGSRDQ
151 GIMLNVVYNS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTSLHDN SFNNESQVK YVSTRFLDWS EGGHGNYSWD NSAFDLNGDG
251 FGDSAYRPNG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

```

a639-1/m639-1 98.8% identity in 344 aa overlap

a639-1.pep	10	20	30	40	50	60
	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	10	20	30	40	50	60
	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
a639-1.pep	70	80	90	100	110	120
	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
m639-1	70	80	90	100	110	120
	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
a639-1.pep	130	140	150	160	170	180
	ISVGNMGGYVLMFSERLKVFVFNIAVGSRDQIMLNVVYNSDIHDNIINKAGKCVFAYNAN					
m639-1	130	140	150	160	170	180
	ISVGNMGGYVLMFSERLKVFVFNIAVGSRDQIMLNVVYNSDIHDNIINKAGKCVFAYNAN					
a639-1.pep	190	200	210	220	230	240
	YDKLSANHFENCQIGIHFTAIEGTSLHDNSFINNESQVKYVSTRFLDWSSEGGHGNYSWD					
m639-1	190	200	210	220	230	240
	YDKLFANHFENCQIGIHFTAIEGTSLHDNSFINNESQVKYVSTRFLDWSSEGGHGNYSWD					
a639-1.pep	250	260	270	280	290	300
	NSAFDLNGDGFGDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
m639-1	250	260	270	280	290	300
	NSAFDLNGDGFGDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
a639-1.pep	310	320	330	340		
	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLN					
m639-1	310	320	330	340		
	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLN					

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGC
51  TATGTCCTGT TTTTCAATCC GCGGTATGTC TCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151 GcggAgcgTc tgcctGATT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201 TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251 GCGtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATCGATA CGCTGATGGC
351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGTCGA TAAGTTCATC
451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCAGCGT
501 GCGCCCGGGC GACATCATCA GcggtGCGAC TgttaCACTG ATGGTGGTTA
551 ACGACAGCAT CCAGCGTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
601 GGTTCGGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651 CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCCGACAAGC
701 AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAAGGC CGTCGGCCAT
751 CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
801 GGCCGGCGTG GCCGATCACG CCGAACAGGG CGATCCTGAC GATACCTTTA
851 TTGATTTGTA TGTTCCTTG GTCAGCCAGC CTTCCATCGG TAAAGCCTG
901 CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACCCGGGCA
951 GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCCG
1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCG TCGAGCTGTC
1101 TGCCGCCGAT GCGCCGCGTT TTAAAGAGT TTCTTGGTTT ACCATCCCTG
1151 AAGCGTAGC GTTTGACGGT GCGGAGCCGT GGCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
1  MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAE VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151 DKYIGLNFIF NPPTPSVAPG DIISGATVTL MVVNSDIQRS YKVIANQYRL
201 GCDKALQTAS ASDVREAAPA SETRPRRMAN PDKQDILSWD ELLKQKAVGH
251 LHITLDQINK LFEKGGKAGV ADHAEQGDPD DTFIDLYVAL VSQPSIGKSL
301 LGEDGWAHLQ KRLKPGQAV LVAGEGRYSW KSGYVRGGI FDRIEMIQGE
351 NSFRTDAQH ERVVELSAAD APRFKEVSWF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCCTGATT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201 TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGTTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGT
351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

	10	20	30	40	50	60
m640.pep	MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAVFVFLTAALPAYAERLPDFLAK					
g640	MIHIISILKSIGISGIAMSCFSIRMSAFRARITAFFTAFVFLTAALPAYAERLPDFLAK					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m64 O.pep  IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITDDAVNTRGYSSKPIDTLMVLAN
            |||||||||||||||||||||||||||||||||||||||||||||||||||
g64 O      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITDDAVNTRGYSSKPIDTLMALAN
            70      80      90      100     110     120

            130     140
m64 O.pep  DGTIAGAKLVDHHEPIMLIGIPH
            |||||||||||||||
g64 O      DGTIAGAKLVDHHEPIMLIGIPQSRVDFIDKYIGLNFINKPPTPSVAPGDIISGATVTL
            130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a64 O.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51 CATGTCCTGT TTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTGT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCTGATT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251 GCGTTTACAA AGCGGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGTT GATCACCATG
401 AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a64 O.pep (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKMSAFR ARITAFFAAF VFLTAALPAY
51 AERLPDFLAK IQPSEIVPGA DRYSKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

            10      20      30      40      50      60
m64 O.pep  MIHIISILKSIGISGIVMSCFSIKMSAFRARITAFFAAVFVFLTAALPAYAERLPDFLAK
            |||||||||||||||||||||||||||||||||||||||||||||||||||
a64 O      MIHIISILKSIGISGIVMSCFSIKMSAFRARITAFFAAVFVFLTAALPAYAERLPDFLAK
            10      20      30      40      50      60

            70      80      90      100     110     120
m64 O.pep  IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITDDAVNTRGYSSKPIDTLMVLAN
            |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
a64 O      IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITDDAVNTRGYSSKPIDTLMALAK
            70      80      90      100     110     120

            130     140
m64 O.pep  DGTIAGAKLVDHHEPIMLIGIPH
            |||||||||||
a64 O      DGTIAGAKLVDHHEPIMLIGIPH
            130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g64 2.seq
1  ATGCGGTATC CGCGCAATC GCGGTTTTG CAGAATGCCG CGCGTTGCCT
51 TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTTGCCCG CTATCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGCTTTCG TGTTCTCTCT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201 TGCCGATGAA GACTTTTTCG AGGGCGCAGG CGTCGGTCAG GGTGTGTTCC
251 TGCAGGAAGC TGCGGATGTC TTCGGGCAAA GCGTAgTcgc gGGCAACGGC
301 GGcaaagcgc ACatcggtTT Gcacggcgtc gagCAGGGtt tggTTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTCTTCGG CCGTGCGCGG GACGAACTGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451 GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAAC
501 CCTTCGCGCC CAAGAGTTTT TGCAACATT GCGCGCGCGc gTAAGTGTAT
551 TCCGTGGCGa ggGTTTTGac gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggGCGcgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCCG
651 AAACCTGATG GCGGCGTTGG ATTTCCGGGC GTTCGTAATC GACGAATCTG

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```

701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCAGGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCACGGCG
851 GTTGCAGGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTCGACGCG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgC CgtttttgCG ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCCTGCCAGT ATTTGCGGGC
1051 GttgACGTAA ATGGTTtgtt cgtcggtata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAT cgCgcgcgcg gaggtTtcgg gttcggtaAc gcccaaacgg
1151 cggctttcgC ctTTGAAAAT CATGTCCAAA CCTTGTCGCA CTTCGcttc
1201 gccgccgaac tCTTGACAGAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

g642.pep

```

1 MRYPPQSAVL QNAARCLLR PKSACRRICP LSAISAVQYI FADVQQEGC
51 GVVFVLLYED KKS GDDFADE DFLQGAGVGQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLVFVQLN ACFFFFGGGA DELVVNFGIK HIVRAFKNRE
151 GADIDGDIAG WVS AFKTLRA QEFLQHLRGG VSVFRGEGFD DVRLHLQMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFHN
251 AVRHADQLQA AADKDVLEA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVCFGDEQQV DDFGEFAVFA LFGGNEEEVA LRIALPVFRG
351 VDVNGLFVGI FVAGLHFACN RRAGGFGFGN AQTAFAFEN HVQTLCDLRF
401 AAELLQRLQH QRAFDAGTQR NGHAVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

m642.seq (partial)

```

1 GCCTGCCGCC GTATTTGCCG GCTACCCGCA ATATCGGCAG TCCAATATAT
51 CTTTGGCGAT GTCGTTACAG AGGAAGGCTG CCGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GCGGATGATT TTGCCGATAA AGACTTTTTG
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTT CTGCAGGAAG CTGCGGATGT
201 CTTCAGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAAGCGGT CGAGCAGGTT TTGGTTTTTG TCCAACCTCA TGCGTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CCGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CCGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TGCGCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTTCG CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGGCGCGCG
601 GATTTCGCGG CGTTCGTAAT CGACGAATTT GATGTCGTG CCGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCGAGC ATTTCGGCAT
801 CGATGCGGTT GACGGCGTAA CCGACGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCAGATTTC CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGG CGTGACGTA AATGTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGACTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CACCCAAACC GCGCCCTCG CCTTGAAAA
1101 TCATCTCCAA ACCTGCGCG ACTTGCGCTT CATCGCCGAA CTCTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

m642.pep (partial)

```

1 ACRRICPLPA ISAVQYIFAD VVQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFQIKHIV RAFKNREGAD VSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADVSTFI FKDVFNHVR HADQLQAAAD KDVLEAQTG
251 SVALGEFHG GCRHFGIDAV DGVTGDAQAF GCEGFAADVC FGDEQQVDDF
301 GEFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVDIFV GLHFACNRRA
351 GGFVGNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHQRA FDAGTQRNGH
401 AVMPRNP

```

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m642/g642 90.4% identity in 407 aa overlap

m642.pep				10	20	30
				ACRRICPLPAISAVQYIFADV	VQEGCGVFVFR	LYED
g642	MRYPPQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADV	VQEGCGVFVFL	LYED			
	10	20	30	40	50	60
m642.pep	40	50	60	70	80	90
	KESGDDFADKDFLQAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLV	FVQLH				
g642	KKSGDDFADEDFLQAGVGQGVFLQEAADVFGQSVVAGNGGKADIGLHGVEQGLV	FVQLN				
	70	80	90	100	110	120
m642.pep	100	110	120	130	140	150
	ACFFFFGGGADKLVVNFGIKHIVRAFKNREGADVSDIAGGVSAFKTLRTQEF	LQHLRGG				
g642	ACFFFFGGGADELVVNFGIKHIVRAFKNREGADIDGDIAGVWSAFKTLRAQEF	LQHLRGG				
	130	140	150	160	170	180
m642.pep	160	170	180	190	200	210
	VSVFRGEGFDDVRLHQLMGDGNRRNGMADVAVKNLGNLMAAPDFAAFVIDE	FDDVADVS				
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVKDFGNLMAALDFAAFVIDE	SDIVADIS				
	190	200	210	220	230	240
m642.pep	220	230	240	250	260	270
	FQIFKDVFNHAVRHADQLQAAADKDVLERAQTSVALGEFHHGGCRHFGIDA	VDGVTDGA				
g642	VQVVKDVFNHAVRHADQLQAAADKDVLERAQTSVAPGEFHHGGCRHFGIDA	VDGVTDGA				
	250	260	270	280	290	300
m642.pep	280	290	300	310	320	330
	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRVALPVFRG	VDVNGLSVDI				
g642	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRIALPVFRG	VDVNGLFGVI				
	310	320	330	340	350	360
m642.pep	340	350	360	370	380	390
	FVVGLHFACNRRAGGFGFGNTQTAAALAFENHLQTLRDLRFIAELLQWLQ	HQRAFDAGTQR				
g642	FVAGLHFACNRRAGGFGFGNAQTAAAFENHVQTLCDLRFIAELLQRLQ	HQRAFDAGTQR				
	370	380	390	400	410	420
m642.pep	400					
	NGHAVMPRNP					
g642	NGHAVMPRNPX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

```

1  GCCTGCCGCC GTATTGCCCC GCTATCCGCA ATATCGGCAG TCCAATATGT
51  CTTTGCGGAT GTCGTTCCAGC AGGAAGGCTG CGGTGTCTTC GTGTTCCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTGT
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTT CTGCAGGAAG CTGCGGATGT
201 CTTGCGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACTTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TGCAGGCGGG CGTAAGTGTA TTCCGTGGCG AGGGTTTGA
501 CGATGTTTCG CTCCATCAGT TGATGGGCGA CGGGTGCAAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGGCGCCCG
601 GATTTCGCGG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTTCCAGGTT TTCAAGGGTG TATTCCATAA TGCCGTGCGT CATGCCGATC

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1020

```

701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCAGGC ATTTCCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GCGGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTCCGGC CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```

a 642 .pep Length: 407
1  ACRRICPLSA ISAVQYVFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
51  QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VSDIAGGVS AFKTLRAQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVSFQV FKGVFHNAVR HADQLQAAAD KDVLERAQTG
251 SVALGEFHHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVAFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFVV RLHFSGNRRR
351 GGFGFGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

m642/a642 95.8% identity in 407 aa overlap

```

m642 .pep      10      20      30      40      50      60
ACRRICPLPAISAVQYIFADVQQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
|||||
a 642          10      20      30      40      50      60
ACRRICPLSAISAVQYVFADVQQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
|||||

m642 .pep      70      80      90     100     110     120
LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLVVNFGIKHIV
|||||
a 642          70      80      90     100     110     120
LQEAADVFGQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLVVNFGIKHIV
|||||

m642 .pep     130     140     150     160     170     180
RAFKNREGADVDSIAGGVSAFKTLRTOEFLQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
|||||
a 642          130     140     150     160     170     180
RAFKNREGADVDSIAGGVSAFKTLRAQEFQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
|||||

m642 .pep     190     200     210     220     230     240
RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVSFQIFKDVFNHVRHADQLQAAAD
|||||
a 642          190     200     210     220     230     240
GRNGMADVAVKNLGNLMAAPDFAAFVIDESDVVADVSFQVFKGVFNHVRHADQLQAAAD
|||||

m642 .pep     250     260     270     280     290     300
KDVLERAQTG SVALGEFHHGGCRHFGIDAVDGVTDGAQAFGCEGFAADVCFGDEQQVDDF
|||||
a 642          250     260     270     280     290     300
KDVLERAQTG SVALGEFHHGGCRHFGIDAVDGVTDGAQAFGCEGFAADVCFGDEQQVDDF
|||||

m642 .pep     310     320     330     340     350     360
GEFAVFALFGGNEEEVALRVALPVFRGVDVNGLSVDIFVVGHLHFACNRRAGGFGFGNTQT
|||||
a 642          310     320     330     340     350     360
GEFAVFALFGGNEEEVALRVALPVFRGVDVNGLSVGIFVVRHLHFSGNRRAGGFGFGNAXT
|||||

m642 .pep     370     380     390     400
AALAFENHLQTLRDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
|||||
a 642          370     380     390     400
AALAFENHVQTLCDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
|||||

```

1021

370 380 390 400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2063>:

g643.seq

```

1   ATGGTGTTC CTTGATGTT GTTGGCGACA ATCAGgTcgg CTACGCTGAC
51  gttgtancGt TTGGcaATGt tGaaCAgggt gtcgccTTCT ACAACGCGGT
101 GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTTGCCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TGCCCGGCGT TtgCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGagaTGTT TCTTCAGCCT GCCGCGCag gTTGTTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGat
351 GACCTGCGCg aGTGtTCCGG TTTGGGTTTC agacgGCATG GCAGTCTGTT
401 TTTcggTTTG a

```

This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>:

g643.pep

```

1   MVLPLMLLAT IRSATLTLXR LAMLN RVSPS TTRWMLAWSG EVSASPSAAL
51  ATRVSKRARR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFGGMTCA SVAVWVSDGM AVCFSV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2065>:

m643.seq

```

1   ATGGTGTTC CTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTTCGG CTTGCCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAGCGGT
201 ATGTTGCGGA GATGCGGAAA TTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGAGATGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAT
351 GATCTGCGCG AGTGTTCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCGGTTTG A

```

This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>:

m643.pep

```

1   MVLPLMLLAT IRSATLTL*R LAMLN RVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAAAVCCG DAEILCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGMICA SVAVWVSDGM AVCFSV*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*.

ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from *N. gonorrhoeae*:

m643/g643

```

              10      20      30      40      50      60
m643.pep      MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR
              |||||
g643           MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEVSASPSAALATRVSKRARR
              10      20      30      40      50      60

              70      80      90      100     110     120
m643.pep      LPSAAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGMICA
              |||||
g643           LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFGGMTCA
              70      80      90      100     110     120

              130
m643.pep      SVAVWVSDGMVAVCFVSX
              |||||
g643           SVAVWVSDGMVAVCFVSX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2067>:

1022

```

a643.seq
1  ATGGTGTTC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCCTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTGCGCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
351 GATCTGCGCG AGTGTTCGGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTGCGTTTG A

```

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

```

a643.pep
1  MVLPLMLLAT IRSATLTL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGTICA SVAVWVSDGM AVCFVS*

```

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAAL	ATRVSKRTRR				
a643	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAAL	ATRVSKRTRR				
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGMICA					
a643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGTICA					
	130					
m643.pep	SVAVWVSDGMVCFVSX					
a643	SVAVWVSDGMVCFVSX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

```

g644.seq
1  ATGCCGTCTG AAAGGccgGC GGATTGTTGC CCGGTGCACT TTGTGGTAAA
51  GTTTAGAAAA TTAACCTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CCATGGACAC GGCTGCTTTT TTAAagcaca tcgaatCCGC
201 ATTCCCCCGC ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC
301 GACAAAAAAC ACGGCGGGCG CAAGGGCAGT CAGTTTGAAA TCCAAGAAGT
351 CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
401 TCGAAGGCGC GCTGTGTGTT CAGCCTCTGC AAGagttcgg cggcgaagcG
451 CAAGTCGCAC AAGGTTTGA CATGATTTTC AAagggcga aa gccgccgttt
501 gggcgTtacc gaacccgaAa cctccggcgc gGcgATTGCA CGCGAAAtgc
551 agtcctgcta cgaatatacc gacgaacaaa CCATTACGT caaCGCCGCG
601 AAATACTGGC AGGGCAATTC GCAAAGCGAC TTCCTcctcg ttgccgccaa
651 agagcgcaaa aacGGcaaac tcgccaaagt CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CCTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAAATC TCCTGGGGCG ACCTGCGCGG TTTGCGCGCG TTCCAAAACA
851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACATCC TTGACAACCT GAACCGATAT GTCCGCAACG ATATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCAACG CCGCATCAG GTTTCGAAA
1001 TCCTTTACCG CTACGCTGTC CATTCGTTT CGcccgctgc GCccgTCGCC
1051 CATCAATTGA TGGAGGCGAA catcgTCAAA ACcctCGCCA CGGAATACAC
1101 TTAcgcCGCC GCGCAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTGT
1151 AACGCGGACA CCCAGCCGGC AATATCGCCA TCGATATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAAGT
1251 CGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATTAAG TTGGACAAAA
1301 accaaaCCCT Gctcgacgcc gtgCAAaccg atGTCcgctt tgCCGCGGTT
1351 GCCcgcgact ACGCTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCTGACC GACGCTGCG CCCTGCAAAA AGTCTTCATC GGCAAAATCA

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1023

1451 TCGCCCGACT TTTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644.pep

1 MPSEPADCC PVHFVVKFRK LTLCNGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKHGGRRKS QFEIQEVLRI AGHYGVVPTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLDMIF KGESRRLGVT EPETSGAIA REMQSCYEY DEQTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNIIFIRSRL QLIGMTHGIM
 301 EYILDNLNRY VRNDIRFVDY ERREIQRHQ VSEILYRYVC HSVSPVAPVA
 351 HOLMEANIVK TLAETTYAA AQMLQKLLGA KGFERGHFAG NIAIDIRPFT
 401 IFEGPNMPLY AEIYDQFVRA TAEKEAGIK LDKNQTL LDA VQTDVRFVAV
 451 ARDYALPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQEEHEDTTA
 501 FLLNDIRKDI LDCRYCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644.seq

1 ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
 51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG CGCGTTTGAC CGGCCGCCGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAG CTATGGACAC GGCTGCTTTT TTAAGCACA TCGAATCCGC
 201 ATTCGCGCGC ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC
 301 GACAAAAAAT ACGGCGGGCG CAAGGCGAGC CAGTTTGAAA TCCAAGAAAT
 351 CcTGCGGATT CCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCCG CGATGAAGCG
 451 CAAGTCGCGC AAGGTTTGGA GATGATTTTC AAAGGCGAGG CCGCGGGTTT
 501 GGGTGTTACC GAACCCGAAA CCTCCGGCGC GCGGATTGCA CGCGAAATGC
 551 AGTCTACTA CGAATATATC GACGGACAAA CCATTTACGT CAACGCCGCG
 601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
 651 AGAGCGCAAA AACGGCAAC TCGCCAAAAGT CATCGACCTG CTGCTCGTCC
 701 CCRAAACATA CATCCGCTGC GAAACCTCG CATCCGAAGG CTTCGCCGCC
 751 GTCCGTTAGC CCGTCAACCG CATCGATGCC GAAATGCTG CAACCGCCGT
 801 GATGAACTC TCCAGAGCG ACGCTGCCGG TTTGCGGCGC TTCCAAAACA
 851 TCTTTATCCG CAGCCGCCCTG CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT
 951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CCGCCATCAG GTTCCGAGA
 1001 TTCTTTACCG CTACGCTGCG CATTCGTTT CGCCTGTGTC CCCCGTCGCC
 1051 CATCAGCTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
 1101 TTACGCCGCC GCGCAATGT TGCAAAAAC CTGGGGTGGC AAGGGTTTGT
 1151 AACGCGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACAGTT
 1251 TGTCGCCGCC ACCGCCGAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
 1301 ACCAAACCTT GCTCGACCGC CTGCAACCG ATGCCCGCTT TGCCGCCGTC
 1351 GCCCGCGACT ACATTTGACC TGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCTGACG GATGCTGCG CCTGCAAAA AGTCTTTATC GGCAAAATCA
 1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGA AACACGAAGA CACCGCAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 GTAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644.pep

1 MPSEPADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKYGGRRKS QFEIQEVLRI AGHYGVVPTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLEMIF KEGGGGLGVT EPETSGAIA REMQSYEYI DGQTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSRL QLIGMTHGIM
 301 EYILENLERY VRNDIKFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
 351 HOLMEANIVK TLAETTYAA AQMLQKLLGA KGFERGHFAG NIAIDIRPFT
 401 IFEGPNMPLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAAV
 451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VOAKHEDTAA
 501 FLLNDIRKDI LDCRYCG*

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSEPADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
g644	MPSEPADCCPVHFVVKFRKLTLCNGRRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					

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	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
g644	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLPFLDKKYGGRKGSQFEIQEVLRI					
	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLPFLDKKHGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	130	140	150	160	170	180
g644	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQAQGLEMI FKEGGGGLGVTEPETSGAAIA					
	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQAQGLDMI FKESRRRLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644.pep	190	200	210	220	230	240
g644	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
	REMQSCYEYTDQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	250	260	270	280	290	300
g644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSRGDAAGLRAFQNI FIRSRLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	310	320	330	340	350	360
g644	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMANIVK					
	EYILDNLNRYVRNDIRFVDYERREIQRRHQVSEILYRYVCHSVSPVAPVAHQLMANIVK					
	310	320	330	340	350	360
m644.pep	370	380	390	400	410	420
g644	TLATEYTYAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	TLATEYTYAAQMLQKLLGAKGFERGHPAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
m644.pep	430	440	450	460	470	480
g644	TAEKEAGMKLDKNQTL DRLQTDARFAAVARDYTL PEDIRSFLOEHTLT DACALQKVF I					
	TAEKEAGIKLDKNQTL DAVQTDVRF AAVARDYAL PEDIRSFLOEHTLT DACALQKVF I					
	430	440	450	460	470	480
m644.pep	490	500	510			
g644	GKIIARLFVVFQAKHEDTAAFLNDIRKDILDCRYCGX					
	GKIIARLFVVFQAEHEDTTAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

a644.seq

```

1  ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTCAG ACGGTATCGA CCTGATCGCA TACCTGCCCG
251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCGGGCG CAAGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGTTTGGG CATGGTTTTC AAAGGCGAGG GCGCGGGTTT
501 AGGCGTTACC GAACCCGAAA CCTCCGGCGC GGCGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTACGT CAACGCCCGC
601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCTCCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCTCG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAAACTC TCCAGAGCG ACGTGCCCGG TTTGCGCGCG TTCCAAAACA

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851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTTG
1151 AACCGCGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAATT
1251 TGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCTT GCTCGACCGC CTGCAAAACG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACCTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCTTGACC GATGCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```

a644 .pep
1  MPERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAAIA REMQSYEYTD GQTIYVNAA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIFFIRSL QLIGMTHGIM
301 EYTLENLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAAV
451 ARDYTELPEDI RSFLQEHTLT DACALQKVFI GKILARLVFV VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

```

m644 /a644 97.3% identity in 517 aa overlap

```

          10      20      30      40      50      60
m644 .pep  MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
          |||
a644       MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
          10      20      30      40      50      60

          70      80      90     100     110     120
m644 .pep  LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI
          |||
a644       LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI
          70      80      90     100     110     120

          130     140     150     160     170     180
m644 .pep  AGHYGVPVTLRTGIEGALVLQPLQEFGDEAQVAQGLEMIKFKEGGGLGVTEPETSGAAIA
          |||
a644       AGHYGVPVXXXXXEGALVLQPLQEFGDEAQIAQGLDMVFKEGGGLGVTEPETSGAAIA
          130     140     150     160     170     180

          190     200     210     220     230     240
m644 .pep  REMQSYEYIDGQTIYVNAAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC
          |||
a644       REMQSYEYTDGQTIYVNAAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC
          190     200     210     220     230     240

          250     260     270     280     290     300
m644 .pep  ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNIFFIRSLQLIGMTHGIM
          |||
a644       ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNIFFIRSLQLIGMTHGIM
          250     260     270     280     290     300

          310     320     330     340     350     360
m644 .pep  EYILENLERIVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK
          |||
a644       EYTLENLERYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK

```

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	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a 644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 . pep	TAEKEAGMKLDKNQTLDRLOTARFAAVARDYTLPEDIRSFLQEHITLDACALQKVFI					
a 644	TAEKEAGMKLDKNQTLDRLOTARFAAVARDYTLPEDIRSFLQEHITLDACALQKVFI					
	430	440	450	460	470	480
	490	500	510			
m644 . pep	GKIIARLFVVFQAKHEDTAAFLNDIRKDILDCRYCGX					
a 644	GKIIARLFVVFQAEHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645.seq

```

1  ATGATGATGG TGTGGCGTT GGGGATGTCG ATGCCGGTTT CGATGATGGT
51  GGAACAGAGC AACACATTGA ATCTTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCACGC AGTTGTCCGT GCGCCACGCC GATACGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAata CCTGTCTCC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTCACG
301 GCGAGGCGGC GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CGCGCAGACC
351 TTCGAGCGCC ATGCTGAGGG TGCGCGGAAT CGGCGTGGCG GTCATGGTTA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGTCGCACG
451 CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
551 CGTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTGCGGGCG AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGAAG GCGGACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGcggcgat ggcggcggc TGGTCTTCGG
851 TTTCTCTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

g645.pep

```

1  MMVVLALGMS MPVSMMEQES NTLNLCKKKS RMTCSRRSR SCPCATPIRA
51  SGRSVSSRSR IFSIVSTSLC RKNTPPRLS SRNTASRTLP SLNGLTKVET
101 ARRLGAVVI SEKSRPSSA MLRVRGIGA VMVRMTLAR RRLSCSFCRT
151 PKRCSIIIN KPRFLNFMSS CTNLCVPITI STVPSAMPSS VALVALLLK
201 RERLATFTGK SAKRSKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT SRSIGFACVK SLITAAMAAA WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645.seq

```

1  ATGATGATGG TGTGGCGTT GGGGATATCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAATA CCTGTCTCC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTAAAGG GTTTGACAAA GGTTCACG
301 GCGAGGCGGC GGCTGGGCGC GGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAACGCC ATACTTAAAG TACGCGGAAT CGGCGTGGCG GTCATGGTAA
401 GGATATCAAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTTGAATTT
501 GATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAAAAGCGT GGTGCGGAGCA AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGGCGATCCA TCGGCTTCGC
801 TTGCGTCAAA TCTTTAATCA CGGCGGCGAT GCGGCGGCGC TGGTCTTCGG

```

851 TTTCTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:

m645.pep
 1 MMMVLALGIS IPVSMVVEQS NTLNRCCKKS RMTCSSSRSR SCPCATPMRA
 51 SGSRVSSRSR IFSIVSTSLC RKNTCPPLRS SRNTASRTLP SLKGLTKVLT
 101 ARRRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
 151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
 201 RERLATFTGK SAKRSKFCFA CCSTKSVVGA STATCLPPIT ATNAARRATS
 251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMMVLALGISIPVSMVVEQSN	TLNRCCKKS	RMTCSSSRSR	SCPCATPMRA	SGSRVSSRSR	
g645	MMMVLALGMSMPVSMVVEQSN	TLNRCCKKS	RMTCSSSRSR	SCPCATPMRA	SGSRVSSRSR	
	10	20	30	40	50	60
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCPPLRSS	RNTASRTLP	SLKGLTKVLT	TARRRLGAV	VISEKSRSPSNA	
g645	IFSIVSTSLCRKNTCPPLRSS	RNTASRTLP	SLKGLTKVLT	TARRRLGAV	VISEKSRSPSNA	
	70	80	90	100	110	120
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRISTLAR	RRLSCSF	XRTPKRCSSSIIT	KPKFLNLMSS	CSTSLCVPITI	
g645	MLRVRGIGVAVMVRISTLAR	RRLSCSF	XRTPKRCSSSIIT	KPKFLNLMSS	CSTSLCVPITI	
	130	140	150	160	170	180
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALLLL	KRERLAT	FTGKS	SAKRSKFC	ACCSTKSVVGA	STATCLPPIT
g645	STVPSAMPSSAALVALLLL	KRERLAT	FTGKS	SAKRSKFC	ACCSTKSVVGA	STATCLPPIT
	190	200	210	220	230	240
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPTSPH	TRRSIGFACVK	SLITAAMAAA	WSSVSSX		
g645	ATNAARRATSVLPKPTSPH	TRRSIGFACVK	SLITAAMAAA	WSSVSSX		
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq
 1 ATGATGATGG TGTGGCGTT GGAATGTCG ATACCGGTTT CGATGATGGT
 51 GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAGTCG CGCATGACTT
 101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
 151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
 201 TTCATTGTGC AGGAAAAATA CTTGCCCGCC GCGTTTGAGT TCGCGCAATA
 251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTGACG
 301 GCGAGGCGGC GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
 351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
 401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
 451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
 501 TATGTCGTCC TGCACCAAGT TGTGCGTACC GATAACAATA TCGACCGTGC
 551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
 601 CGCGAAAGGC TGGCGACTTT CACGGGGAAG TCGGCGAAGC GGTCCGCAAA
 651 ATTTTGC GCG TGTGCTCGA CCAGAAGCGT GGTCGGTGGC AGTACGGCAA
 701 CTTGTTTGCC ACCCATTACC GCCACAAACG CGGCGCGCAG GGCGACTTCG
 751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
 801 CTGCGTCAA TCTTTAATCA CGGCGGCGAT GGCGGCTGCC TGGTCTTCGG
 851 TTTCTTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

a645.pep
 1 MMMVLALGMS IPVSMVVEQS NTLNRCCKKS RMTCSSSRSR SCPCATPMRA

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```

51  SGRVSSRSR MFSMVSTSLC RKNTCPPLRS SRNTASRTLP SLNGLTKVLT
101 ARRRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLK
201 RERLATFTGK SAKRSAKFCA CCSTRSVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/a645 96.9% identity in 286 aa overlap

```

          10      20      30      40      50      60
m645.pep  MMMVLALGISIPVSMVQSNLTNRCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
          |||||:|||||
a645      MMMVLALGMSIPVSMVQSNLTNRCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
          10      20      30      40      50      60

          70      80      90     100     110     120
m645.pep  IFSIVSTSLCRKNTCPRLSSRNATSLPSLKGLTKVLTARRRLGAVVISEKSRSPSNA
          :||:|||||:|||||:|||||:|||||:|||||:|||||
a645      MFSMVSTSLCRKNTCPRLSSRNATSLPSLNGLTKVLTARRRLGAVVISEKSRSPSSA
          70      80      90     100     110     120

          130     140     150     160     170     180
m645.pep  ILKVRGIGVAVMVRISTLARRLSCSFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
          |||||:|||||:|||||:|||||:|||||:|||||
a645      ILKVRGIGVAVMVRMSTLARRLSCSFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI
          130     140     150     160     170     180

          190     200     210     220     230     240
m645.pep  STVPSAMPSSAALVALLLKRRERLATFTGKSAKRSKFCACCSTKSVVGASTATCLPPIT
          |||||:|||||:|||||:|||||:|||||:|||||
a645      STVPSAMPSSAALVALLLKRRERLATFTGKSAKRSKFCACCSTRSVVGASTATCLPPIT
          190     200     210     220     230     240

          250     260     270     280
m645.pep  ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
          |||||:|||||:|||||:|||||
a645      ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
          250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

```

g647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTTAAAGAG CGTGCACGCT
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

```

g647.pep
1  MQRLAADGIQ IFFVGVGQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
51  GFKGTVGQTE RGTVAADTV FRQIVGVDD TDAERTAVHS RGRTRFYRIS
101 LII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

```

m647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTGCA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

```

m647.pep
1  MQRLAADGIQ IFFVSDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

```

1029

51 GFKGTVGQTE RGTAVADTV FRQIISIVNH ADAERTAHS RGRGFYRIS
101 LII*

m647/g647 91.3% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	: : : : : :					
g647	MQRLAADGIQIFFVSDGQFALRINGLVKERARSVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGRGFYRISLIIX					
	: : : : : :					
g647	RGTAVADTVFRQIVGVDDTDAERTAVHSRGRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2085>:

a647.seq
1 GTGCAAAGGC TCGTTACACA CAGCGTCCAA GTCTTTTGTG TAGGTGTCGA
51 TGGGCAGTTT GCCTTGGCAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCGCTGTAGC
201 GGACACCGTT TTTGCCAAA TAATACGCAT AGTTGATCAC GCCGATACCG
251 AGCGAACGGC GGCCCATAGT GGAGGTACGC GCGGCTCTA CCGGATATCC
301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2086; ORF 647.a>:

a647.pep
1 VQRLVTHSVQ VFFVGVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
51 GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAHS GGTRGFYRIS
101 LII*

m647/a647 87.4% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	: : : : : :					
a647	VQRLVTHSVQVFFVGVDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGRGFYRISLIIX					
	: : : : : :					
a647	RGAVAVADTVFRQIIRIVDHADTERTAHSGGTRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2087>:

g648.seq
1 ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51 CGACGTTTTG AATGTAGATG CGCCCGGTCC CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCGGCAGC CGGAATGATA CGCTTGGCTA TGTTCGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAACCCGAA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCATA
301 ATCAAGCTGG CGGATACGGT TGTCTTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCA ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCACC TTGCGAACAA GATTGACCG CCGCCTGAAA
451 CATCTTAAAG AAGGGAATGC AGCCGGTATG CCGGGCTTCA CCGCCCGGA
501 TTTCCTGTC CAGCCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCG
551 CGTTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGCATTCAA TCAGCACACA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2088; ORF 648.ng>:

g648.pep

1030

```

1   MNRRNARIER AVRIAVIDVL NVDAPGPGTL LHQRGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAAALNQAG VQQAVIDLHAI
101 IKLADTVVFH APVVFQHQQA FGFMPPQGV E QGCRAAAHAT LRTFRDRLK
151 HLKEGNAAGM PGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

```

m648.seq
1   ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTGG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTGCGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTCCAC ACCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCGCC TTGCGAACAG GATTGACCG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGCGCTTCG CCGCCCGGA
501 TTTGCTGTC CAAACCGCGG ATACGTCCGG CATTGATGCC GATGCCGCA
551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGCATTCAA TCAGCACACA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:

```

m648.pep
1   MNRRDARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAAALNQAG VQQAVIDLHAI
101 IKLTDTVVFH TAVVFQHQQA FGFDMPQGV E QGCRAAAHAA LRTGFDRRLK
151 HFKEGNAAGM PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

m648/g648 91.5% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
	: : : : : : : : : :					
g648	MNRRNARIERAVRIAVIDVLNVDAPGPGTLLHQRGKQVGSRNDTLAYVRVLLVFRIEPLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQNRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
	: : : : : : : : :					
g648	FVLVGKKRFVQPRNLVGRKQNRNVAALNQAGVQQAVIDLHAIKLADTVVFHAPVVFQHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPQGVQGCRAAAHAALRTGFDRRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
	: : : : : : : : :					
g648	FGFMPPQGVQGCRAAAHATLRTFRDRLKHLKEGNAAGMPGFTAPDFAVQPADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX					
	: : : : : : : :					
g648	DARALGNVFHNRAGSGIDGIQTIVAFNQHTAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

```

a648.seq
1   ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTGG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTGCGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCACC TTGCGAACAG GATTGACTG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGTCTTCG CCGCCCGGA

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1031

501 TTTCGCTGTC CAGTCCGCGG ATACGTCGCG CATTGATGCC GATGCCCCGCA
 551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
 601 CAGGCTGTCTG TCGCATTCTGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648 . pep
 1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
 101 IKLTDTVVFH APVVVFHQQA FGFDMPQVE QGCRAAAHAT LRTGFDCLRK
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
 201 QAVVAFDQYA A*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648 . pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGS	RNDALADIRVLLVFRIEPLK				
a648	MNRRNARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGS	RNDALADIRVLLVFRIEPLK				
	10	20	30	40	50	60
m648 . pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVVFHQQA					
a648	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHAPVVVFHQQA					
	70	80	90	100	110	120
m648 . pep	FGFDMPQVEQGCRAAAHAALRTGFDRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
a648	FGFDMPQVEQGCRAAAHATLRTGFDCLRKHFKEGNAAGMPCFAAPDFAVQSADTSGIDA					
	130	140	150	160	170	180
m648 . pep	DARTLGNVFHN	RAGSGIDGIQTIVAFNQHTAX				
a648	DARTLGNVFHN	RAGSGVDGIQAVVAFDQYAAAX				
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649 . seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGAAGTGGTAT CAACAACGTC
 51 CGTGCCCGGT ACGTCAGAAC CCGCCACCG ACATACCAA CATATCAGCA
 101 AGGCAAAACAA GCAGATGCTG CACCCGAAT GCAGAAATA TTTGGAACGC
 151 CGTGCCCGGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGCACCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

g649 . pep
 1 MLAILLSAIL GLVSTTAAAG TSEPARRHTK HISKANKQML HPECKRYLER
 51 RAAWYRSQGN VQELRENKKA RKAFRTLPPY EQKIQCAAAY EAFDDFDGGR
 101 FRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649 . seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGAAGTGGTAT CGACAACGTC
 51 CGTGCCCGGT ACGTCAGAAC CCGCCACCG CGATACCAA CATATCCGCA
 101 AGGCAAAACAA GCAGATGCTG CACCCGAAT GCAGAAATA TTTGGAACGC
 151 CGTGCCCGGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGT
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649 . pep

1032

1 MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
 51 RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCAAAY EAFDDFDGGS
 101 FRR*

m649/g649 96.1% identity in 103 aa overlap

	10	20	30	40	50	60
m649.pep	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN					
g649	MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERRAAWYRSQGN					
	10	20	30	40	50	60

	70	80	90	100
m649.pep	VQELRENKKARKAFRSLPYAEQKIQCAAAYEAFDDFDGGSFRRX			
g649	VQELRENKKARKAFRTLPHYAEQKIQCAAAYEAFDDFDGGRFRRX			
	70	80	90	100

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

a649.seq
 1 ATGCTTGCCA TACTGTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAA CATATCCGCA
 101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TCGCGGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
 251 CCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCAGCAGG
 301 TTCCGCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:

a649.pep
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
 51 RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQKTQCAAAY EAFDDFDGSR
 101 FRR*

m649/a649 96.1% identity in 103 aa overlap

	10	20	30	40	50	60
m649.pep	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN					
a649	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN					
	10	20	30	40	50	60

	70	80	90	100
m649.pep	VQELRENKKARKAFRSLPYAEQKIQCAAAYEAFDDFDGGSFRRX			
a649	VQELRENKKARKAFRSLPYKEQKTQCAAAYEAFDDFDGSRFRRX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

g650.seq
 1 ATGTCCAAAC TCAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
 51 TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
 101 CGATTATGCG GTTAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
 151 TATTTCCAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
 201 GGGCGAAGTC AATCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
 251 CRAAGCCGAG CTATTTGAC AGGGTCGTCA ACCGGAGCCG ACCCTATATG
 301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
 351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACAGC
 401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
 451 GGCTTGGAAG AAACaccgGT TTACGacggc aggcacGacy TTacgcaGc
 501 taccgatgcc gcacTCAACT AtctGcaATA TCTCTatggA CTGTTCCGGC
 551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
 601 CGCGCCGTCA ACCGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
 651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
 701 TGGCAACAT TATTGCCACC CCCCAATCTT TCGGCATGAA TATCAGCGAC

1033

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751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATGCCCCGGC TTGCCGGCAT CACGCAAGC GAGCTGCTCG
851 CCTGAATCC TGCAATCAAC GTCCCCGgt teatCCCCAA AAacaaacgc
901 aaacTGCTGC TTCCTGTCGC GTCCGTCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCGTTTC CATCGACATC GACAATACGC CcgacacCta ccgttccaat
1201 ATGCGggcag gcaCGGTGAA CGTCAGCATT gccCgaatcc aacCCgccgc
1251 cgcaCAGACA gcggacatta ccgtcgcacc tttgccgcaa gaaaccgtcc
1301 gtacgggaac ccgatccct tgtccgcaTt accgaaccgc ccctTGCGAC
1351 AGCCGCAGCG CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

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This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

```

g650.pep
1 MSKLKTIALT ASGLSVCPGF LYAQTSSHQ VGLAIMRLNS SILDLPPTKO
51 YFQSGSLWDE LRQGFMRGEV NPFLVRRHES KFIASRSYFD RVNRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVSI ARIQPAQAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

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m650.seq
1 ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTTCGAAT CCGGCAGCCT GTGGGCGGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTTCATCG
251 CAAGGCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
451 GGCCTGGAAA AAACACCGGT TTACGACGGC AGGCACGACG TTACGCGCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCCGCT TGCCCTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCCAAG CTGCTCGCCG
701 TGCGCAACAT TATTGCCACT CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATGCCCCGGC TTGCCGGCAT CACGCAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCCGCGT TTATCCCCAA AAGCAAACGC
901 AAACGCTGTC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCCGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCGCG
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTGTCCGCGA AAAACCGTCC
1301 GTACGG.AAC CCGATCCCTT TGTCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

```

m650.pep
1 MSKLKTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKO
51 YFQSGSLWGE LRQGFMRGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

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m650/g650 96.1% identity in 465 aa overlap

1034

m650.pep	10	20	30	40	50	60
	MSKLTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	MSKLTIALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
	10	20	30	40	50	60
m650.pep	70	80	90	100	110	120
	LRQGRMGEVNPVLVRRHESKFIAHSYFNRVINRSRPYMYHIANEVKKRNMPAEAAALLP					
g650	LRQGRMGEVNPVLVRRHESKFIAHSYFDRVVNRSRPYMYHIANEVKKRNMPAEAAALLP					
	70	80	90	100	110	120
m650.pep	130	140	150	160	170	180
	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	190	200	210	220	230	240
	LFGDWPLAFAAYNWGEGNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
g650	LFGDWPLAFAAYNWGEGNVGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
	190	200	210	220	230	240
m650.pep	250	260	270	280	290	300
	PQSGFMNISDIDNKPYPQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	PQSGFMNISDIDNKPYPQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
	250	260	270	280	290	300
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLNAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLQTASESVVSIIDNTPDTPYRSNMPAGTVNVGIARIRPAAAQT					
g650	NLVNAGRSILVAKNGKTLHTASESVVSIIDNTPDTPYRSNMPAGTVNVSIARIQPPAAAQT					
	370	380	390	400	410	420
m650.pep	430	440	450	460		
	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
g650	ADITVAPLPQETVRTGTRSPCPHYTRPCDSRSATSNRKTDCHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

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a650.seq
1   ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCGTCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGAGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCC CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 GGCCTGGAAA AAACACCGGT TTACGACGGC AGGCACGACA TTTACGCCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTTCCCAAG CTGCTCGCCG
701 TGCGCAACAT CATTGCCGCC CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCCTATTT TCAGGCAGTC GAACCGGACC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCCGCGT TCATCCCAA AAGCAAACGC

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1035

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901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CTTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTGCGCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

a650 .pep

```

1   MSKLKTIALT ASGLSVCPGF LYAONTSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWSE LRQGRMGEV NPVLRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDYIATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNVPK LLAVRNIIAA PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

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m650/a650 99.1% identity in 465 aa overlap

	10	20	30	40	50	60
m650 .pep	MSKLKTIALTASGLSVCPGF LYAONTSSHQ IGLAIMRLNS SILDLPPTKQ YFQSGSLWSE					
a650	MSKLKTIALTASGLSVCPGF LYAONTSSHQ IGLAIMRLNS SILDLPPTKQ YFQSGSLWSE					
	10	20	30	40	50	60
m650 .pep	LRQGRMGEVNPVLRRHESKFIASHSYFN RVINRSRPYMYHIANEVKKRNMPAEALLP					
a650	LRQGRMGEVNPVLRRHESKFIASHSYFN RVINRSRPYMYHIANEVKKRNMPAEALLP					
	70	80	90	100	110	120
m650 .pep	LRQGRMGEVNPVLRRHESKFIASHSYFN RVINRSRPYMYHIANEVKKRNMPAEALLP					
a650	LRQGRMGEVNPVLRRHESKFIASHSYFN RVINRSRPYMYHIANEVKKRNMPAEALLP					
	70	80	90	100	110	120
m650 .pep	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
a650	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650 .pep	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
a650	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650 .pep	LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNVPKLLAVRNIIAT					
a650	LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNVPKLLAVRNIIAA					
	190	200	210	220	230	240
m650 .pep	LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNVPKLLAVRNIIAT					
a650	LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNVPKLLAVRNIIAA					
	190	200	210	220	230	240
m650 .pep	PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAPFIPKSKR					
a650	PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAPFIPKSKR					
	250	260	270	280	290	300
m650 .pep	PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAPFIPKSKR					
a650	PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAPFIPKSKR					
	250	260	270	280	290	300
m650 .pep	KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
a650	KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650 .pep	KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
a650	KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650 .pep	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTYRSNMPAGTVNVGIARIRPAAQT					
a650	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTYRSNMPAGTVNVGIARIRPAAQT					
	370	380	390	400	410	420
m650 .pep	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTYRSNMPAGTVNVGIARIRPAAQT					
a650	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTYRSNMPAGTVNVGIARIRPAAQT					

1036

	370	380	390	400	410	420
	430	440	450	460		
m650 - pep	ADITVAPLPQKTVRTXTRSPCPYCRTPCDSRSATSNRKTDHRAVX					
a650	ADITVAPLPQKTVRTXTRSPCPYCRTPCDSRSATSNRKTDHRAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

g652.seq

```

1 ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTTGG GTGCGAATGC
51 GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGCG GACGAAGCGG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCCGG CTACAAGCGG GCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATACTTGGAA GGCTTGTTA
551 ACGAATTCCC GATTATTTC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATG GGCAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTCTGTA CCAATCCGAA AATCTTGCC GAAGGCATCG
701 AAAAAGCGT AGCAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCCTGAAAGC cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCAccgct ccggCGAAAC CGAAGACAGT Accattgccc
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTA AAAAccgG TTCTTTGAGC
901 cgtTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCcgctACT ACCCGGCA AGCCGCATTC TACCAACTGG
1001 GCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

g652.pep

```

1 MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51 VPMMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
201 EGVKLLTEKL GKQVQLVDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAKYNQ LLRIEELAE AAYYPGKAFF YQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

m652.seq

```

1 ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTTGG GTGCGAATGC
51 GACTTTGGCG GTTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGCCCAGT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGCG GACGAAGCGG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCCGG CTACAAAGCG GCGAAGACG TATTATTCGC ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATATCTGGAA GGCTTGTTA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATG GGCGGTAGAG TTCAATTGGT
651 TGCGGACGAC TTGTTCTGTA CCAATCCAAA AATCTTGCC GAAGGCATCG
701 AAAAAGCGT AGCAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAAACCG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAa CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCGGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

m652.pep

```

1 MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51 VPMMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC

```

1037

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
 151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
 201 EGWKLLETKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
 301 RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGK*

m652/g652 98.2% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
g652	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
g652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
g652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFFIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
g652	GLVNEFFIISIEDGMDENDWEGWKLLTEKLGKVKQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGTILSETLKAVDLAKRNRYASVM SHRSGETEDSTIADLAVATNCMQIKTGSLS					
g652	LLVKVNQIGTILSETLKAVDLAKCNRYASVM SHRSGETEDSTIADLAVATNCMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAYNQLLRIEELAEAAADYPSKAAFYQLGKX					
g652	RSDRMAYNQLLRIEELAEAAAYPGKAAFYQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

a652.seq

1	ATGATCGAAT	TGGACGGTAC	TGAAAACAAA	GGCAATTGGG	GTGCGAATGC
51	GACTTTGGCG	GTTTCTATGG	CGGTTGCACG	CGCCGCTGCC	GAAGACTCAG
101	GCCTGCCGCT	TTACCGCTAC	TTGGGCGGCG	CAGGCCCGAT	GTCCCTGCCC
151	GTACCGATGA	TGAACGTCAT	CAACGGCGGC	GAACACGCCA	ACAACAGCCT
201	GAACATCCAA	GAGTTTATGA	TTATGCCCGT	CGGCGCAAAA	TCTTTCCGCG
251	AAGCGTTGCG	CTGCGGTGCG	GAAATTTTCC	ACGCCTTGAA	AAAACGTGTC
301	GACAGCAAAG	GCTTCCCGAC	CACAGTCGGC	GACGAAGCGG	GTTTCGCCCC
351	CAACCTGAAC	AGCCACAAAG	AAGCCCTGCA	ACTGATGGTC	GAGGCGACCG
401	AAGCCGCGCG	CTACAAAGCG	GGCGAAGACG	TATTATTGCG	ATTGGACTGC
451	GCGTCCAGCG	AGTTCTACAA	AGACGGCAAA	TACCACTTGG	AAGCCGAAGG
501	CCGCTCCTAC	ACCAACGCGG	AATTTGCCGA	ATATCTGGAA	GGCCTGGTCA
551	ACGAGTTCCC	CATCATCTCC	ATCGAAGACG	GGATGGATGA	AAACGACTGG
601	GAAGGCTGGA	AACTGCTGAC	CGAAAAACTG	GGCGGCAAG	TCCAACTCGT
651	TGGCGACGAC	CTCTTCGTTA	CCAACCCGAA	AATCCTTGCC	GAAGGCATTG
701	AAAAAGGCGT	GGCAAACGCA	CTATTGGTCA	AAGTCAACCA	AATCGGTACT
751	TTGAGTGAAA	CCCTGAAAGC	CGTCGACTTA	GCCAAACGCA	ACCGCTACGC
801	CAGCGTAATG	AGCCACCGCT	CCGGCGAAAC	CGAAGACAGC	ACCATTGCCG
851	ACTTGGCAGT	CGCCACCAAC	TGTATGCAGA	TCAAACCGG	TTCTTTGAGC
901	CGTTCGACCC	GCATGGCGAA	ATACAACCAA	CTGCTGCGTA	TCGAGGAAGA
951	ATTGGCGGAA	GCCGCGGACT	ACCCAGCAAA	AGCCGCATTG	TACCAACTGG
1001	GCAAATAA				

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

a652.pep

1	MIELDGTENK	GNLGNATLA	VSMVARAAA	EDSGLPLYRY	LGGAGPMSLP
51	VPMNVINGG	EHANNSLNIQ	EFMIMPVGAK	SFREALRCGA	EIFHALKKLC
101	DSKGFPTTVG	DEGGFAPNLN	SHKEALQLMV	EATEAAGYKA	GEDVLFALDC

1038

151 ASSEFYKD GK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
 201 EGWKLLETKL GGVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
 251 LSETLKAVDL AKRNRYSVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
 301 RSDRMAKYNQ LLRIEELAE AADYPSKAAF YQLGK*

m652/a652 99.7% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGANATLAVSMAVARAAEDSGLPLYRYLGAGFMSLPVPMNIVINGG					
a652	MIELDGTENKGNLGANATLAVSMAVARAAEDSGLPLYRYLGAGFMSLPVPMNIVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN					
a652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
a652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFFIISIEDGMDENDWEGWKLLETKLGGVQLVGDDLFVTNPKILAEGIEKGVANA					
a652	GLVNEFFIISIEDGMDENDWEGWKLLETKLGGVQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGTILSETLKAVDLAKRNRYSVM SHRSGETEDSTIADLAVATNCMQIKTGSLS					
a652	LLVKVNQIGTILSETLKAVDLAKRNRYSVM SHRSGETEDSTIADLAVATNCMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAKYNQLLRIEEEELAEAAADYPSKAAFYQLGKX					
a652	RSDRMAKYNQLLRIEEEELAEAAADYPSKAAFYQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1   ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GTGCGGCCGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGCTATTCC GGCAAGGCG TATTGAAGGC
201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TCTCTATGGC
351 GGTTCACGCG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGGCGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCGCTC GCGCAAAAT CTTTCCGCGA AGCGTTGCGC TGCGGTGC GG
551 AAATTTTCCA CGCCTTGAAA AAATGTGCG ACAGTAAAGG CTTCCCGACC
601 ACAGTCGCGC ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AAGCGGCCGA AGCCGCCGGC TACAAGGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TACTTGGAAG GCTTGGTTAA CGAATTTCCG ATTATTTC CA
851 TTGAAGACGG GATGGACGAA AACGACTGGG AAGGCTGGA ACTGCTGACC
901 GAAAAATTGG GCAAAAAAGT TCAATTGGTC GGCACGACT TGTTTCGTAAC
951 CAATCCGAAA ATCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1051 GTCGACTGG CAAATGCAA CCGCTACGCC AGCGTGATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGTA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT TAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCTACTA
1251 CCCCGGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

1039

g652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDVLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNLSL NIOEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKQVLV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSSETLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAYYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCAGCGCG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTGCGCAGC GCGACAAATC CCGTTATTCT GGCAGGGGCG TATTGAAGGC
201 GGTGGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAACAAAG GCAATTGGG TCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCACGCG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTTCCGCGA AGCGTTGCGC TCGGTTGCGG
551 AAATTTTCCA CGCCTTGAAA AAATGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGCGACCGA AGCCGCGGCG TACAAAGCGG
701 CGGAAGACGT ATTATTGCGA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGCCAAAT ACCACTTGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGTAGAGT TCAATTGGTT GCGGACGACT TGTTCGTAAC
951 CAATCCAAAA ATCTTGGCCG AAGGCATCGA AAAAGGCGTA GCAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CTTGAAAGCC
1051 TCGCACTTAG CCAAAACGAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACGACA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDVLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNLSL NIOEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKQVLV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAADYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLESGVMGRAAVPSGASTGQKEALELRDGDKSRY					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLESGVMGRAAVPSGASTGQKEALELRDGDKSRY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNLSLNIQEFMIMPVGA					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNLSLNIQEFMIMPVGA					
	130	140	150	160	170	180

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKLCDSKGFPPTVVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA					
g652-1	CGAEIFHALKKLCDSKGFPPTVVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFIISIEDGMDENDWEGWKLLT					
g652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFIISIEDGMDENDWEGWKLLT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGRRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA					
g652-1	EKLGGRRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEADYPSK					
g652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEADYPSK					
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACCA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAGA GGCTTTGGAA
151 CTTGCGGACG GCGACAATC CCGTTATTCG GGCAAGGCG TATTGAAGGC
201 GGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCACGCG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGCGCGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCGCTC GCGCAAAAT CTTTCCGCGA AGCGTTGCCG TCGGTTGCCG
551 AATATTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCCTGACC
601 ACAGTCCGCG ACGAAGCGCG TTTGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGCGC TACAAGCGCG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGAA ACTGCTGACC
901 GAAAACTGG GCGGCAAGT CCAACTCGTT GCGGACGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGGCGTG GCAACGCGAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAC CCTGAAAGCC
1051 GTCGACTTAG CCAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCGGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pap

```

1  MSAIVDIFAR EILDSRGNPT VECVLLLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGAHA TLAVSMAVAR AAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFF IISIEDGMD NDWEGWKLLT
301 EKLGGKVQLV GDDLFVTNPK ILAEGIEKGV ANALLVKVNQ IGTLSLTKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEE LAEADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNTVECDVLESVGMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNTVECDVLESVGMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

m652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

m652-1      AAAEDSGLPLYRYLGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
a652-1      AAAEDSGLPLYRYLGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
              130     140     150     160     170     180

m652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
              190     200     210     220     230     240

m652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFPIISIEDGMDENDWEGWKLIT
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFPIISIEDGMDENDWEGWKLIT
              250     260     270     280     290     300

m652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
a652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
              310     320     330     340     350     360

m652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEADYPSK
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEADYPSK
              370     380     390     400     410     420

m652-1      AAFYQLGKX
a652-1      AAFYQLGKX
              429

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1  ATGGCGGcgccg aaccgatgcg gAtgcggag gtaAcgtaCG GTTTTCCGG
51  ATCGTTCGGG ATGGCGTTTT TGTtgacggT GATGTGCGCt ttgccccAAG
101 CGGCTtcggc ggctttgcCg gtgaTTTTCA TCGGTTGCAG GtcgacgaGG
151 AAAacgTGGC TTTCGGTGCG GCCGGAaacy atgcgCaaac cgCGTttaac
201 caactcttcc gcCATGACGG CAGCATTGAT TTCACTTGT TTTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgCGCGCG
301 ATAACGTgca tcaACGGAcc gCCTTGCAGG CTTGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTGTGG GTGGTAGTgG ttACgaaGtc GCAGaatgyc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1  MAAEPMRME VTYGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMTALIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGMEEFSAF SWVLSRHKIT PPRGPRRLV VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCGTTCGGA ATGGCGTTTT TGTGACGGT GATGTGCGCT TTGCCCAAAG
101 CGGCTTCGGC GGCTTTGCCG GTAATTTCA TCGGTTGCAG GTCAACGAGG

```

1042

```

151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCACCTGT TTTGCGTATT
251 GTTTGAACCTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAAG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```

m653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRLVW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/g653 96.9% identity in 163 aa overlap

```

m653.pep      10      20      30      40      50      60
MAAEPMRMPEVTKGFSGSFGMAFLLTMCAALPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||
g653          10      20      30      40      50      60
MAAEPMRMPEVTYGFSGSFGMAFLLTMCAALPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||

m653.pep      70      80      90      100     110     120
MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
|||||
g653          70      80      90      100     110     120
MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF
|||||

m653.pep      130     140     150     160
SWVLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATRPAX
|||||
g653          130     140     150     160
SWVLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATSPAX
|||||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```

a653.seq
1  ATGGCGGCGG AACCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCATTCCGG ATGGCGTTT TGTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGC GGCTTTCGGC GTAATTTCA TCGGTTGCAG GTCAACGAGG
151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCACCTGT TTTGCGTATT
251 GTTTGAACCTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGGCC ACCTTGCAAG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGGATTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```

a653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRLVW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/a653 100.0% identity in 163 aa overlap

```

m653.pep      10      20      30      40      50      60
MAAEPMRMPEVTKGFSGSFGMAFLLTMCAALPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||
a653          10      20      30      40      50      60
MAAEPMRMPEVTKGFSGSFGMAFLLTMCAALPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||

m653.pep      70      80      90      100     110     120
MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
|||||
a653          70      80      90      100     110     120
MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
|||||

m653.pep      130     140     150     160
SWVLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATRPAX
|||||
a653          130     140     150     160
SWVLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATRPAX
|||||

```

130 140 150 160

```
g656. seq
  1  ATGCCGCGTT TCTCCGGTTC GATTTCCTCG ATGATTTCCTCA TCGCGCGGAC
51  TTTtggcGCG CCGGAGAGTG TGcggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGCT AACGCCTCT TTCAAACAGC ctTCGACGTT GGAACGATG
151 TGCATCAGAT GGGAGTATT TTCAATCACC ATTTTGTGCG TGACTTTGAC
201 TTCGCCTGTT TTGCTGATGC GTCCGACATC GTTGCGCCCC AAATCGATAA
251 GCATAACGTG TTCGGGgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTCTG
301 TTGGCAAGCT CTTCCGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGCGCGAGC ATGACGTcat CGCGTTCGCG CGGACGAGG ATTTCGGGCG
401 AGGAACCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

g656 - pep

1	MPRFGSGSISS	MISIARTFGA	PESVPAGKVA	ARMSILVTPS	FKQPSTLETM
51	CITWEYFSIT	ILSVTLTSPV	LLMRPTSLRP	KSISITCSAI	SLASLNKSCS
101	LARSSAGVLP	RRRVPAMGRT	MTSSRSRRTR	ISGEEPTMWK	SPKS*

```
m656.seq
  1  ATGCCCGGTT  TGCTCGGTTT  GACTTCTTCG  ATGATTTCCT  TGGCGCGGAC
51  TTTGGGTGCG  CCGGAGAGTG  TGCCGGCAGG  GAAGGTAGCG  GCGAGGATGT
101 CCATGTTGGT  CATCGCGTCT  TTCAGACGGC  CTTTCGACGT  GGAACCGATG
151 TGCATTACAT  GGGAGTATTT  TTCAATCACC  ATTTTGTCCG  TAACTTTGAC
201 TTCGCCGGTT  TTAATGATGC  GGCCGACGTC  GTTGCGTCCT  AAGTCAATCA
251 ACATGACGTG  TTCGGCGATT  TCCTTGGCAT  CGCTTAACAA  ATCTTGTTCT
301 TTGGCAAGGT  CTTTCGGCGG  GGTTTTCGCG  CGCAGGCGCG  TGCCGGCGAT
351 GGGGCGGACG  ATAACCTCGT  TCGCTTCGCG  TCGGAGCAGG  ATTTTCGGCG
401 AGGAGCCGAC  GATGTGGAAT  TCGCCGAAT  CGTAG
```

m656.pep

1	MPRLLGSTSS	MISMARTLGA	PESVPAGKVA	ARMSMLVMPs	FRRPSTILETM
51	CITWEYFSIT	ILSVTLTSPV	LLMRPTSLRP	KSINMTCsAI	SLASLNKSCS
101	LARSSAGVLP	RRRVPMGRT	ITSLRSRRT	ISGEEPTMWK	SPKS*

Homology with a predicted ORF from *N. gonorrhoeae*

```

      10      20      30      40      50      60
m656.pep  MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSLVMPFSFRPSTLETMCITWEYFSIT
          |||: || |||||:||||:||||:||||:||||:||||:||||:||||:||||:
g656      MPRFSGSISSMISIARTFGAPESVPAGKVAARMSILVTPSFKQPSTLETMCITWEYFSIT
          10      20      30      40      50      60

      70      80      90      100     110     120
m656.pep  ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLPRRRVPMGRT
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g656      ILSVTLTSPVLLMRPTSLRPKSISITCSAISLASLNKSCSLARSSAGVLPRRRVPMGRT
          70      80      90      100     110     120

      130     140
m656.pep  ITSLRSRRTRISGEEPTMWKSPKSX
          :|| |||||:||||:||||:||||:||||:||||:||||:
g656      MTSSRSRRTRISGEEPTMWKSPKSX
          130     140

```

1044

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTG GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
51  TTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTGACGTT GGAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTGTCTCG TAACTTTGAC
201 TTCGCGGTT TTAATGATGC GGCCGACGTC GTTGCCTCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCG
301 TTGGCAAGGT CTTGCGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTTGCGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRT R ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT					
a656.	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
m656.pep	ITSLRSRRT R ISGEEPTMWKSPKSX					
a656	MTSSRSRRT R ISGEEPTMWKSPKSX					
	130	140				
m656.pep	ITSLRSRRT R ISGEEPTMWKSPKSX					
a656	MTSSRSRRT R ISGEEPTMWKSPKSX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTA ggcagAATGT TTGCCGTTGC CGCTAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCCGCT TGGACGAATT
201 GGCAAAATGC GCGGCGGTTa cgACCGAATT TGAAAacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATACCAACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTCAGGAA AAAGCGTGGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCGGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattcc ATCGTccccg CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GGCACAACgc tTGGCGGACG AATTGGATTA TGTGCGGcgt
751 TTGGCGGTAG AAATGTTTGT TGTGCGGAC ACACATGAAT TGCTCGTCAA
801 TGAAACCGCC CCGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
851 GCGCCGACAG CAGTTCCAA CAGCAGGTAC GCATTATGTG CAacctGCCG
901 cccGccgACA CCAAATTATT aTCCCcttgC TGTATGGCGA ATATTTTGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGCGCGAA TGCACACCTG CACCTATACG GAAAAAAAAC CGCACAGAAA
1051 GGTGCGAAAA TGGGACACTT TaccgTTTGG ACCACCGATT CGGACaccgC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657 - pep

1	MNT	PILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC	
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL	
151	GYDGKGQIRV	CTLDELKAAF	AHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE	
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADEL DYGVG	

1046

251 LAVEMFVVD THELLVNETA PRTHNSGHHT IDACAAADQFQ QQVRIMCNLF
 301 PADTKLLSPC CMANILGDVW QEDGGEPDWL PLQSRPNAHL HLYGKKTAQK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2131>:

m657.seq
 1 ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTTGCCA TCCTCGGCGG
 51 CGGACAATTA GGCAGAATGT TTACCGTTGC CGCCAAAACC ATGGGCTACA
 101 AAGTAACCGT TCTCGACCCC GATCCGGACG CGCCGGCAGC AGAATTTGCC
 151 GACCGCCATT TGTGCGCGCC GTTTAACGAC CAAGCTGCTT TGGACGAATT
 201 GGCAAAATGC GCGGCGGTGA CCACTGAATT TGAAAACGTC AATGCCGATG
 251 CGATGCGCTT TTTGGCAAAA CATACCAATG TTTCCCTAG CGGCGATTGT
 301 GTGGCGATTG CACAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAAGC
 351 GGGATTGCAA ACCGCGCCGT ATCAAGTGGT TTGTAAGGCT GAAGACATCA
 401 CTGAAGCAAG CGCGCAATT TTGCCGGCA TCCTGAAAAC GGCTACGTTG
 451 GGCTACGACG GCAAAGGTCA AATCCGCGTA AAAACATTGG ATGAACTCAA
 501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
 551 TGGATTGCG CAGTGAAATT TCCGTAATCG TATGCCGTTT GAACAATGAC
 601 AACGTGCAA CTTTCGACCC TGCCGAAAAC ATCCACGAAA ACGGCATCTT
 651 GGCTTATCC ATCGTCCCG CGCGACTGAG TGCCGACGTG CAGCAACAGG
 701 CGCGGCAGAT GCGCAACGC TTGGCGGACG AATTGGATTA TGTGCGCGTA
 751 TTGGCGGTAG AAATGTTTGT TGTCGGTGAC ACGCATGAAT TGGTCGTCAA
 801 CGAAATCGCC CCGCGCCCGC ACAATTCCGG ACACCATACG ATAGATGCCT
 851 GCGCAGCAGA CCAGTTCAG CAGCAGGTAC GCATTATGTG CAACCTGCCG
 901 CTGCCGATA CCAAATTACT GAGTTCTTGC TGTATGGCAA ATATTTTGGG
 951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGCTG CCCTTGCAAA
 1001 GCCATCCGAA TGCACACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
 1051 GGGCGGAAAA TGGGACACTT TACCGTTTGA ACCACCGATT CGGACACCGC
 1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

This corresponds to the amino acid sequence <SEQ ID 2132; ORF 657>:

m657.pep
 1 MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGKVTVLDP DPDAPEAEFA
 51 DRHLCAPFND QAALDELAKE AAVTTEFENV NADAMRFLAK HTNVSPSGDC
 101 VAIAQNRIQE KAWIRKAGLQ TAPYQVCKA EDITEASQF LPGILKTATL
 151 GYDGGKQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRSEI SVIVCRLNND
 201 NVQTFDPAEN IHENGILAYS IVPARLSADV QQARQMAQR LADELQYVGV
 251 LAVEMFVVD THELVVNEIA PRPHNSGHHT IDACAAADQFQ QQVRIMCNLF
 301 PADTKLLSSC CMANILGDVW QEDGGEPDWL PLQSHNAHL HLYGKKTAHK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m657/g657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGKVTVLDP	DPDAPEAEF	ADRHLCAPFND
g657	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGKVTVLDP	DPNAPAEF	ADRHLCAPFDD
	10	20	30	40	50	60
m657.pep	QAALDELAKE	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC	VAIAQNRIQE	KAWIRKAGLQ
g657	RAALDELAKE	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC	VSIAQNRIQE	KAWIRKAGLQ
	70	80	90	100	110	120
m657.pep	TAPYQVCKA	EDITEASQFL	PGILKTATL	GYDGGKQIR	VKTLDELKAA	FAEHGGVDCVL
g657	TAPYQAVCKA	EDITEASQFL	PGILKTATL	GYDGGKQIR	VKTLDELKAA	FAEHGGVDCVL
	130	140	150	160	170	180

1047

	190	200	210	220	230	240
m657 . pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNDENVQTFDPAENIHENGILAYSIVPARLSADVQQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657 . pep	LADEL DYVGV LAVEMFVVGDTHEL VVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
g657	LADEL DYVGV LAVEMFVVGDTHELLVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657 . pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLOSHRNAHLHLYGKKTAKHGRKMGHFTVL					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLOSRPNAHLHLYGKKTAKHGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657 . pep	TTDSDTAFQEAKKLHQSXLX					
g657	TTDSDTAFQEAKKLHQSXLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

a657 . seq

1	ATGAAAAACA	TATCTCTTTC	TCCGCCCGCC	ATGCTCGGCA	TTCTTGGCGG
51	CGGACAATTA	GGCAGAAATG	TTACTGTTGC	TGCCAAAACC	ATGGGCTACA
101	AAGTAACCGT	ACTCGATCCC	AACCCGAATG	CGCCGGCAGC	GGAATTTGCC
151	GACCGCCATT	TGTGTGCGCC	GTTTGACAAC	CAAACCGCTT	TGGAAGAATT
201	GGCAAAATGT	GCGGCTGTTA	CGACCGAGTT	CGAAAACGTC	AATGCCGATG
251	CGATGCGTTT	TCTCGCCAAA	CATACCAATG	TTTCCCCCAG	CGGCGACTGC
301	GTTGCCATCG	CGCAAAACCG	CATTCAGGAA	AAGGCATGGA	TACGCAAAGC
351	AGGCCTGCAA	ACCGCGCCGT	ATCAAGCAAT	TTGCAAAGCC	GAAGACATCA
401	CTGAAGAAAG	CATACAATTT	CTGCCCGGCA	TCCTGAAAAC	CGCTACATTG
451	GGCTATGACG	GCAAAGGCCA	AATCCGCGTC	AAAACGGTGG	ATGAACTCAA
501	AGCCGCGTTT	GCCGAACACC	GCGGCGTGGA	TTGCGTTTTG	GAAAAAATGG
551	TGGACTTGCG	CGGCGAAATT	TCCGTTATCG	TATGCCGCTCT	GAACAATGAC
601	AACGTGCAAA	CTTTCGATCC	TGCCGAAAAC	ATTCACGAAA	ACGGTATCCT
651	CGCCTACTCC	ATCGTCCCAG	CCCGACTGAG	TGCCGACATT	CAGCAACAGG
701	CGCGACAAAT	GGCGCAGCGT	TTGGCCGATG	AATTGAACTA	CGTCGGCGTA
751	TTGGCGGTAG	AAATGTTTGT	TGTCGGCGAC	ACGCATGAAT	TGGTCGTCAA
801	CGAAATCGCG	CCGCGTCCGC	ACAATTCCGG	CCACCATAAC	GTCGACGCCCT
851	GCGCGGCAGA	CCAATTCCAG	CAACAGGTCC	GCCTGATGTG	CAACCTGCCA
901	CCTGCTGACA	CCAAATTGCT	GAGTTCCTGC	TGTATGGCGA	ATATTTTGGG
951	CGACGTTTGG	CAGGAAGACG	GCGGCGAACC	GGATTGGTTT	CCCCTGCAAA
1001	GCCGGCCGGA	CGCGCACCTG	CACCTTTACG	GCAAAAAAAC	CGCGCACAAA
1051	GGGCGGAAAA	TGGGACACTT	TACCATTTTA	AGCACCGATT	CGGACACCGC
1101	ATTTCAGAA	GCAAAAAAAC	TGCATCAGTC	CCTATAA	

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

a657 . pep

1	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	NPNAPAAEFA
51	DRHLCAPFDN	QTALEELAKC	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC
101	VAIAQNRIQE	KAWIRKAGLQ	TAPYQAICKA	EDITEESIQF	LPGILKTATL
151	GYDGKGQIRV	KTVDELKAAF	AEHRGVDCVL	EKMVDLRGEI	SVIVCRLNND
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADI	QQQARQMAQR	LADELNYVGV
251	LAVEMFVVGDT	THELVVNEIA	PRPHNSGHHT	VDACAADQFQ	QQVRLMCNLP
301	PADTKLLSSC	CMANILGDVW	QEDGGEPPWF	PLQSRPDAHL	HLYGKKTAKH
351	GRKMGHFTIL	STDSDTAFQE	AKKLHQSXL*		

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657 . pep	MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDAFAAEFADRHLCAFPND					

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|||||
a 657      MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAPAAEFADRHLCAFPDN
              10      20      30      40      50      60

              70      80      90      100     110     120
m657 . pep  QAALDELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
              |||||
a 657      QTALEELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
              70      80      90      100     110     120

              130     140     150     160     170     180
m657 . pep  TAPYQVVCKAEDITEASAQFLPGILKTATLGVDGKGQIRVKTLDLKAFAEHGGVDCVL
              |||||
a 657      TAPYQAICKAEDITEESIQFLPGILKTATLGVDGKGQIRVKTLDLKAFAEHRGVDCVL
              130     140     150     160     170     180

              190     200     210     220     230     240
m657 . pep  EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQARQMAQR
              |||||
a 657      EKMVDLRGEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADIQQARQMAQR
              190     200     210     220     230     240

              250     260     270     280     290     300
m657 . pep  LADEL DYVGV LAVEMFVVGDTHEL VVNEI APRPHNSGHHTIDACAADQFQQQVRIMCNLP
              |||||
a 657      LADEL NYVGV LAVEMFVVGDTHEL VVNEI APRPHNSGHHTVDACAADQFQQQVRLMCNLP
              250     260     270     280     290     300

              310     320     330     340     350     360
m657 . pep  PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHPNAHLHLYGKKTAAHKGRKMGHFTVL
              |||||
a 657      PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSRPDAHLHLYGKKTAAHKGRKMGHFTIL
              310     320     330     340     350     360

              370     379
m657 . pep  TTSDS TAFQEAKKLHQSLX
              :|||
a 657      STSDS TAFQEAKKLHQSLX
              370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2135>:

```

g658. seq
1  ATGGTGGCCG GAATTGTGCG TGCGCGGGGC GGTTCATTG ACGAGCAATT
51  CATGTGTGTC GCCGACAACA AACATTTCTA CCGCCAAtac GCCGACATAA
101 TCCAATTCGT CCGCCAagcG TTGCGCCGTC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGCCGCGcgg gGACGATGga atAAGCCAAG ATGCCGTTT
201 CGTGGATGTT TTCGGCGGGG TCGAAGGTTT GCACGTTTC ATCGTTCAGA
251 CGGCATACGA TCACGGAAAT CTCGCCGCGC AAGTCCACCA TTTTTCCAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAAA CGCGGCTTTG AGTTCGTCCA
351 ACGTTTGTAC GCGGATTGA CCTTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGGCAAAAA TTGCGCGCTT GCTTCAGTAA TGTCTTCGGC
451 CTTGCAAACC GCCTGATACG GCGCGGTTTG CAAGCCTGCT TTGCGTATCC
501 ACGCTTTTTC CTGAATGCGG TTTTGTGCAA TGGACACGCA GTCGCCGCTG
551 GGGGAAACGT TGGTATGCTT TGCCAGAGAG CGCATCGCGT CGGCAttgac
601 gtTTTCAAAT TCGGTcgtaA CCGCCGCGCA TTTTGCCAAT TCGTCCAACG
651 CGGCCCGGTC GTCAAACGGC GCGCACAAAT GGCGGTGGC AAATTCCGCC
701 GCCGGCGCAT TCGGGTCGGG ATCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTTAGCGGCA ACGGCAAACA TTctgcctAA

```

This corresponds to the amino acid sequence <SEQ ID 2136; ORF 658.ng>:

```

g658. pep
1  MVAGIVRARG GFIDEQFMCV ADNKHFYRQY ADIIQFVRQA LRLRLRLLH
51  VGTQPRGDDG ISQDAVFVDV FGGVEGLHVF IVQTAYDHGN LAAQVHHFFQ

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1049

101 NAIHAAVFGK RGFEFVQRF ADLTFVAVQA RSRFQDAGQK LRACFSNVFG
 151 LANRLIRRGL QACFAYPRFF LNAVLCNGHA VAAGGNVGM L CQRAHRVGID
 201 VFKFGRNRRR FCQFVQRGPV VKRRAQMAVG KFRRRRIRVG IENGYFVAHG
 251 FSGNGKHS*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

m658 . seq
 1 ATGGTGTCCG GAATTGTGCG GGCGCGGGGC GATTTCGTTG ACGACCAATT
 51 CATGCGTGTC ACCGACAACA AACATTCTA CCGCCAATAC GCCGACATAA
 101 TCCAATTCGT CCGCCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC
 151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTTT
 201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTGTG ATTGTTCAAA
 251 CGGCATACGA TTACGGAAAT TTCACTGCGC AAATCCACCA TTTTTCCTAA
 301 AACGCAATCC ACGCCGCCGT GTTCGGCAA CGCGGCTTGT AGTTCATCCA
 351 ATGTTTTTAC GCGGATTGA CCTTTGCCGT CGTAGCCCAA CGTAGCCGT
 401 TTCAGGATGC CGGGCAAAA TTGCGCGCTT GCTTCAGTGA TGTCTTCAGC
 451 CTTACAAACC ACTTGATACG GCGCGGTTT CAATCCCGCT TTGCGTATCC
 501 ATGCCTTTTC CTGAATGCGG TTTTGTGCAA TCGCCACACA ATCGCCGCTA
 551 GGGGAAACAT TGGTATGTTT TGCCAAAAG CGCATCGCAT CGGCATTGAC
 601 GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAT TCGTCCAAAG
 651 CAGCTTGGTC GTTAAACGCG GCGCACAAAT GGCGTTCGGC AAATTCGTCT
 701 GCCGCGCGCT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGGT
 751 TTTGGCGGCA ACGGTAAACA TTCTGCCTAA

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

m658 . pep
 1 MVSGIVRARG DFVDDQFMRV TDNKHFYROY ADIIQFVROA LRHLPRLLH
 51 VGTQSRGDDG ISQDAVFVDV FGRVESLHV IVQTAYDYG N FTAQIHFFQ
 101 NAIHAAVFGK RGFEFIQCFY ADLTFVAVQA RSRFQDAGQK LRACFSDVFS
 151 LTNHLIRRGL QSRFAYPCLF LNAVLCNRHT IAARGNIGMF CQKAHRIGID
 201 VFKFSGHRRR FCQFVQSSLV VKRRAQMAVG KFCCRRVRIG VENG YFVAHG
 251 FGGNGKHS*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

	10	20	30	40	50	60
m658 . pep	MVSGIVRARGDFVDDQFMRVTDNKHFYROYADIIQFVROALRHLPRLLHVG	VTQSRGDDG				
g658	MVAGIVRARGGFIDEQFMCVADNKHFYROYADIIQFVROALRRLPRLLHVG	TQPRGDDG				
	10	20	30	40	50	60
m658 . pep	ISQDAVFVDVFGGRVESLHVIVQTAYDYG N FTAQIHFFQNAIHA	AVFGKRGFEFIQCFY				
g658	ISQDAVFVDVFGGVEGLHVFIVQTAYDHGNLAAQVHHFFQNAIHA	AVFGKRGFEFVQRF				
	70	80	90	100	110	120
m658 . pep	ADLTFVAVQAQRSRFQDAGQKL	LRACFSDVFS	LTNHLIRRGLQSRFAYPCLF	LNAVLCNRHT		
g658	ADLTFVAVQAQRSRFQDAGQKL	LRACFSNVFGLANRLIRRGLQACFAYPRFF	LNAVLCNGHA			
	130	140	150	160	170	180
m658 . pep	IAARGNIGMF	CQKAHRIGIDVFKFSGHRR	AFQFVQSSLVVKRRAQMAVG	KFCCRRVRIG		
g658	VAAGGNVGM	LQRAHRVIGIDVFKFGRNRR	AFQFVQRGPPVKRRAQMAVG	KFRRRRIRVG		
	190	200	210	220	230	240
m658 . pep	VENG YFVAHG	FGGNGKHS				
g658	VENG YFVAHG	FGGNGKHS				
	250	260				
m658 . pep	VENG YFVAHG	FGGNGKHS				

1050

```

          :|||||:|||||
g658      IENGYFVAHGFGNGKHSAX
          250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

```

a658.seq
1  ATGGTGGCCG GAATTGTGCG GACGCGGCGC GATTTCGTTG ACGACCAATT
51  CATGCGTGTG GCCGACAACA AACATTTCTA CCGCCAATAC GCCGACGTAG
101 TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT
151 GTCGGCACTC AGTCGGGCTG GGACGATGGA GTAGGCGAGG ATACCGTTTT
201 CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTTGTC ATTGTTCAGA
251 CGGCATACGA TAACGGAAAT TTCGCCGCGC AAGTCCACCA TTTTTCCAA
301 AACGCAATCC ACGCCGCGGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
351 CCGTTTTGAC GCGGATTGCG CCTTTGCCGT CATAGCCCAA TGTAGCGGTT
401 TTCAGGATGC CGGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC
451 TTTGCAAATT GCTTGATACG GCGCGGTTTG CAGGCTGCTT TTGCGTATCC
501 ATGCTTTTTT CTGAATGCGG TTTTGCSCGA TGGCAACGCA GTCGCCGCTG
551 GGGGAAACAT TGGTATGTTT GCGGAGAAAA CGCATCGCAT CGGCATTGAC
601 GTTTTCGAAC TCGGTCGTAA CAGCCGCACA TTTTGCCAAT TCTTCCAAAG
651 CGGTTTGGTT GTCAAACGGC GCACACAAAT GCGGGTCGGC AAATTCGCT
701 GCCGCGCAT TCGGGTTGGG ATCGAGTACG GTTACTTTGT AGCCCATGGT
751 TTTGGCAGCA ACAGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

```

a658.pep
1  MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGQT LRHLSRLLLN
51  VGTQSGWDDG VGEDTFVFNV FGRIESLHV IVQTAYDNGN FAAQVHHFFQ
101 NAIHAAVFGK RGFEFIHRFD ADLAFAVIAQ CSGFQDAGQK LYAFFSDVFG
151 FANCLIRRLG QACFAYPCLF LNAVLRDNGA VAAGGNIGMF GEKTHRIGID
201 VFELGRNSRT FCQFFQSGLV VKRRTQMAVG KFCRRIRVG IEYGYFVAHG
251 FGSNSKHS*

```

m658/a658 75.3% identity in 259 aa overlap

```

          10      20      30      40      50      60
m658.pep  MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLVGTQSRGDDG
          ||:||||:| ||:||||:| ||:||||:| ||:||||:| ||:||||:| ||:||||:|
a658      MVAGIVRTRRDFVDDQFMRVADNKHFYRQYADVQFIGQTLRHLSRLLLVNVTQSGWDDG
          10      20      30      40      50      60

          70      80      90      100     110     120
m658.pep  ISQDAVFVDVFRVESLHVIVQTAYDYGNTAQIHFFQNAIHAAVFGKRGFEFIQCFY
          ::||:||||:| ||:||||:| ||:||||:| ||:||||:| ||:||||:| ||:||||:|
a658      VGEDTFVFNVFGRIESLHVIVQTAYDNGNFAAQVHHFFQNAIHAAVFGKRGFEFIHRFD
          70      80      90      100     110     120

          130     140     150     160     170     180
m658.pep  ADLTFVAVQSRFQDAGQKLRACFSDVSLTNHLIRRLGQSRFAYPCLFLNAVLCNRHT
          ||:||||:| ||:||||:| ||:||||:| ||:||||:| ||:||||:| ||:||||:|
a658      ADLAFAVIAQCSGFQDAGQKLYAFFSDVFGFANCLIRRLGQACFAYPCLFLNAVLRDNGA
          130     140     150     160     170     180

          190     200     210     220     230     240
m658.pep  IAARGNIGMFQCAHRIGIDVFKFSGHRRAFQCFVQSSLVVKRRAQMAVGKFCRRVRIG
          :|| ||:||||:| ||:||||:| ||:||||:| ||:||||:| ||:||||:| ||:||||:|
a658      VAAGGNIGMFGEKTHRIGIDVFELGRNSRTFCQFFQSGLVVKRRTQMAVGKFCRRIRVG
          190     200     210     220     230     240

          250     260
m658.pep  VENGYFVAHGFGNGKHSAX
          :| ||:||||:| ||:||||:|
a658      IEYGYFVAHGFGSNGKHSAX
          250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

g661.seq
 1 ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51 GGCGGGCATT GCCGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
 151 ACCGGA AAAA CCTgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
 201 TGCCGTGCAG ATTGCCGGCA GCGACCcga acaGATGGCG Gatgcgggcgc
 251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
 301 cccgccaaga AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
 351 CGAGccgctg gttgcCgcca tTTtggaggc ggtggtcAAG GCGGCGGgcy
 401 TACCCGTTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
 451 ctgcCcgccg tcgcca aaat cgccgaagat tgcggcattg ccgccCttgc
 501 cgttccacgg ggcCGCgcgC ACGCCAAATGT ACAAAGGCGA GGCgcGTTAC
 551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
 601 CGGCGACATC actTCgccc AAAAAGCCGC CGccgTCCTC AAACAAACCG
 651 CCGCCGACGG CATCATGATA GGGCGCGCGC CGCAAGGCAG GCCGTGGTTT
 701 TTCCGCGATT TGAAGCATT TGC CGAACAC GGCCTTTTAC CGCCTGCCTT
 751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACCACATC CGCGCCATGC
 801 ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
 851 GGCTGGTACA TCGCGAAAT GCCCGACGGC GAACAGGCGC GCGGTGA

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

g661.pep
 1 MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
 51 TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
 101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDHDDQN
 151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
 201 RRHFHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFRFEAL CRTRRFTACL
 251 EFGRMQSRHF EPHPRHARVL WDRRCARHT QTHRLVHRRN ARRTTGA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

m661.seq
 1 ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51 GGCGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
 151 ACTAGAAAAA CCTTGACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
 201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
 251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
 301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
 351 CGAGCCGCTG GTTGCCGCCA TTTTGAAGC CGTCGTCCGT GCGGCAGGCG
 401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
 451 CTGCCCCTCA TCGCCAAAAT CGCCGAAGAT TCGGGCATCG CCGCCCTTGC
 501 CGTCC.ACGG ACGCACGCGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
 551 GAACTCATCG CCGAAACCAA ATGCCGCTGT AACATCCCGG TCTGGGTCAA
 601 CGGCGACATT ACTTCGCCGC AAAAAGCCCA AGCCGTCCCT AAACAAACCG
 651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
 701 TTCCGCGATT TGAACATTA TGCCGAACAC GGTGTTTTGC CGCCTGCCTT
 751 GAGTTTGGCA GAATGCGCCG CCGCTATTTT GAACCACATC CGCGCCATAC
 801 ACGCGTTTTA CCGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
 851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

m661.pep
 1 MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
 51 TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
 101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDHDDQN
 151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
 201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPRFETL CRTRCFAACL
 251 EFGRMRRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRTTDS*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
	: : : : :					
g661	MHIGGYFIDNPIALAPMAGIADKPFRRLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
	: : : : :					
g661	ADEGGIVAVQIAGSDPEQMADAARYNVSLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
	: : : : :					
g661	VAAILEAVVKAAGVPVTLKTRLGWHDHDDQNLPVAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRNRRHYDRARRARQAVVLPFRFETL					
	: : : : : :					
g661	GALRTHRRDQKPSEHPGLGQRRHHFAAKSRRRPQTNRNRRHHDRARRARQAVVFPRFEAL					
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFAACLEFGMRMRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
	: : : :					
g661	CRTRRFTACLEFGMRQSRHFEPHPRHARVLWDRRCARHTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGGAGGC GGTGGTCAA GCGGCGGGCG
401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCAGCGC ACGCAAATGT ACAAAGGCGA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGGCGACATT ACCTCGCCGC AAAAAGCCCA AGCCGTCTC AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGCGC CGCAAGGCAG ACCGTGGTTC
701 TTCCGCGATT TGAAACATTA CGCCGAACAC GGTGTTTTAC CGCCTGCCTT
751 GAGTTTGGCA GAATGTACCG CCACTATTTT GAACCATATC CGAGCCATGC
801 ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCAGC CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWHDHQN
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRHYLAAKSP SRPQTNRNRR HYDRARRARQ TVVLPFRFETL RRTRCFTACL
251 EFGRMYRHYF EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRTDTS*

```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					

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a661      MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60

           70      80      90      100     110     120
m661.pep  ADEGGIVAVQIAGSDPQOMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMONEPL
           |||||
a661      ADEGGIVAVQIAGSDPQOMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMONEPL
           70      80      90      100     110     120

           130     140     150     160     170     180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||:|||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180

           190     200     210     220     230     240
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPREFETL
           |:| |||||:|||||
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPREFETL
           190     200     210     220     230     240

           250     260     270     280     290     299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           |||||:|||||:|||||
a661      RRTRCFACLEFGRMYRHYFEPHPSHARVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAACCG TGTTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGtctGC CAAATGCCTG AAATCGCTGG TGCCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggctg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTCGGAC GCAACAATTC GGTTTTTGTG
601 GATTTTTTCG GCATtcagac GGCAACGATT ACGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCCTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTGGAAATC CTTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCGCTTA TCGAAGAACG
801 CGTGCGCGAA CACCCGGAAC AATATTCTG GCTGCACAAG CGTTTCAAAA
851 CCCGTCGCGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLOFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVILLYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRRNSVFV
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPIV READNTVTIQ FYPAWKSFFS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DEFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAACCG TGTTGAAACA

```

1054

```

201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCTGC CGGACGTTTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAG GCCGCAACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCTCG TCAAACAGTT CCGCAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTCGGAC GCAACGATTG GGTTTTGTG
601 GATTTTTTCG GTATTCAGAC GGCAACGATT ACCGGATTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCGC CATTCCTGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGAAATC CTTCCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACCGTTTTA TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTG GCTGCACAAG CGTTTAAAAA
851 CCCGTCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
51 KCFSEWSEEK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFV
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPV READNTVTLH FYPAWSFPG
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKP	RRRIGEINLAKCFSEWSEEK				
g663	10	20	30	40	50	60
	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKP	RRRIGEINLAKCFPEWDEEK				
m663.pep	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
g663	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYWYASAKCLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
m663.pep	130	140	150	160	170	180
	AFEMAVYALNQDIPLISMYSHQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
g663	130	140	150	160	170	180
	AFEMAVYALNQDVPLISMYSHQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
m663.pep	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAAL	ANAKVIPAIPVREADNTVTLH				
g663	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAAL	ANAKVIPAIPVREADNTVTLQ				
m663.pep	250	260	270	280	290	
	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHK	RFKTRPEGSPDFYX				
g663	250	260	270	280	290	
	FYPAWSFPGEDAQADAQRMNRFIEERVREHPEQYFWLHK	RFKTRPEGSPDFYX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAACCTGC TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGGCGAAAT CAATTTGGCA

```

```

151 AAA.TGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAACCG TGTGAAACA
201 GCA.TTTCAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACG.CGCCCCG CGGGCGTTTG AAATCACTGG TCGCTACCG CAACAAACAT
301 TAT.TTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCA.CTTACCC GCGTTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTT
401 CGC.TGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATT.TTGAAAG GCCGCAACCG CTATCACAAAC GTTTTCCTTA TCGGGCGCAC
501 CGA.AGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTC.TGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTG GGTTTTGTG
601 GAT.TTCTTCG GTATTTCGGAC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGC.GCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACA.ATACGGT TACATTGCAT TTCTACCCTG CTTGGGAATC CTTTCCGAGT
751 GAA.GATGCCG AGGCCGACGC GCAGCGCATG AACCCTTTTA TCGAGGAACG
801 CGT.GCGCGAA CATCCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCC.GTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

a663.pep

```

1 MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51 KCFPEWDGKK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFV
201 DFFGIRTATI TGLSRIAALA NAKVIPAI PV READNTVT LH FYPWESFSP
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

m663/a663 96.2% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP RRRIGEINLAKCFSEWSEEK					
a663	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP RRRIGEINLAKCFPEWDGKK					
	10	20	30	40	50	60
m663.pep	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH YLDDALAAGEKVIILYPHFT					
a663	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH YLDDALAAGEKVIILYPHFT					
	70	80	90	100	110	120
m663.pep	130	140	150	160	170	180
	AFEMAVYALNQDIP LISMYS HQNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
a663	AFEMAVYALNQDVPLISMYS HQNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
	130	140	150	160	170	180
m663.pep	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVT LH					
a663	SAPFLYLPDQDFGRNDSVFVDFFGIRTATITGLSRIAALANAKVIPAI PVREADNTVT LH					
	190	200	210	220	230	240
m663.pep	250	260	270	280	290	
	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX					
a663	FYPAWSFPGEDAKADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

g664.seq

```

1 ATGATACATC CGCACCCTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51 AGAAATTGTT CATCTCCTCA TAGCTGAcg gCGGCACCGG ATGGGCGGTC
101 GGGCCTGCGT CTTGGGGGAA CTGGTTCTGG CGCAGCAGGC GGATGTTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGAAAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGAAA TATTCGTGTC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCTT TGTTTTCCAT CGCGCCATA
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCcaa
451 cCgaagcgc gtttcgtcCc acttcacgC gtTTTTTCAA cgaTTCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAaa ACTCGATTTT

```

g664.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

m664.seq

This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:

m664.pcp

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m664/g664 91.8% identity in 183 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

a664.seq

1	GTGATACATC	CGCACCACCT	CCGCGCCTTT	TTCATAAACG	GTCATGGTGT
51	AGAAATTGTT	CATCTCCTCA	TATCGGGCGG	GGCGCACC	GGTATGCGGTC
101	GGACCTGCGT	CTTCGGGGAA	CTGGTGCTGG	CGCAGCAGGC	GGATGTTTTC
151	GATACGGCGC	ACGGCGCGGC	TGGCGCGGTC	GCCGGAATAA	TCTTGGTTCG


```

2 01 GGAACACGGT CAACCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
2 51 GTCACGCGGT TGCCCGTCCA GTTGTGAAA TATTCGTGTC CGACCACGGA
3 01 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
3 51 CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTTCCAT CGCACCATA
4 01 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
4 51 ACCGAAGCGC GTTTCGTCC ACTTCATTGC GTTTTT.CAG CGATTCCACG
5 01 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGATAA ACTCGATTTT
5 51 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
1  VIHPHHFRAF FINGHGVEIV HLLISGGAHR MCGRTCVEGE LVLAQQADV
51  DTAHGAAGAV AGKFLVAEHG QPFLQKLEP VAAGHAVARP VVEIFVSDHG
101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
151 TEARFVPLHC VFXAIPQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

m664.pep      10      20      30      40      50      60
VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGRACVFGELVLAQQADVFDAHGAAGAV
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a664          10      20      30      40      50      60
VIHPHHFRAFFINGHGVEIVHLLISGGAHRMCGRTCVEGE LVLAQQADVFDTAHGAAGAV

m664.pep      70      80      90     100     110     120
AGKFLVAEHGQPFLQKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAGVKDELG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a664          70      80      90     100     110     120
AGKFLVAEHGQPFLQKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG

m664.pep     130     140     150     160     170     180
VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVEXTIPQSRPWACPLRWCK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a664         130     140     150     160     170     180
VKDVQTLVFHRTHEIAHGDDHENIQVVFQTEARFVPLHCVFXAIPQSRPWACPLRWCK

m664.pep      TRFX
||||
a664          TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
1  atgaagtGg acgaaacgcg cttcgGgttg GAAatgact tggatatttt
51  CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACC GCC
151 ACCGATACCG ATTTCGAAGG CATTGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
301 CGCGCCGGCC GCGCCGTGCG CCGCATCGAG AACATCCGCC TGCTGCGCCA
351 GAACCACTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCcccg
401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TGGTGGCGAT GTATCATACC CTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGC ATGAAGCTAT ATTTcCaacg CCACGACGGA CAGGCAGTGA
551 CCTGCGACGA TTTCCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
601 GACCACTTCG CCTTGTGGTA CAGCCAGGCG GGCACGCCCC TTTTGGAAAGC
651 CGAAGGCCGT CTGAAAAACA ATGTTTTTGA GTTAACCATT AAACAAACCG
701 TGCCGCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
801 GGGCAAAACG GCAACCGAAG CCGTGTTCCT GATGACCGAA GCCGAACagg
851 CCTTCCCGCT CGAAGGTGTA ACCGAAGCGG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCAGTGTA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCACG ACAGCGACG TTTACAGTGC TGGGAAGCCG

```

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10 01 CCCAAACGCT CTACCGTCGC GCCGTCGCCG CCAACCTTGC CGCGCTTTCA
10 51 GACGGCATCG GGTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
11 01 AGTCATTTCG GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
11 51 GCGTGCCGTC CGAAGCCGAA ctGTGGGACG GCACGAAAAA CATcgaCCCG
12 01 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
12 51 CttcctgcCG AAATGGCAGC AATTGGaccg tcaggcggcg aagCaggaaa
13 01 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
13 51 AACGTCTGCC GCGCCTtctgt cctGCGCGCC GACCCCGCGC acatcgAAAC
14 01 TGTGTCGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
14 51 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
15 01 CTGGCGCAGT TTGCCGacaa gTtttcAGAC GACGCGCTGG TGATGGACAA
15 51 ATATTTTCGCC CTTATCGGCT CAAGccgccg cagCGACACC CTGCAACAGG
16 01 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
16 51 GCCCGTTTCG TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTTCACGC
17 01 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
17 51 ACCGCTTCAA cCCGcaggtc gccGCCCGCC TGGTGCAGGC GTTCAACCTC
18 01 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTgGTGAAAC AAGAATTGCA
18 51 GTGCATTCCG GCGCAGGAAG GATTGTCGAA AGacGTGGGC GAaatcgtCG
19 01 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

g665.pep

```

1 MKWDETRFGL EYDLDFMVV AVGDFNMGM ENKGLNIFNT KFLVADSRTA
51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPTAHP VRPVSYEEMN NFYTMTVYEK
151 GAENVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNVFELTI KQTVPTTDPD ADKQPMPIPV
251 KVGILLNRNGE AVAFDYQGRK ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYLYN PYSDDDL LLL LAHDSDAFTC WEAAQTLYRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDROQA KQENQSYEYS PETADWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESDTRNCL
501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQVQVQALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

m665.seq

```

1 ATGAAATGGG ACGAAACGCG CTCGGTTTG GAATACGACT TGGATATTTT
51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAAACACC AAGTTCGTCC TTGCCGACAG CCGCACC GCC
151 ACCGATACCG ATTTCAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACCTG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAATT TTCCGCGCAC
301 CGCGCCAGCC GCGCGTGC GCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCACTTC CCCGAGACG CAGGCCCCGAC CGCCCATCCG GTGCGCCCCG
401 CCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGC CGGGAAG TAGTGC GGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCAACG CCACGACGGA CAGGCGGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCAGTTCG CTTGTGTGTA CAGCCAGGCG GGCACGCCCG TTTTGGGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCAC GCGGATATG ACGGATAAAC AGCCGATGAT GATTCCCGTC
751 AAGGTCGGGC TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGTGCT GCTGACCGAA GCCGAACAGA
851 CCTTCCTGCT CGAAGCGGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAACAT CCGTACAGCG ACGACGACCT
951 CTGCTCCTG CTCGCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CCCAAACGCT CTACCGCCGC GCCGTGCGCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCG GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
1251 CTTCTGCGC AAATGGCAGC AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGGCG CACGCTGCGC

```

```

13 51 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
14 01 CGTTGCCGAA AAATACGGCG AAATGGCGCA AACATGACC CACGAATGGG
14 51 GCATCCTGTC CGCGCTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
15 01 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
15 51 ATATTTTGCC CTCGTCGGCT CAAGCCGCGG CAGCGACACC CTGCAACAGG
16 01 TTCGAACCGC CTTGCAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
16 51 GCCCGTTCGC TCATCGGCAG CTTAGCCGCG AACGTCCCGC ATTTCCACGC
17 01 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
17 51 ACCGCTTCAA CCCGAGGTC GCCGCCGCT TAGTGCAGGC GTTCAACCTC
18 01 TGCAACAAGC TCGAGCGCA CCGCAAAAAC TTGGTGAAAC AAGCATTGCA
18 51 GCGCATTCGG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
19 01 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
  1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFLVADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNIFELTV KQTVPTPDM TDKQPMIIPV
251 KVGLLNRRGE AVAFDYQGR ATEAVLLTE AEQTFLLGV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDL LLAHDSDAFTR WEAQAQTL YRR AVAANLATLS
351 DGVELPKHEK LLAIVEKVIS DDLNDAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNROAA KOENQSYEYS PEAAGWRTL R
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNM T HEWGILSAVN GNESDTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGSFSR NVPFHAEDEG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQRIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

```

m665.pep      10      20      30      40      50      60
MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES
|||||
g665          10      20      30      40      50      60
MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES

m665.pep      70      80      90     100     110     120
VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
|||||
g665          70      80      90     100     110     120
VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQNF

m665.pep     130     140     150     160     170     180
PEDAGPTAHPVRPASYEEMN NFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG
|||||
g665         130     140     150     160     170     180
PEDAGPTAHPVRPVSYEEMN NFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG

m665.pep     190     200     210     220     230     240
QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM
|||||
g665         190     200     210     220     230     240
QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPTPDM

m665.pep     250     260     270     280     290     300
TDKQPMIIPVKVGLLNRRGEAVAFDYQGRATEAVLLMTEAEQTFLLGVTEAVVPSLLR
|||||
g665         250     260     270     280     290     300
ADKQPMIIPVKVGLLNRRGEAVAFDYQGRATEAVLLMTEAEQAFFLEGVTEAVVPSLLR

```

1060

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTWEAAQTLRYRAVANLATLSDGVELPKHEK					
g665	GFSAPVYLNYPYSDDDLLLLLAHDSDAFTCWEAAQTLRYRAVANLAALSDGIGLPHKEK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNFAKALLLGVPEAEWLDGAENIDPLRYHQAREALLDTLAVHFLP					
g665	LLAAVEKVISDDLLDNFAKALLLGVPEAEWLDGTENIDPLRYHQAREALLDTLAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNQAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNM					
g665	KWHELDQAAKQENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNM					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQH					
g665	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
g665	PKFSLENPNKARSLIGSFSRNVPHFHAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILD					
g665	CNKLEPHRKNLVKQELQCIRAQEGLSKDVGEIVGKILGX					
	610	620	630			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

```

a665.seq
1  ATGAAGTGGG ACGAAACGCG CTTCGGTTTG GAATACGACT TGGATATTTT
51  CATGGTCGTC GCCGTGGGCG ATTCAATAT GGGTGGCATG GAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGTACCGCC
151 ACCGATACCG ATTTTGAAGG CATCGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACGCG ACGGGCAACC GCGTGACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGTTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGTATCGAA AACATCCGCC TGCTGCGCCA
351 GACCCAGTTC CCCGAAGACG CAGGTCCGAC CGCACATCCG GTGCGCCCGC
401 CCCGATATGA GGAGATGAAC AATTCTACA CCATGACCGT TTATGAAAAA
451 GGCAGCGAAG TGGTGGCGAT GTATCACACC TTGCTCGGCG AAGAGGGCTT
501 CCAAAAGGAT ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCTGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGTGG ACGCGAACGG CATCAACCTC
601 GACCAATTCG CTTGTGGTA CAGCCAAGCA GGTACGCCGG TTTTAGATGC
651 TCAAGGGCGT CTGAAAAACA ATGTGTTTCA GTTAACCATC AAACAAACCG
701 TGCCGCCACG GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAATCGGGC TGCTGAACTG CAACGGCGAA GCGGTGGCAT TTGATTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CTTTCAGTT CGAAAGCGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTTCTG CTCGCCCATG ACAGCGACGC CTTACAGCGC TGGGAAGCCG
1001 CACAAACGCT CTACCGCCGT GCCGTGCGCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCGTCG AGTTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCG GACGACCTCT TAGACAACGC TTTCAAAGCC CTGCTTTTGG
1151 GTGTGCCGTC TGAAGCCGAG CTGTGGGACG GCGCGGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATATAC TTGCCGTCCG
1251 CTTTCTGCCG AAATGGCAGC AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAGTACAGC CCCGAAGCCG CCGGTGGCG CACGCTGCGC
1351 AATGTCTGCC GCGCCTTCGT CTGCGCGCC GATCCGCGC ACATCGAAAC

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
 1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACCGG CAACCGCCTG
 1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
 1551 ATATTTCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
 1601 TTCAAACCGC CTTGCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
 1651 GCCCGCTCGC TCATCGGCAG CTTACGCCGC AACGTCCCGC ATTTCCACGC
 1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
 1751 ACGGCTTTAA CCCGAGGTC GCCGCCGCC TGGTGCAGGC GTTCAACCTC
 1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
 1851 GCGCATTCCG GCGCAGGAAG GATTGTGAA AGACGTGGGC GAAATCGTCG
 1901 GCAAAATTTT GGATTGA

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

a 665.pep

1 MKWDETRFGL EYDLDFMVV AVGFENMGAM ENKGLNIFNT KFLVADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
 101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
 151 GAEVVRMYHT LLGEEGFQKG MKLYFORHDG QAVTCDDFRA AMVDANGINL
 201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPTPDM ADKQPMMPV
 251 KIGLLNCNGE AVAFDYQGRK ATEAVLLLE AEQTFQFESV TEAVVPSLLR
 301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAQAOTLYRR AVAANLAALS
 351 DGVELPKHEK LLAAVEKVIS DDLNDNAFKA LLLGVPSEAE LWDGAENIDP
 401 LRYHQAREAL LDILAVRFLP KWHELNQAAA KOENQSYEYS PEAAGWRTLR
 451 NVCRAFLVRA DPAHIETVAE KYAEMAQNM T HEGWILSAVN GNESDTRNRL
 501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLENPNK
 551 ARSLIGSFSR NVPHFHAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
 601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

m665/a665 97.3% identity in 638 aa overlap

m665.pep	10	20	30	40	50	60
a665	MKWDETRFGLEYDLDIFMVVAVGFENMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES					
m665.pep	70	80	90	100	110	120
a665	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD RASRAVRRIE NIRLLRQHOF					
m665.pep	130	140	150	160	170	180
a665	PEDAGPTAHPVRPARYEEMN NFYTMTVYEK GAEVVRMYHT LLGEEGFQKG MKLYFORHDG					
m665.pep	190	200	210	220	230	240
a665	QAVTCDDFRAAMADANGINLDQFALWYSQA GTPVLEAEGRLKNNIFELTVKQTVPTPDM					
m665.pep	250	260	270	280	290	300
a665	TDKQPMMPV KVGLLNRNGE AVAFDYQGRK RATEAVLLLEAEQTFLEGVTEAVVPSLLR					
m665.pep	310	320	330	340	350	360
a665	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEAQAOTLYRR AAVANLATLS DGVELPKHEK					

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNROAAKQENQSYEYSPEAGWRTLNRNVCRAFLRADPAHIETVAEYQEMAQNMT					
a665	KWHELNROAAKQENQSYEYSPEAGWRTLNRNVCRAFLRADPAHIETVAEYQEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQOVRTALQH					
a665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQOVQRTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFNRNVPFHAEADGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFNRNVPFHAEADGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQRIQAEGLSKDVGEIVGKILD					
a665	CNKLEPHRKNLVKQALQRIQAEGLSKDVGEIVGKILD					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAAACG CTGCCTACCG
51  CATTCTTGAA ACCGAAGTGC ATTTCGACAT TGCCGAACCG CAAACCGTGC
101 TGAAGTCGCG TTTGACGGTC GAGCCGCGA GGGCGGGCGA GCCGCTGGTG
151 TTGGACGGTT CGGCAAAACT CTTGTCCGTC AAAATCAACG GCGCGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGCG GGAACACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATCTGTTTA CCCAGTGGCA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCAAC ATCGTCGCGG ACAAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTTT CAGACGGCGC
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTCCG GGGCGATTTC GCGGTAACGG AAGACCGTTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAAC
651 CAAGTCGCGC TTGCGCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGTTGGAA TATGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTAGGCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATTTT
801 TAACACCAAG TTCGTCCTCG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCT CAACCTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGGCGACCGC GCCGGCCGCG
1001 CCGTGCGCCG CATCGAGAAC ATCCGCTTGC TGCGCCAGAA CCACTTCCCC
1051 GAAGACGCGA GCCCGACCGC CCATCCGGTG CGCCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCATACCCCTG CTCGGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG GCAGTGACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTCGCTC
1301 TGTGTTACAG CCAGGCGGGC ACGCCCGTTT TGGAGCCGA AGGCCGCTCTG
1351 AAAACAATG TTTTCGAGTT AACCATTAAA CAAACCGTGC CGCCACGCGC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAAA GTCGGGCTTC
1451 TGAACCGCAA CGCGGAAGCG GTGGCATTCT ATTATCAGGG CAAACGCGCA
1501 ACCGAAGCCG TGTGCTGAT GACCGAAGCC GAACAGGCC TCCCGCTCGA
1551 AGGTGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGATCTT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCACGACA GCGACGCTTT CACGTGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGTCGCGCC GTCGCCGCA ACCTTGCCG GCTTTCAGAC GGATCGGGT

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1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCCT CAAAGCCCTG CTTTGGGGCG TGCCGTCGCA
1851 AGCCGAACCTG TGGGACGGCA CGGAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATACGCTT CCGTCCGCTT CCTGCCGAAA
1951 TGGCAGCAAT TGGACCGTCA GGCGGCGAAG CAGGAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACGCCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCCT GCGCGCCGAC CCCGCGCACA TCGAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGCGCAAAA CATGACCCAC GAATGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTGCCCTT
2251 ATCGGCTCAA GCCGCCGAG CGACCCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCCTACCGT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCCTGG TGCAGGCGT CAACCTCTGC AACAGCTCG
2501 AGCCGCAACC CAAAACTTG GTGAAACAAG AATTGCAGT CATTCGGCG
2551 CAGGAAGGAT TGCGAAAGA CGTGGCGGAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pap

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPORAGEPLV
51 LDGSAKLLSV KINGAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDBGHWV KWEDPFAKPS YLFALVAGDL AVTEDRETTM
201 SGRNVKIEFY TTEADKPKVG FAVESLRNAM KWDETRFGL EYLDIFMVVA
251 VGDFFMGMME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRWF QLSLKEGLTV FRDQEFSGDR AGRVVRRIEN IRLLRQNFPP
351 EDAGPTAHVP RPVSYEEMNN FYTMTVYKGG AEVVRMYHTL LGEEGFQKGM
401 KLYFORHGO AVTCDDFRAA MADANGINLD QFALWYSOAG TPVLEAREGL
451 KNNVFELTIK QTVPTPDMA DKQPMMPVK VGLLNRNGEA VAFDYQKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVLYNYP YSDDDLLLLL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNAFKAL LLGVPSEAEL WDGTEINIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROAAK QENQSYEYSP ETADWRTLNR VCRAFLVRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSRRSDTL QQVQALQHP KFSLENPNKA RSLIGSFSRN VPHFHAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVGE IVGKILG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAAA ACCGATTAC ATTTTGATAT TAATGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTT GAGCCGCGA GGGTAGGGGA GCCGCTGGTG
151 TTGACCGGTT CGGCGAAACT CTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACGAAA TCCTGCCGGC GGAAACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATTGTGTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCAAATT CACCACCACC ATCGTCGCGC AAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGCAACAA AATCGACGGC GGCGAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAG ACCCGTTTC CAAACCGAGC TATCTGTTG
551 CTTTGGTCCG GGGCGATTG GCGGTAACGG AAGACTATT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGGCGATT TCAATATGGG CGCGATGGA AACAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACAG AGTATTTCCA CAACCTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG CATCGAAAAC ATCCGCTTGC TCGCCAGCA CCAAGTTCCC
1051 GAAGACGCGA GCCCGACCGC CCATCCGGTG CGCCCGCCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAGAGGC GCGGAAGTAG
1151 TCGGATGTA TCACACCTG CTCGCGGAAG AGGGCTTCCA GAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTACCT GCGACGATT
1251 CCGCGCGGCG ATGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CAGGCGGGC ACGCCCGTT TGAAGCGGA AGGTCGCTG
1351 AAAACAATA TTTTCGAGT GACCGTCAA CAAACCGTGC CGCCACGCC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCCGTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTG ACTATCAGG CAAACCGCGC

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1501 ACCGGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
1551 AGGCCTAACC GAAGCCGTCG TTCCTCTGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCATGACA GCGAGCCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGCCGCGCC GTGCGCGCCA ACCTTGCCAC GCTTTCAGAC GCGGTTGAGC
1751 TGCCGAAACA CGAAAACTG CTTGCCGCGG TCGAAAAAGT CATTTAGAC
1801 GACCTCTTAG ACAACGCCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA
1851 AGCCGAGCTG TGGGACGGCG CAGAAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCCTGCGA AGCCTTGTG GATACGCTTG CCGTCCACTT CCTGCGGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGGCGAAG CAGGAAAAAC AAAGTACGA
2001 ATACAGCCCC GAAGCCGCGG GCTGCGCAC GCTGCGCAAC GTCTGCGCGG
2051 CCTTGTCTCT GCGCGCGGAC CCGCGGCACA TCGAAACCGT TGCCGAAAAA
2101 TACGCGGAAA TGGCGCAAAA CATGACCCAC GAATGGGCGA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGTGTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGCCTC
2251 GTCGGCTCAA GCCGCCGAG CGACACCCTG CAACAGGTTT GAACCGCCTT
2301 GCAGCATCCG AATTCAGCC TCGAAAAACC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCGCGATT TCCACGAGA AGACGGCAGC
2401 GGCTACCGTT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAAAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG CATTGCAGCG CATTCGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTGGCA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSEFTVEV ETEILPAENK
101 SLMGLYASGG NLFQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL YDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLRQHQFP
351 EDAGPTAHPV RPASYEEMNN FYTMTVYERK AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNIFELTVK QTVPTPDMT DKQPMIPVK VGLNLRNGEA VAFDYQKRA
501 TEAVLLLEA EQTLLEGVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVLPKHEKL LAAVEKVISD
601 DLLDNFAKAL LLGVSEAEEL WDGAENIDPL RYHQAREALL DTLAVHFLPK
651 WHELNRAAK QENQSYEYSP EAAGWRLRN VCRFVLRAD PAHETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPOVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVGE IVGKILD*

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m665-1/g665-1 96.1% identity in 866 aa overlap

	10	20	30	40	50	60
m665-1.pep	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTVVKSRLTV	EPQRVGEPLV	LDGSAKLLSV
g665-1	MSKTVRYLKD	YQTPAYRIEL	TELHFDIAEP	QTVVKSRLTV	EPQRAEPLV	LDGSAKLLSV
	70	80	90	100	110	120
m665-1.pep	KINGAAADYV	LEGETLTIAG	VPSEFTVEV	ETEILPAENK	SLMGLYASGG	NLFQCEPEG
g665-1	KINGAAADYV	LEGETLTIAD	VPSEFTVEV	ETEILPAENK	SLMGLYASGG	NLFQCEPEG
	130	140	150	160	170	180
m665-1.pep	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDGRHWV	KWEDPFSKPS
g665-1	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDGRHWV	KWEDPFAKPS
	190	200	210	220	230	240
m665-1.pep	YLFALVAGDL	AVTEDYFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGL
g665-1	YLFALVAGDL	AVTEDRFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGL
	250	260	270	280	290	300
m665-1.pep	YDLDFMVVAV	VGDFNMGAMEN	KGLNIFNTK	FVLADSRAT	DTFEGIESV	VGHEYFHNWT
g665-1	YDLDFMVVAV	VGDFNMGAMEN	KGLNIFNTK	FVLADSRAT	DTFEGIESV	VGHEYFHNWT

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV					
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQHQPEDAGPTAHPV					
	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
	RPASYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
g665-1	RPVSYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPDMDKQPMPIPVK					
g665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPPTPDMDKQPMPIPVK					
	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
	VGLLNRNGEAVAFDYQGKRATEAVLLLTAEQTFLLLEGVTEAVVPSLLRGFSAPVHLNYP					
g665-1	VGLLNRNGEAVAFDYQGKRATEAVLLMTAEQAFPLEGVTEAVVPSLLRGFSAPVHLNYP					
	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
	YSDDDL LLLLAHDSDAFTRWEAAQTL YRRAVANLATLS DGVLPKHEKLLAAVEKVISD					
g665-1	YSDDDL LLLLAHDSDAFTCWEAAQTL YRRAVANLAALSDGIGLPKHEKLLAAVEKVISD					
	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
	DLLDNAFAKALLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNROAAK					
g665-1	DLLDNAFAKALLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDROAAK					
	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
	QENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
g665-1	QENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQHPKFSLENPNKA					
g665-1	NESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQHPKFSLENPNKA					
	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
	RSLIGSFSRNVPFHAEADGSGYRFIADKVI EIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
g665-1	RSLIGSFSRNVPFHAEADGSGYRFIADKVI EIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	790	800	810	820	830	840
m665-1.pep	850	860				
	VKQALQIRIRAQEGLSKDVGEIVGKILD					
g665-1	VKQELQCIRIRAQEGLSKDVGEIVGKILGX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTTAC ATTTTGATAT TAACGAACCG CAAACCATTG
101  TGAAGTCGCG TTTGACGGTC GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151  TTGGACGGTT CGGCGAAACT CTGTCCGTC AAAATCAACG GCGTGGCGGC
201  GGATTATGTG TTGAAGGCG AGACGCTGAC GATTGCGGAC GTGCCGTCCG
251  AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAACAAA
301  TCGCTGATGG GGCTGTATGC GTCCGCCGGT AACCTGTTA CCCAGTGCGA
351  GCCGGAGGGC TTCCGCAAAA TCACGTCTA TATCGACCGT CCGGATGTCA
401  TGTCCAAGTT CACGACCACC ATCGTCGGG ACAAAAACG CTATCCCGTT
451  TTGCTCTCCA ACGCAACAA AATCGACGGC GCGAGTATT CAGACGGCGC

```

```

501 CCAATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGGTCGC GGGCGATTTC GCGGTCACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAAGGTCGGC TTTGCCGTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
701 AAAACGGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGGCGATT TCAATATGGG TGCATGGAA AACAAGGTTT TGAACATCTT
801 TAAACCAAG TTCGTCTTGC CCGACAGCCG TACCGCCACC GATACCGATT
851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGC AACCGCG TGACCTGCCG CGACTGGTTC CAGCTTTTCG TGAAGGAAGG
951 GTTGACCGTG TTCGCGGACC AAGAAATTTT CGGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG TATCGAAAAC ATCCGCTGCG TCGCCAGCA CCAATTCCCC
1051 GAA GACGAG GTCCGACCGC ACATCCGGTG CGCCCCGCCC GATATGAGGA
1101 GAT GAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGG CCGGAAAGTG
1151 TGC GGAATG TGCACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCTGTACCT GCGACGATTT
1251 CCGCGCGCGC ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTCGCCT
1301 TGTGGTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
1351 AAAAAACATG TGTTTCGAGT AACCATCAAA CAAACCGTGC CGCCACGCC
1401 CGATATGCGG GACAAACAGC CGATGATGAT TCCCGTCAAA ATCGGGCTGC
1451 TGA ACTCAA CGGCGAAGCG GTGGCATTTC ATTATCAGGG CAAACGCGCG
1501 ACCGAAGCCG TGTTGCTGCT GACCGAAGCC GAACAGACCT TCCAGTTCGA
1551 AAGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCACTT GAACTATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
1651 GCCCATGACA CGGACGCCCT CACGCGCTGG GAAGCCGCAC AAACGCTCTA
1701 CCGCGCGTGC GTCCCGCCA ACCTTGCCGC GCTTTCAGAC GCGCTCGAGT
1751 TGC CGAAACA CGAAAACTG CTGCGCGCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCTTT CAAAGCCCTG CTTTGGGTG TGCCGTCTGA
1851 AGCCGAGCTG TGGGACGGCG CGGAAAACAT CGACCCGCTG CGTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATATACTTG CCGTCCGCTT TCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGCGCGAAG CAGGAAAACC AAAGCTACGA
2001 GTACGACCCC GAAGCCGCGG GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAT CCCGCGCACA TCGAAAACCG TGCCGAGAAA
2101 TACGCGGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGCTGA TGGACAAATA TTTCCGCCCTC
2251 GTCGGCTCAA GCCGCGCAG CGACACCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAGTTCAGCC TCGAAAATCC CAACAAAGCC CGCTCGCTCA
2351 TCGGCAAGCT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2401 GGCTACCCTG TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTTAACCC
2451 GCAGGTGCGC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG CATTGCAGCG CATTGCGGCG
2551 CAGGAAGATG TGTCGAAAGA CGTGGCGGAA ATCGTCGGCA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPILV
51 LDGSAKLLSV KINGVAADYV LEGETLTIAD VPSERFTEV ETEILPAENK
101 SLMGLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEYS DGRHWV KWEDPFAKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYLDIFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTDFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRQHOF
351 EDAGPTAHVP RPARYEEMNN FYTMTVYK EGVVVMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAQGRL
451 KNNVFELTIK QTVPTPDMA DKQPMMPVK IGLLNCNGEA VAFDYQKRA
501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLAALSD GVLPKHEKL LAAVEKVISD
601 DLLDNAFKAL LLGVPSEAE LWDGAENIDPL RYHQAREALL DILAVRFLPK
651 WHELNROAAK QENQSYEYSP EAAGWRTL RNVCRAFLRAD PAHIETVAEK
701 YAEMAQNMT H EWGILSAVNG NESDTRNRL ALQFADKFSDD ALVMDKYFAL
751 VGSRRSDTL QVQVTAHQH KFSLENPNKA RSLIGSFERN VPHFAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVGE IVGKILD*

```

a665-1/m665-1 97.2% identity in 867 aa overlap

```

          10      20      30      40      50      60
a665-1.pep MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPILV LDGSAKLLSV
          |||
m665-1      MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPILV LDGSAKLLSV
          10      20      30      40      50      60

          70      80      90     100     110     120

```


	790	800	810	820	830	840
	850	860				
a665-1.pep	VKQALQRI	RAQEGLSKDV	GEIVGKILD	X		
m665-1	VKQALQRI	RAQEGLSKDV	GEIVGKILD	X		
	850	860				

g666.seq

1	ATGCTTTGTA	TGAATTATCA	ATCAAACCTCA	GGCGAAGGAG	TGCTTGTAGC
51	TAAAACATAT	TTATTGACTG	CATTGATAAT	GTCTATGGTA	ATCTCCGGAT
101	GTCAGTCAT	CCATGCCAAT	CAAGGTAAAG	TTAATACTAA	TTCTGCTGTC
151	ATCGCAGGTG	CAGACGCTCA	CACGCCTGAA	CATGTAAACGG	GACTGACCCA
201	ACAAAAGCAG	GTGATTGCCA	GTGATTTTAT	AGTAGCGCTCA	GCCAACTCCAT
251	TAGCAACACA	AGCTGGCTAT	GATATCTTAA	AGCAAGGCGG	TAGCGCTGCA
301	GATGCGATGG	TGGCGGTGCA	GACGACACTA	AGCTTGGTAG	AGCCACAGTC
351	GTCAGGCTTG	GGCGGTGGTG	CATTTGTGTT	GTATTGGGAC	AATACGCCCA
401	AAACATTGAC	CACATTTGAT	GGGCGTGAGA	CGGCACCGAT	GCGTGCGACG
451	CCAGAATTAT	TTTTGGATAA	AGATGGTTAA	CCATTGAAAT	TTATGGAAGC
501	GGTGGTCGCT	CGGTAGGTAC	GCCTGCTATC	CCTAAACTGA	

g666.pap

1	MLCMNYQSNS	GEGVLVAKTY	<u>LLTALIMSMV</u>	<u>ISGCQVIHAN</u>	QGKVNNTSAV
51	IAGADAHTPE	HVTGLTEQKQ	VIASDFIVAS	ANPLATQAGY	DILKQGSAA
101	DAMVAVQTTL	SLVEPQSSGL	GGGAFVLYWD	NTAKTLTTFD	GRETAPMRAT
151	PFLFDKDGX	PLKFMEAVVA	RXVRLLSLN*		

```
m666.seq
1 ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGC GAAGGAG TGCTTGTGGC
51 TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTC AAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCCA
201 ACAAAGCAGG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTGTGTT GTATTGGGAT AATACGCCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGGCAGC
451 CCGGAATTAT TTTTGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA
```

m666.pap

1	MPCMNHQSNS	GEGVLVAKTY	<u>LLTALIMSMT</u>	<u>ISGCQVIHAN</u>	QGKVNTHSAV
51	ITGADAHTPE	HATGLTEQKG	VIASDFMVAS	ANPLATQAGY	DILKQGGSA
101	DAMVAVQTTL	SLVEPQSSGL	GGGAFVLYWD	NTAKTLTTFD	GRETAPMRAT
151	PELFLEKDKGQ	PLKFMFAVVV	VARVVRLLSL	N*	

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m666.pep	MPCMNHQSN	GEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE				
	:	: : : :				
g666	MLCMNYQSN	GEGVLVAKTYLLTALIMSMVISGCQVIHANQGKVNTNSAVIAGADAHTPE				
	10	20	30	40	50	60
	70	80	90	100	110	120
m666.pep	HATGLTEQKQVIASDFMVASANPLATOAGYDILKQGGSAADAMVAVOTTL	SIVEPSSSGL				

```
a666.seq
1 ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTTGGC
51 TAAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CAGCCTGAA CATGAACAAG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGTTAG AGCCACAGTC
351 GTCAGGCTTG GCGGTTGGTG CATTTGTGTT GTATTGGGAT AATACGCCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCAAT GCGTGCAGCG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CATTGGAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA
```

a666.pap

1	MPCMNHQSNS	GEGVLVAKTY	<u>LLTALIMSMT</u>	ISGCQVIHAN	QGKVNTHSAV
51	ITGADAHTPE	HATGLTEQKQ	VIASDFMVAS	ANPLATQAGY	DILKQGSAA
101	DAMVAQVTTL	SLVEPQSSGL	GGGAFVLYWD	NTAKTLTTFD	GRETAPMRAT
151	PELFLDKDGO	PLKFMEAVVV	VARVRRLSI	N*	

		10	20	30	40	50	60
m666.pep		MPCMNHQSNSEGVLVAKTYLLTALIMSMTISGCQVIHANQGVNTHSAVITGADAHTPE					
a666		MPCMNHQSNSEGVLVAKTYLLTALIMSMTISGCQVIHANQGVNTHSAVITGADAHTPE					
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGSAADAMVAVQTTLSLVEPQSSGL					
a666		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGSAADAMVAVQTTLSLVEPQSSGL					
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLYWDNTAKTLTTFDGREAPMRATPELFLDKDGQPLKFMEAVVVVARVWRLLSL					
a666		GGGAFVLYWDNTAKTLTTFDGREAPMRATPELFLDKDGQPLKFMEAVVVVARVWRLLSL					
		130	140	150	160	170	180
m666.pep	NX						
a666	NX						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
1  atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51  tttccAtttg gtattcgctc gcgtcgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggttttcgc aatAAttgcg
151 GAtttccttc agcgtgcccg cgtgGAacgc ttcccacact ttgctgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTCgcCat atcgtccagC
251 GGCACATTcg ccctcggtG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCGCGC GGC GTTGTATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCGGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATAACG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651 GCTGCGCGAA CAGCACCAC TCGTCATCCG GCAGGGAAGA CGGCAAGTCA
701 TACAACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTA TTCATGGCag tACCTTGCAT tcaAAAACAG ActTGC GCCT
801 ATTgTgtcaT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
1  MRFVFLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVARIPIAR GVDVAVYQAV MQYQVETAA
151 VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMLVLPP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHHFVIRQGR RQVIQRTDTL HIGYGFNIES
251 QNRHGSTLH SKTDLRLCH *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
1  ATGCGGCTTT TCCCCGGCTT GTGCGGACAG GTAATTCCGC ATCCGTTTGA
51  TTTCCATTTT GTATTCTGTC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GGC GTTGTATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCGGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TGCATATGAC CACTTCTTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCAC TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
1  MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFALIA
51  DFLQPARMEC LPNLAHVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVAHIPIAR GVDVAVYQAV MQYQVETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHL
201 MKMMLHKIAA RLSTAFVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

              10      20      30      40      50      60
m667.pep  MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFALIIADFLQPARMEC
           ||:  | |: : | ||: |||: : |||||: ||| : : ||||| ||| ||: |
```

1071

```

g667      MRFVFCLGGEIVSDPCDFHLVFRVESAADQTETQIHQIRIHGIGFAIIADFLQRRARVER
           10      20      30      40      50      60
           70      80      90      100     110     120
m667.pep  LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVALVITADVVPLEIAAAVE
           |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
g667      FPHFAAVHTQLARKAAQFRHIVQRHVRPRLVKREQIHQIAVALVITADVVPLEIAAAVE
           70      80      90      100     110     120
           130     140     150     160     170     180
m667.pep  IAVAHIPIARGVDAVYQGAVMVGQIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD
           |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
g667      IAVARIPIARGVDAVYQGAVMVGQVETAAPADQLRRMFFNQFEKLGNDHFFAIVHLAD
           130     140     150     160     170     180
           190     200     210     220
m667.pep  GADMYFILPPTHAARNRHNLMKMLHKIAARLSTAFVLGNQHHL
           |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
g667      GADMNLVLPPAHTAGNRHNLMEVVLHKIAAGLCAAFLLREQHHFVIRQRRQVIQRTDTL
           190     200     210     220     230     240
g667      HIGYGFNIESQNRIHGSTLHSKTDLRLLLCHX
           250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2181>:

```

a667.seq
1  ATGCGGTTTG TCTTCTGTTT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51  TTTCCATTTC GTATTCGTCT GCGTCGAATC TGCCGCTGAC CAGACAGAAA
101 CGCAGATACA TCAGATAGGT ATTTACCGCA TCGGTTTCGC AATAATTGCG
151 GATTTCCCTC AGCCTGCCCG CGTGGAACGC CTCCACACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAAC
251 GGCACATTCG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 ATGACGTTGG TGGTAGCGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GCGGTTGATG
401 CCGTGTAGCA GCGAACGTA ATGCAGAAC GGCAGGTCGA AACCGCCGCC
451 GTTCCAACTG ACCAGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAATT
501 TGGCGATAAC CACTTCCTCG CCGTCATCCA TCTCGCGGAT TGTACCGACA
551 TGGACTTTAT CTGCCCCCA ACGCATGCAG CACGAAATCG CCACAATCTG
601 ATGAAGATGA TGCTGCATAA AATCCCCACC CGTCTGAGCA CGGCGTTTTT
651 GCTGGGCAAA CAGCACCCTC TCATCGTCGG GCAGCGAGGA CGGCAAGTCA
701 TACAGCGTAC GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTG GTCATGACAG CACCTGTAT TAAAA.CAG ACTTGCGCCT
801 ATTGTGTCAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2182; ORF 667.a>:

```

a667.pep
1  MRFVFCLGGE IVSDPLDFHF VFVCVESAAD QTETQIHQIG IYRIGFAIIA
51  DFLQPARVER LPHLAAVHTQ LARKTAQFRH IVQRHVRPRL VKREQIHQIA
101 MTLVVAADV VPLEIAAAVE IAVAHIPIAR GVDV*QRTV MQRQVETAA
151 VPTDQLRRMF FNQLEKFGDN HFLAVIHLAD CTDMDFILPP THAARNRHNL
201 MKMMLHKIPT RLSTAFLLGK QHHEFIVQRG RQVIQRTDTL HIGYGFNIES
251 QNRGHDSTLY LKXDLRLLLCH *

```

m667/a667 79.0% identity in 224 aa overlap

```

           10      20      30      40      50      60
m667.pep  MRLFPGLCGQVIPHPFDHFVFRVRIQPAADQTETQVHQISVCRVGFIAIDFLQPARMEC
           |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
a667      MRFVFCLGGEIVSDPLDFHFVFVCVESAADQTETQIHQIGIYRIGFAIIADFLQPARVER
           10      20      30      40      50      60
           70      80      90      100     110     120
m667.pep  LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVALVITADVVPLEIAAAVE
           |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
a667      LPHLAAVHTQLARKTAQFRHIVQRHVRPRLVKREQIHQIAMTLVVAADVVPLEIAAAVE

```

	70	80	90	100	110	120
m667.pap	130	140	150	160	170	180
	IAVAHIPIARGVD	AVYQGAVM	QYQIETAA	VPTDQLRR	MFNFQEFK	FSNDHFLAVIHLAD
a667	IAVAHIPIARGVD	AVXQRTVM	QNRQVETA	AVPTDQLRR	MFNQLEKFG	DNHFLAVIHLAD
	130	140	150	160	170	180
m667.pap	190	200	210	220		
	GADMYFILP	PTHAARNR	NHLMKML	LHKIAARL	STAFVLGN	QHHL
a667	CTDMDFILP	PTHAARNR	NHLMKML	LHKIPTRL	STAFILGK	QHHFIVGQRGRQVIQRTDTL
	190	200	210	220	230	240
a667	HIGYGFNIES	QNRGHD	STLYLKX	DLRL	LCHX	
	250	260	270			

```
g669.seq
1  ATGCGCCGCA TCGTTAAAAA ACACGAGCCC GTAAACGCGC CACATATCGT
51  TTTGGA AATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAACGTC CCATCATCAT GACCGCAGCC TTCGCGGCGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A
```

g669.pep
1 MRRIVKKHQF VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLLRQHG
51 EGMGDFDKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQAL SRPAVEGYNA
101 DIKRIL*

```
m669.seq
1  ATGCGCCGCA TCATTAAAA ACACCAGCCC ATAAACGCGC CACATATCGT
51  TTTGGA AATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAACGTTCC CCATCATCAT GACACGAGCC TTCGCGGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACC AAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACGTGA A
```

```
m669.pap
  1  MRRIIKKHQP INAPHIVLEI RIMKLHRAFV FLGRKRPHHH DSSLRRQHG
 51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQAL SRPAVFGYNA
101  DIKRIL*
```

	10	20	30	40	50	60
m669.pep	MRRRIKKHQPINAPHIVLEIRIMKLHRAVFVFLGRKRPHHHDDSSLRROHGIEGMGDFDKQI					
	: : : : : : : :					
g669	MRRIVKHKQPVNAPHIVLEIRIMKLHRAVFVFLGRKRPHHHDRSLRROHGIEGMGDFDKQI					
	10	20	30	40	50	60
	70	80	90	100		


```

m669.pép    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1   ATGCGCCGCA TCATTAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTTCG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pép
1   MRRIKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRL*

```

m669/a669 98.1% identity in 106 aa overlap

```

m669.pép    10      20      30      40      50      60
             MRRIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHHHDSLSLRQHGI EGMGFDFKQI
             |||||:|||||
a669        10      20      30      40      50      60
             MRRIKKHQPVNAPHIVLEIRIMKLHRAFVFLGRKRPHHHDSLSLRQHGI EGMGFDFKQI

m669.pép    70      80      90      100
             FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
a669        70      80      90      100
             FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1   ATGACTTGTT GCAGGAACGT CTTGGCGCGT TCGTGTTCG GGTGGTGAA
51  AAACGCTTCC GCGGTTTCGT CTTCAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CCGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TGCTGCTGG
301 CCGCCGAAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pép
1   MTCCRNLAR SCFGLVKNAS GVSSSRICPL STKITSATS RANPISWVTH
51  IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNTVRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1   ATGACCTGTT GCAGGAACGT CTTGGCGCGT TCGTGTTCG GGTGGTGAAA
51  AAACGCTTCC GCGGTTTCGT CTTCGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CCGTTCGTCA AACAAACATTA

```

1074

```

2 51 CCGCGCGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
3 01 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
3 51 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
4 01 CCTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
4 51 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151 G*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              |||||
g670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep      FITFNTSPTISGSSAEVGSSNNITRGSIAK PRAIATRCWPPESWEGKASFLCASPTRSK
              |||||
g670           FITFNTSPTISGSSAEVGSSNSITRGSIASPRAIATRCWPPESWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep      SSIAFFSACS AFCPLTFIGARVMSNTVRCGX
              |||||
g670           SSIAFFSACS AFCPLTFIGARVMSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1 ATGACCTGTT GCAGGAACGT CTTGGCGCGT TCGTGTTTCG GGTGCGTAAA
 51 AAACGCTTCC GGCGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTTACGCAC
151 ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTCGTCA AACAACTTA
251 CCGCGCGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGTTCCATCG CTTTTTCTC TGCCTGTTCC GCATTTTGAC
401 CTTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151 G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              |||||
a670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```

1075

	70	80	90	100	110	120
m670.p ep	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPESWEGKASFLCASPTRSK					
a670	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPESWEGKASFLCASPTRSK					
	70	80	90	100	110	120
	130	140	150			
m670.p ep	SSIAFFSACS AFCPLTTFIGARVMFSNTVRCGX					
a670	SSIAFFSACS AFXPLTTFIGARVMFSNTVRCGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

g671.s eq

1	ATGATCAGCA	GGGTAACAAT	CAAAACGCCT	TTCAATGCAC	CGAATACACC
51	GCCCAAAATG	CGGTTGGCAA	AGCCAGACC	GACCGCCGAA	ACTGCGCCGG
1 01	TCAGCAGCGA	ACGAGGCATT	TTCTGGATCA	GACAGGCAAT	GACGAACAGG
1 51	GAAATGAATG	ACAGagccaa	TGCAAACAgg	cggggTTGGA	ACGaggCAAA
2 01	GGCGAGGTcg	gcgaaggGTG	CGGCaaAGAG	TTTggcaaAA	AAGAaggAAA
2 51	ccaccCATGC	cACCATCgaa	ccTGCTCCG	CAATCAGCC	GCGCATCGTG
3 01	GAAATGACGA	TGCAGGCGGC	GATGACGGcg	gAGGCGAGGA	GGTCGGCAAT
3 51	GGGGAGGCTA	TTCATTTCGTT	ACCTGGCCGG	CGATGCCGTG	CACGCGCAGT
4 01	TTGTTCAAAT	CGCGTTCGGC	ATCCCTTGCG	TTTTTATAGT	TGCTTGA

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

g671.p ep

1	MISRVTIKTP	FNAPNTPPKM	RLAKPRPTAE	TAPVSSERSI	FWIRQAMTNR
51	EMNDRANANR	RGWNEAKARS	AKGAAKSLAK	KKETTHATIE	PASAITPRIV
1 01	EMTMQAAMTA	EARRSAMGRL	FIRYLAGDAV	HAQFVQIAFG	IPCVFIVA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

m671.s eq

1	ATGACCAGCA	GGGTAACAAT	CAAAACGCCT	TTCAATGCAC	CGAATACGCC
51	GCCCAAAATG	CGGTTGGCAA	AGCCCAAACC	GACCGCCGAA	ACTGCGCTGG
1 01	TCAGCAGCGA	ACGAGGCATT	TTCTGGATCA	GACAGGCAAT	GACGAACAGG
1 51	GAAATGAACG	ACAGAGCCAA	TGCAAACAGG	CGGGGTTGGA	ACGAGGCAAA
2 01	GGCGAGGTG	GCGAAGGAGG	CGGCAAAGAG	TTTGGCGAAA	AAGAAGGAAA
2 51	CCACCCATGC	CGCCATTGAG	CCTGCCTCCG	CAATCAGCC	GCGCATCGCG
3 01	GATAGCAGCA	TGCAGGCGGC	GATGACGGCG	GAGACGAGGA	GGTCGGCAAT
3 51	GGGGAGGCTA	TTCATTTCGTT	ACCTGACCGG	CGATACCGTG	TACGCGCAAT
4 01	TTGTTCAAAT	CGCGTTCGGC	ATCCCTTGCG	TTTTTATAGT	TGCTTGA

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

m671.p ep

1	MTSRVTIKTP	FNAPNTPPKM	RLAKPKPTAE	TALVSSERSI	FWIRQAMTNR
51	EMNDRANANR	RGWNEAKARS	AKEAAKSLAK	KKETTHAAIE	PASAITPRIA
1 01	DSTMQAAMTA	ETRRSAMGRL	FIRYLTGDTV	YAQFVQIAFG	IPCVFIVA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

	10	20	30	40	50	60
m671.p ep	MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
g671	MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.p ep	RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL					

1076

```

|||||
g671      RGWNEAKARSAKGAAKSLAKKKTTHATIEPASAITPRIVEMTMOAAMTAEARRSAMGRL
              70      80      90      100      110      120

              130      140      149
m671.pep   FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
              |||||:|||||:|||||:|||||
g671      FIRYLAGDAVHAQFVQIAFGIPCVFIVAX
              130      140

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2199>:

```

a671.seq
1   ATGACCAGCA GGGTAATAAT CAAAATGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTGGCAA AGCCCAAACC GACCGCCGAA ACTGCCCGCG
101 TCAGCAGCGA GCGGAGTATT TTCTGGATCA GACAGGCAAT GACGAATAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTGGA ACGATGCAAA
201 GCGGATGTCG GCGAAGGGTG CCGCAAAGAG TTTGGCGAAA AAAAAGGCAA
251 CCACCCATGC CGCCATTGAG CCAGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGATGGCG GAGACGAGGA GGTGCGCAAC
351 GGGGAGGTTA TTCATTGCTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2200; ORF 671.a>:

```

a671.pep
1   MTSRVIKMP FNAPNTPPKM RLAKPKPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNAKAMS AKGAAKSLAK KKATTHAAIE PASAITPRIA
101 DSTMQAAMMA ETRRSATGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

m671/a671 93.9% identity in 148 aa overlap

```

              10      20      30      40      50      60
m671.pep     MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDANANR
              ||||| ||||| ||||| ||||| ||||| |||||
a671         MTSRVIKMPFNAPNTPPKMRLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDANANR
              10      20      30      40      50      60

              70      80      90      100      110      120
m671.pep     RGWNEAKARSAKEAAKSLAKKKTTHAAIEPASAITPRIADSTMQAAMTAEARRSAMGRL
              ||||| ||||| ||||| ||||| ||||| |||||
a671         RGWNAKAMSAKGAAKSLAKKATTHAAIEPASAITPRIADSTMQAAMMAETRRSATGRL
              70      80      90      100      110      120

              130      140      149
m671.pep     FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
              ||||| ||||| ||||| ||||| ||||| |||||
a671         FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
              130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2201>:

```

g672.seq
1   ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCCCG GCGCAGACGC ATTGGGACTG GTTTTACC
101 CCCAAAGCCC CCGCGCTATC GACATCATT AAGCACAAA AATCGCCGCC
151 GCACTGCCGC CGTTTGTCTAG CGTTGTCTGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAT GCATTCTGCC GGCAGTTCGA CCGCCCCTAT
301 ATTAAAGCCA TTCGTGTCTA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC AACGCTCAGG CACTGCTGTT CGATGCCTAT CACCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGact GGacgctgtt ggcggAATAT
451 TCGGGCAAGC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAAGC GGTGACGTA TCCGGCGGCG
551 TGAAGCGTC TAAAGGCAAA AAAGACCCG CCAAAGTCGC CGCCTTTATC
601 GCAACCGCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```

g672.pep
  1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATRF NAQALLFDAY HPSEYGGTGH RFDWTLAEY
151 SGKPWVLGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDKPAKVAEFI
201 ATANRLSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```

m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCC GCGCCAAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTGTC CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGCGCA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GCGGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAATC GGTTCGATGA TCCGCGGGTG
551 TGAAGCGTC TAAAGGCAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACCGCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```

m672.pep
  1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQGSSRAV DIARAKKITA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATRF DAQALLFDAY HPSEYGGTGN RFDWTLAEY
151 SGKPWVLGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDAKVAEFI
201 ATANRLSR*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

```

          10      20      30      40      50      60
m672.pep  MRKIRTKICGITTPEDAAAAAAGADAVGLVFFQGSSRAVDIARAKKITAALPPFVSVVA
          |||||
g672      MRKIRTKICGITTPEDALYAAHAGADALGLVFYQSPRAIDIKAQKIAALPPFVSVVA
          10      20      30      40      50      60

          70      80      90      100     110     120
m672.pep  LFNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATRF
          |||||
g672      LFNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFDRPYIKAIRVQTASDIRNAATRF
          70      80      90      100     110     120

          130     140     150     160     170     180
m672.pep  DAQALLFDAYHPSEYGGTGNRFDWTLAEYSGKPWVLGGGLTPENVGEAVRITGAESVDV
          :|||
g672      NAQALLFDAYHPSEYGGTGHFRFDWTLAEYSGKPWVLGGGLTPENVGEAVRITGAESVDV
          130     140     150     160     170     180

          190     200     209
m672.pep  SGGVEASKGKKDAKVAEFIATANRLSRX
          |||||
g672      SGGVEASKGKKDKPAKVAEFIATANRLSRX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

1078

```

1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51 ACTGTATGCC GCCACGCCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
1 01 CCCAAAGCCC CCGCGTGTG GACATCATTA AAGCACAAAA AATCACCGCC
1 51 GCACTGCCGC CGTTGTGTC CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
2 01 GCAAAACATC CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
2 51 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
3 01 ATCAAGGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
3 51 CCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
4 01 AATACGGCGG CACCGGACAC CGCTTCGACT GGACGCTGTT GCGCGAATAT
4 51 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGA
5 01 CGAAGCCATC CGCATCACCG GAGCGGAAGC GGTGATGTA TCCGGCGGCG
5 51 TGGAAGCGTC TAAAGGCAAA AAAGACCCAG CCAAAGTGC CGCCTTTATC
6 01 GCAACGCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

```

a672.pep
1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAV DIIKAQKITA
51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAADRFP DAQALLFDAY HPSEYGGTGH RFDWTLAEY
151 SGKPWVLAGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAAFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

```

          10      20      30      40      50      60
m672.pep  MRKIRTKICGITTPEDAAGADAVGLVFFQSSRAVDIARAKKITAALPPFVSVVA
          |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
a672      MRKIRTKICGITTPEDALYAAHAGADALGLVFYQSPRAVDIIKAQKITAALPPFVSVVA
          10      20      30      40      50      60

          70      80      90      100     110     120
m672.pep  LFNESAQNIRILAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATRF
          |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
a672      LFNESAQNIRILAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAADRFP
          70      80      90      100     110     120

          130     140     150     160     170     180
m672.pep  DAQALLFDAYHPSEYGGTGNRFDWTLAEYSGKPWVLAGGLTPENVGEAVRITGAESVDV
          |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
a672      DAQALLFDAYHPSEYGGTGNRFDWTLAEYSGKPWVLAGGLTPENVDEAIRITGAEAVDV
          130     140     150     160     170     180

          190     200     209
m672.pep  SGGVEASKGKKDAKVAAFIATANRLSRX
          |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
a672      SGGVEASKGKKDPAKVAAFIATANRLSRX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

```

g673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CGGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGTGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGGATGCGC CTTACCGATG CCGACCGCGT
351 CGTGTGTTAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGATCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTGCG GCGGCGGAGG CGGTCAGTGC
501 GAAACACGGT TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCGAAAG CGTACCGATG TATCCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAACTCT TCCGCTATTT

```

```

6 51 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
7 01 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
7 51 AGCCAAAAGG CGATTTTGTAT CGGTAAAGGC GGGGAGCGTT TGAATAAAT
8 01 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGTAT AACAAAGTAT
8 51 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
9 01 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
1 01 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
1 51 AQVRAEFEDA AAEAVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
2 01 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEGDGLNR IYIAVLVDKE
2 51 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
3 01 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
1 01 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
1 51 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
2 01 GTTCGTGTTT GTCGATACGC CCGGCTTTCA AACCGACCAC CGCAACGCGC
2 51 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CCGCGTGGAT
3 01 GTGGTGGTTT TCGTCGTGGA GCGGATGCGC TTTACCGATG CCGACCGCGT
3 51 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
4 01 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTGTT
4 51 GCCCAAGTGC GCGCGGAATT TGAATTTGCG GCGGCGGAGG CCGTCAGCGC
5 01 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
5 51 TGCCCGAAAG CGTGCCGATG TATCCGAAG ATATGGTTAC GGACAAATCG
6 01 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAAATTGT TCCGCTATTT
6 51 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
7 01 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
7 51 AGCCAAAAGG CAATTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
8 01 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGTAT ACCAAAGTAT
8 51 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
9 01 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
1 01 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VVINKIDKDKA KDRYALEAFV
1 51 AQVRAEFEDA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
2 01 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
2 51 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
3 01 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

          10      20      30      40      50      60
m673.pep MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
          |||
g673      MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
          10      20      30      40      50      60

          70      80      90     100     110     120
m673.pep YDDTAQFVFVDTPGFQTDHNRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK
          |||

```

1080

```

g673      YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVEAMRLTDADRVVLK
           70      80      90      100     110     120

           130     140     150     160     170     180
m673.pep  QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELL
           130     140     150     160     170     180

           190     200     210     220     230     240
m673.pep  KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           190     200     210     220     230     240

           250     260     270     280     290     300
m673.pep  IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDNKVFLKVWVKVKS GWADDIR
           250     260     270     280     290     300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51  TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGCGC
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTTGTGTTT GTCGATACGC CCGGTTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGGCGTGGAT
301 GTGGTGTTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTGAA CAACTGCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGT
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAAGCG
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51  QTTRNRVTGI YTDDTAQFVF VDTPEGFQDH RNALNDRLNQ NVTEALGGVD
101 VVVVFVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFefa AAEAVSAKHG LRIANLLELI KPYPLESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGK GERLKKISTE ARLDMEKLF DT KVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

           10      20      30      40      50      60
m673.pep  MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a673      MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           10      20      30      40      50      60

```


	70	80	90	100	110	120
m673.pep	YTDDTAQFVFDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
a673	YTDDTAQFVFDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEDGLNR					
a673	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEDGLNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR					
a673	IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR					
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAGGCAGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TGCAGCGGAC TATATCCGAC AAATCCGCCC
201 GCTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCGACGA GCCCAAACGC CGTTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
  
```

1082

51 FFGTQTNAAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 1 01 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	::					
g674	YIQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq

1	ATGAAAACAG	CCCGCCGCCG	TTCCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCCGCGCC	CGAGATTGCT	AAAAACATCC
101	GCGAAATGCC	CGACTTTGCC	AAGGCAGACG	AAGAATTGTT	CAACAACTT
151	TTCTTCGGCA	CGCAAACCAA	TGCGGCAGAG	TACATCCGAC	AAATCCGCCC
201	CCTGCTCGAC	CGCGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTCC
251	TGCTGACCGC	CTGCCACGAG	CTGTCCGCCA	TGCCCCGAAAC	GCCCTACCCC
301	GTATCATCA	ACGAAGCCAT	CGAAGTAACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCGTCAACG	GCATCCTCGA	CAAACCTGCC	GCCCAAATCC
401	GTCCCGACGA	GCCCAAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMPDFA	KADEELFNKL
51	FFGTQTNAAE	YIRQIRPLLD	RDEKDLNPIE	RAVLLTACHE	LSAMPETPYP
101	VIINEAIEVT	KTFGGTDGHK	FVNGILDKLA	AQIRPDEPKR	R*

m674/a674 99.3% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

g675.seq

```
1 ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
1 01 GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcaccgtc
1 51 gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
2 01 CTCTTCGAA AAATTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
2 51 GCGAAACCTA CCATTTCGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
3 01 GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
3 51 CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
4 01 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
4 51 GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

1084

g675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
101 GRVALDYNIP IANAVLTEN DAQAIERIGE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGTC GAATGCGCCA ACCTCGTCAA CCGTCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV
101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFELVANESGAGIGRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130 140 150 159					
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIGEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCTGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
251 GCGAAACCTA CCATTTGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
351 CACGGAAAAC GACGACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV

```

1085

1 01 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
1 51 EEQFEDEE*

m675/a 675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCRTLQELGVADENITVATVPGALEIP					
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
a675	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
a675	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq
1 ATGCCGAGA TTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTg
51 ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGGC CTTCCGGCGT
151 GTTCAAAACC ACTTCGTGCG CTTCCGCGCG TTTAATCAGG CAACGCGCCA
201 ACGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGACG
251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
301 GGTCCGCGCG AAAAATACTT GGTCCGTGCG TTCGCGCAAT TCGGGATCGA
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTG
401 ATTTCCGCGA TACGGCGTTT GCCGTAAAGA TAGTCGCGT TTTGCTGCG
451 GTCGCGGTTG CTTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep
1 MPQILVRIFL IRYSEFIWETV RLCRRFRHSR SVDFDVFDRK DFNFLTAFFR
51 VQNHVAFAR FNQATRRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT
101 GRAEKYLVR FAQFGIDDDG SLQTFGOETD AAVDFAHATF AVKIVAVFAA
151 VAVACRPVDD LDDEGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq
1 ATGCCGAGA TTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTG
51 GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCCGGCGT
151 GTTCAAAACC ACTTCGTGCG CTTCCGCGCG TTTAATCAGA CAACGAGCCA
201 GCGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGATG
251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCCGAC
301 CGTCGCGCG AAAAATACTT GGTCCGTGCG TTCGCGCAAT TCGGGATCGA
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTG
401 ATTTCCGCGA TACGGCGTTT GCCGTAAAGA TAGTCGCGT TTTGCTGCG
451 GTCGCGGTTG CTTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep
1 MPQILVRIFL IRYSEFIWETA RLCRRFRHSR SVDFDVFDRK DFNFLTPFRR

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51 VQNHFAFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQSD
 1 01 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
 1 51 VAVACRPVDD LDDEGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

m677.pep	10	20	30	40	50	60
	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLT	PFRRVQNHFAFAR				
g677	10	20	30	40	50	60
	MPQILVRIFLIRYSFIWETVRLCRFRHRSVDFDVFDRKDFNFLT	AFRRVQNHFAFAR				
m677.pep	70	80	90	100	110	120
	FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQSDRRAEKHLVGRFAQFGIDDDG					
g677	70	80	90	100	110	120
	FNQATQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGDAEKYLVGRFAQFGIDDDG					
m677.pep	130	140	150	160	170	180
	SLQTFGQETDAAVDFAHTAFVAVFAAVACRPVDDLDDEGAFFVDQLIKLVFQCL					
g677	130	140	150	160	170	180
	SLQTFGQETDAAVDFAHTAFVAVFAAVACRPVDDLDDEGAFFVDQLIKLVFQCL					
m677.pep	190	199				
	PSGGRNVVFGFGTHIVCGX					
g677	190					
	PSGGRNVVFGFGTHIVCGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

a677.seq

1	ATGCCG	CAGATA	TTTGGT	GCGGAT	GATTTTC	CCTCATT	CCTTTATT	TG
51	GGAAAC	GGCGCG	CGTTTG	TGCGCC	GTTTCAG	ACGCGA	TCAGTC	GATT
101	TTGATG	TATT	CGACAG	AAAG	GATTTCA	ATTTCAC	CGCC	CTTCCG
151	GTTTAA	AAACC	ACTTCG	TCGC	CTTCAC	GCGCGC	TTTAAT	CAGACA
201	GCGGCG	GAAAT	CCAAGAA	ATT	TTGTTT	TGCG	CGGTAT	CGAT
251	CCGACG	ATT	TGACGG	TTTG	CTCGCG	CCCG	TCGCGC	GCA
301	GGTCG	GCGCG	AAAAACA	CTT	GGTCGG	TGCG	TTCGGC	CAAT
351	CGACG	ACGGC	GGCTT	CCAAA	CGCTTG	GTCA	GGAAAC	GGAT
401	ATTT	CGCGCA	TACGGC	GTTT	GCCGTA	AAAG	TAGTCG	CCGT
451	GTCG	CCGTTG	CCTGCC	GCCC	AGTTGA	CGAT	TTGGAC	GATT
501	CTTT	TATTAAC	CAGTTG	AATA	AGCTCG	TCTT	TCAATG	CCTG
551	GGCG	TAAATG	AGTTT	TGTTG	TTCGGT	ACTC	ATATTG	TGTG

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

a677.pep

1	MPQILVRIFL	IRYSFIWETA	RLCRFRHRS	SVDFDVFDRK	DFNFLT	PFRR
51	V*NHFVAFTR	FNQTSQRRN	PRNFVLRGID	FIDADDFDGL	LAPVAAQ	QTD
101	GRAEKHLVGR	FAQFGIDDDG	GFQTLGQETD	AAVDFAHTAF	AVKVVAV	FAA
151	VAVACRPVDD	LDDEGAFFIN	QLIKLVFQCL	PSGGRNVVFG	FGTHIVCG*	

m677/a677 93.4% identity in 198 aa overlap

m677.pep	10	20	30	40	50	60
	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLT	PFRRVQNHFAFAR				
a677	10	20	30	40	50	60
	MPQILVRIFLIRYSFIWETARLCRFRHRSVDFDVFDRKDFNFLT	PFRRVXNHFAFTR				
	70	80	90	100	110	120

1087

```

m677.pép      FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRAEKHLVGRFAQFGIDDDG
a677          FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGAEKHLVGRFAQFGINDDG
              70      80      90      100     110     120

m677.pép      SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDFFGAFFVDQLIKLVFQCL
a677          GFQTLGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDFFGAFFINQLIKLVFQCL
              130     140     150     160     170     180

m677.pép      PSGGRNVVFGFGTHIVCGX
a677          PSGGRNVVFGFGTHIVCGX
              190     199

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1   ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTccgCCG TCATCGCCGC
51  CTGCATCGTC ATTCCACGA TCGCGGCGGT GATTGCGGAA GCAGgttcGA
1 01 TGGTgGCATG ggtggTTTcc tTCTTTTttg ccAAACTCTt tGCCGCACcc
1 51 ttcgcccACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
2 01 tCTGTcATTc ATTTCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
2 51 TCCGTTcGCT GCTGACCgGC GCAGTTTCGG CGGTcGGTCT GGGCTTTGCC
3 01 AACCGcATTT TGGGCGGTGT ATTcGGTGCA TTGAAAGGCG TTTTGATTGT
3 51 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCC GATACCGAAG
4 01 AATGGCAACA GTCCTATACC GTACCGTTTT TCGTATCGCT TTCCGAAGCC
4 51 GTGTTAAACC atacggaCAA CGCaccgaa tCCctcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pép
1   MNSLPIADLL ASAVIAACIV ISTMrgVIAE AGSMVAWVVS FFFAKLFAAP
51  FADLAFASfQ PRLfALALSF ISLfvIACLI QKMLRSLLTG AVSAVGLGFA
1 01 NRILGGVfGA LKGVLIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
1 51 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1   ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCGC
51  CTGCATCGTG CTATCCGCGA TCGCGGCGGT GATTGCGGAG GCAGGCTCAA
1 01 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTTT TGCCGCCTCC
1 51 TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCgcCTGT TTGCATTGGC
2 01 TCTGTcGTTc ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
2 51 TCCGTTcGCT GCTGACCAGC GCAGTTTCGG CGGTcGGTTT GGGCTTTGCC
3 01 AACCGcATTT TGGGCGGCGT ATTcGGTGCA TTGAAAGGCG TTTTGATTGT
3 51 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCC GATACCGAAG
4 01 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
4 51 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pép
1   MNSLPIADLL VSAVIAACIV LSAMrgVIAE AGSMAWVVS FFFAKLFAAS
51  FADLAFASfQ PRLfALALSF ISLfvIACLI QKMLRSLTTS AVSAVGLGFA
1 01 NRILGGVfGA LKGVLIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
1 51 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1088

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
	: : : : : :					
g678	MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAWVVSFFFAKLFAAPFADLAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	: : : : : :					
g678	PRLFALALSFISLFVIACLIQKMLRSLTGAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	: : : : : : :					
g678	IMLASKTDLPDTEEWQSYTVPFFVSLSEAVLNHTDNAPESLDDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

```
a678.seq
1  ATGAATAACC TCCCCGTTGC CGACCTCCTC GTCTCCGCCA TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTTTCCTCG CCAAACCTTT TGCCGCACCC
151 TTCGCCGACA TCGCCTTTGC ATCGTCCAA CCCCAGCTGT TTGCATTGGC
201 TCTGTCGTC ATTCCCTAT TCGTCATTGC CTGTCTGATC CAGAAAATAC
251 TCCGCTCGCT GCTGACCGGG GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATTT TGGCGGCGT ATTCGGTGCA TTGAAAGGCA TTTTGATTAT
351 TACCCTGCTG GTCATGCTCG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGCGGAA ACTCCGAAG ACGATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

```
a678.pep
1  MNNLPVADLL VSAIIAACIV LSAMRGVIAE AGSMAAWVVA FFFAKLFAAP
51  FADIAFASFQ PRLFALALSF ISLFVIACLI QKILRSLTGA AVSAVGLGFA
101 NRILGGVFGA LKGILIITLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*
```

m678/a678 93.9% identity in 165 aa overlap

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
	: : : : : :					
a678	MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFAKLFAAPFADIAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	: : : : : :					
a678	PRLFALALSFISLFVIACLIQKILRSLTGAVSAVGLGFANRILGGVFGALKGILIITLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	: : : : : :					
a678	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2237>:

```
g680.seq
1  ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51  GCGGACGAGG ACGCGCAGGC TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCTGCTTTC TTGGGAACGG TCGCCGTGTA TCGCTGTGC GGACAGGTTG
```



```

151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAACC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTGT TTTAACTGA TGTTTTTCTG TTTCACATGG TCGAGCAGCC
551 GTCCGACGGT GGCACGACT ATTTTCGAGC CGGCACGCAG GTCGGCGGTT
601 TGTTTGTCCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAELV AEKSRVWRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMEFCFTW SSSRPTVATT ISQPARRSAV
201 CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
1 ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
51 GCGGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGCA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CCGCGCACCA GTTCGCGCGT TACGCGGTCTG ACGCTTTGTT TGGTTTTCGA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTTTTGGCG GGCGACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAG CATAAGGTCT GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTTCTG TTTCACGTGG TCGAGCAGCC
551 GTCCGACGGT GGCACGACG ATTTTCGAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTGTATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVFCAATS TVSGAFMKSC ASLRIGAELV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFECFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPNK TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

```

m680.pep      10      20      30      40      50      60
MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680          10      20      30      40      50      60
MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

m680.pep      70      80      90     100     110     120
TLCLVLQNTMTWFICKSTISRSSRLRFKXVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680          70      80      90     100     110     120
TLCLVLQKTIITWFICRSTISRSSRLRFWKVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

m680.pep     130     140     150     160     170     180
ASLRIGAELVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFECFTW

```

1090

```

|||||
g680      ASLRIGA EKVAEKSRVWRWRG SICMILRMSSINPISNMRSASSRTTISALFKLMFFCFTW
           130      140      150      160      170      180

           190      200      210      220
m680.pep  SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX
           |||||
g680      SSSRPTVATTISQPARRSAVCLSM LTPPKRTVCRSGRFLMX
           190      200      210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2241>:

```

a680.seq
1  ATGACGAAGG GCAGTTCGGC AATATCCAGC CCCC GCGCGG CGATATCGGT
51  GGCGACGAGG ACGCGCAGGT TGCCGCTCTT GAAGGCGTTG AGTGTTCGCA
101 GCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTGTG TGGTTTTGCA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTGCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGCTTGCGC GCGGACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAG CATAACGGTC GCTTCGTCCA AAACGACGAT
501 TTCGACTTGG TTCAAATGGA TGTTTTCTG TTTACGTGG TCGAGCAGCC
551 GTCCGACGGT GGCACGACG ATTTCCGAGC CGGCACGAG GTCGGCGGTC
601 TGTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2242; ORF 680.a>:

```

a680.pep
1  MTKGSSAISS PRAAISVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51  RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVSCAATS TVSGAFMKSC ASLRIGA EKVAEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPNK TVWRSGRFLM *

```

m680/a680 98.6% identity in 220 aa overlap

```

           10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
           |||||:|||||:|||||:|||||:|||||:|||||
a680      MTKGSSAISSPRAAISVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
           10      20      30      40      50      60

           70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSRLRF*MVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
           |||||:|||||:|||||:|||||:|||||:|||||
a680      TLCLVLQNTMTWFICKSTISRSSRLRF*MVSTAMMCCSTLALVVS CAATSTVSGAFMKSC
           70      80      90      100     110     120

           130     140     150     160     170     180
m680.pep  ASLRIGA EKVAEKSRVWRWRG SICMILRMSSIKPISSIRSASSKTTISTL FKWMFFCFTW
           |||||:|||||:|||||:|||||:|||||:|||||
a680      ASLRIGA EKVAEKSRVWRWRG SICMILRMSSIKPISSIRSASSKTTISTL FKWMFFCFTW
           130     140     150     160     170     180

           190     200     210     220
m680.pep  SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX
           |||||:|||||:|||||:|||||:|||||:|||||
a680      SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX
           190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2243>:

```

g681.seq
1  ATGACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTCAAGCGC GCCGGGTACG GTGGcgacgg

```

```

101 t gatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 T TGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTCGcgt cgaggttgGG GCGCATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 T TGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTGGT GGTCTGCGGT
451 GTATTCGTCG GTTTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTTTG
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCTG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTCGCGA
651 TTTTACCACG ATTCGCCCGT TGTCCGCAGA CGGCGCGGTT TGGTGGTAC
701 AATGTGCGCC GTTTCAGGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751 AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

g681.pep

```

1 MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51 LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGNLECA AVFGKLPRAA FGLGKQCGGF RVGFGDVGEA DDAEVVGVVG
151 VFVGFVAEE TPAAVVFKNG GFAVKEADGP VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTL GGGKLADFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
251 KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

m681.seq

```

1 ATGACGACGC CGATGGCAAT CAGTGCCTCA AACTTTTTCGG AAGAGGCAAA
51 GTTCATCAGC GCGATGGGGA TTTCAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTCGCGT CGAGGTTGGG GCGCATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTTGGCGATG CGGCGAGGCT GACGATGCTG AAGTTGTCCG GATCGTGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTTTG
551 GCGACGGTGT TGGTGGCGAT ACAGCGGTCTG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATTT
651 TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCGGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGAAA
751 CGCATTCCGG CTGTTTTTTT CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

m681.pep

```

1 MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51 LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGDGLEC AVFGKLPCAA FGLGEQCGGF RVGFGDVGEA DDAEVVRIIVG
151 VFVGLVAEE TPAAVVFKNG GFAVEEADGP VLFGDGVGGD TAVECRGKCL
201 CKCVHYGNTL GXKLTDFTTI RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

          10      20      30      40      50      60
m681.pep  MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
          |||||
g681      MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV
          10      20      30      40      50      60

```

```

a681.seq
1   ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCCAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCGGGGTACG GTGGCCACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GAGGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GGCATGGTG TTCAATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGCTGAAGG TCAGTCCCTT
301 AGGTTGCCAG TCGCGACGCG TTTGGAATGT CCGCTCTTCT GCCAATTCCT
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGCGGGTTTC AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCTGTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGCTCGTTTT
501 CAAAAACGGG GGCTTCGCGC TAGAGGAAGC GCACGGGCTG GTTTTGTGTT
551 GCGACGGTGT TGGTGCGCAT GCAGCGGTCT AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTGCGG GAATACGTT. GGGGGAAAC TTGCGGATTT
651 TACCACGATT CTTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTTCCG CTGTTTTTTC CGGAAGACGG TAA

```

```
a681.pep
1  ITPMAISAS  NFSEEAKFIS  AMGISSAPGT  VATVMFSSAT  FNSWRVRQOT
51  LSISLPISLV  KRAC TPMRR  CLPSRLGAMV  FIECPLVFVG  FGMPSEGSVL
101 RLPVGDGLEC  AVFCQFPRAA  FRLGEQCGGF  RVGFGDIGEA  DDAEVRVRVG
151 VFVGLVAAEE  TPAAVVFKN  GFAVEEADGL  VLFGDGVGGD  AAVECRGKCL
201 CKCVHCGNTX  GGKLAFTTI  LALSADGGGL  VVQCPAFAAL  RCFCIFGVWK
251 RIRAVFCGRR  *
```

	10	20	30	40	50	60
m681.pep	MTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPSISLV					
	:					
a681	ITTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPSISLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m681.pep	KRACTMPMRRLCP SRLGAMVFIGCPLVFGVSECR LKVSVLRLPVGDGLCAVFGKLPCAA					
a681	KRACTMPMRRLCP SRLGAMVFIECPLVFGGFGMPSEGSVLRLPVGDGLCAVFCQFPRAA					
	70	80	90	100	110	120

	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGFVDGEADDAEVVRIVGVFVGLVAAEETPAAVVFKNGGFAVEEADGP					
a681	FRLGEQCGGFRVGFVDIGEADDAEVVRVGVFVGLVAAEETPAAVVFKNGGFAVEEADGL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGXKLTDFTTIRALSADGGGLVVQCAPFAAL					
a681	VLFGDGVGGDAAVECRGKCLCKCVHCGNTXGGKLADFTTILALSADGGGLVVQCAPFAAL					
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIRAVFCGRRX					
a681	RCFCIFGVWKRIRAVFCGRRX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAT GCGTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTTC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWIQTAFCM AGFIREFTDR
101 PILTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTG
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTC AACTGACCGA
301 CCCATTTCGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDFTVWVS YGKWRKNWDIR YCLLHLIHL STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY... EMAMPSEP DWIQTAFCA YGFIREFTDR
101 PIITRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

1094

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
      |||:|||| ||: ||||| |||: || ||||| ||||| ||||| ||||| |||||
g682      MRDFAVWVVPYGERRKNWDIRYCLPHLIRLSPTLRKCGRILSGICEPFCLITPDLTMHYC
      10      20      30      40      50      60

      70      80      90      100     110
m682.pep  PILILIDY-----EMAMPSEPDWQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFR
      ||||| ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g682      PILILIDYICVNDKMPSEPDWQTAFCMAGFIRFPTDRPILTRQSGVVRISPRTGFR
      70      80      90      100     110

      120     130
m682.pep  YPTRSLPKSKKAYGX
      ||||| |||||
g682      YPTRSLPKSKKAYGX
      120     130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2253>:

```

a682.seq
1  ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 ATAT.....
251 .....TATA TTCGGTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCCGAC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2254; ORF 682.a>:

```

a682.pep
1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHL SSTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIEY..
101 PILTRPTGVV RISPTGFRY PTRSLPKSKK AYG*

```

m682/a682 80.6% identity in 129 aa overlap

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a682      MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
      10      20      30      40      50      60

      70      80      90      100     110     120
m682.pep  PILILIDYEMAMPSEPDWQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFRYPTRS
      ||||| ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a682      PILILIEY-----YIRFPTDRPILTRPTGVVRISPRTGFRYPTRS
      70      80      90      100

      130
m682.pep  LPKSKKAYGX
      ||||| |||||
a682      LPKSKKAYGX
      110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2255>

```

g683.seq
1  ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTACT
51  CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATTAATAAA
151 GACAGTGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTTACCAAT CTGAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AGTTATTGTA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 CTACACAGCC TCTTCCTCC GCCCGATGAG CATCTGTCC GGGACATTAA

```

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683>:

g683.pep

1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPSILS GTLTEKQYET VCGKKL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTATT
51 CCC TATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGT TACCAAT CTAACAACAG AACGTTTTCG CAACACCCCG GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGT TCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 CTAACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep..

1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPSILS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
g683	MIKETLMRPIFLSFVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPSILSGTLTEKQYETVCGKKLX					
g683	SSLRPSILSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTATT
51 CCC TATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
201 TGT TACCAAT CTAACAACAG AACGTTTTCG CNACACCCCG GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGT TCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep

1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFXDKKVVVN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL

101 SSLQLFDTKN TEISTQXYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
a683	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVTNLQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
a683	IFXDKKVVTNLQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMISLSGTLTEKQYETVCGKKLX					
a683	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

g684.seq

1	ATGCGCCTTT	TCCCCATCGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACCGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCATCAACAC
201	CGCACAAAAC	CATGTTTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAC	CTTTGTTCTT
301	GCCTCAGGCA	GCGGCAGTAC	CGACAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

g684.pep

1	MRLFPAAAL	TAAACGTVQS	TQYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGGLVYQT	DPYRINTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRTFVP
101	ASRSGSTDKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRN	FHIETEQQGD
151	GYAAMTAAL	QGLKQAAQOM	VE*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

m684.seq

1	ATGCGCCTTT	TCCCGATTGC	CGCCGCCCTG	TCGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTCTT
301	GCCTCAGGCA	GCGGCAGTAC	CGAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CGATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

m684.pep

1	MRLFPAAAL	SLAACGTVQS	TQYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGGLVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRTFVP
101	ASRSGSTEKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRN	FHIETEQQGD

151 GYAAMTAALE QGLKQAAQOM VE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

m684/g684 97.7% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
g684	MRLFPAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
g684	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
	70	80	90	100	110	120
	130	140	150	160	170	
m684.pep	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
g684	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

a684.seq

1	ATGCGCCTCT	TCCCGATTGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGCTCTGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTTGAGCA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTTCT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCAGATA			

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

a684.pep

1	MRLFPAAAL	TLAACGTVQS	TQYFVLPDSR	YIRPATQGG	TAVEVRLAEP
51	LKRGGGLVYQT	DPYRLNTAQN	HWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTKWT	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAALE	QGLKQAAQOM	VE*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

m684/a684 99.4% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
a684	MRLFPAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
a684	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
	70	80	90	100	110	120
	130	140	150	160	170	

1098

```

m684.pep      YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
               ||||||||||||||||||||||||||||||||||||||||||||
a684          YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
               130       140       150       160       170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2267>

```

g685.seq
1   TTGTTTGGCC GTATCGGGAA TTTGCGTTT TCGCGCGTGG TTTCTGCAGG
51  TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGcct GCGCCGTCCT GCCGGCCGCC
151 TGTTCGCCCG AACCTGCCGC CGAAAAAAct GTATccgCCG CATCCCAAGC
201 CGCAATCCACA CCTGTGCCCA CGGTGACCGT GCCGACCGCG CGGGGCGATG
251 CCGTTGTGCC GAAGAATCCC GAACgcgctcg ccgtgtAcga CtggCGCGCG
301 TtggaTACGC TGACCGAGCC GGGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTG GACTATTTCG AGCCTGCATT TGACAAGCGG GCAACGGTGG
401 GGACGCTGTT TGAGCCCGAT TGCGAATCCC TGCACCGCCA CAATCCGCAG
451 TTTGTCATTA CCGGCGGGCC GGGTGCAGAA GCGTATGAAC AGTTGGCGAA
501 AAACGCGACC ACCATAGATT TGACGGTGGG CAACGGCAAT ATCCGCACCA
551 GCGGCGAGAA GCAGATGGAG ACCCTGTCGC GGATTTCGG TAAGGAAGCG
601 CGCGTGCGCG AATTGAATGC GCAGATTGAC GCGCTGTTCG CCCAAAAGCG
651 CGAAGCCGCC AAAGGCAAAG GACGCGGGCT GGTGCTGTCT GTTACAGGCA
701 ACAAAGGTGTC CGCCTTCGGC ACGCAATCGC GGTGGCAAG TTGATACAC
751 GCGGACATCG GCCTGCCGCC CGTGGACGAA TCTTTACGCA ACGAAGGGCA
801 CCGGCGAGCC GTTTCCTTCG AATACATCAA AGAGAAAAAC CCCGGCTGGA
851 TTTTCATCAT CGACCGCACC GCCGCCATCG GGCAGGAAGG GCCGGCTGCC
901 GTGGAGTGTG TGGATAACGC GCTGGTATGC GGCACGAACG CTGGAAGCG
951 CAAGCAAATC ATCGTCATGC CTGCCGCGAA CTACATTGTC GCGGGCGGCG
1001 CCGGCGAGTT GATACAGGCG GCGGAACAGT TGAAGCGCGC GTTTGAAAAA
1051 GCAGAACCCG TTGCGGCGCA GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685>:

```

g685.pep
1   LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLPAA
51  CSPEFAAEK VSAASQAAS PVATLTVPPTA RGDVAVPKNP ERVAVYDWA
101 LDTLTPEPGV VSGATTAPVRV DYLPQAFDKA ATVGTLFEPD CESLHRHNPO
151 FVITCGPGAE AYEQLAKNAT TIDLTVDNNG IRTSGEKOME TLSRIFGKEA
201 RVAELNAQID ALFAQKREAA KGKGRGLVLS VTGNKVSAFG TQSRSLASWIH
251 GDIGLPPVDE SLRNEGHGQP VSFYIKEKN PGWIFIIDRT AATGQEGPAA
301 VEVLDNALVC GTNAWKRRQI IVMPAANYIV AGGARQLIQ AELKAAFEK
351 AEPVAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2269>:

```

n685.seq
1   TTGTTTGGCC GTATCGGGAA TTTGCGTTT TCGCGCGTGG TTTCTGCAGG
51  TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTCGCCCG AACCTGCCGC CGAAAAAAct GTATCCGCGC CATCCGCATC
201 TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG TCGCGGTGGA
351 TTATTGTCAG CCTGCATTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCATTACC
451 GCGGGGCGCG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGCAATAT CCGCACCAGC GCGGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCCGCCAA
651 AGGCAAGGA CGCGGGCTGG TGCTGTCCGT TACGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG
851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGTACGCGG CACGAACGCT TGAAGCGCA AGCAAATCAT
951 CGTCATGCTT CCGCGAAGT ACATTGTCGC GGGCGGCGCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGCGGCGT TTAAGAGGC AGAACCCGTT
1051 GCGGCGGGGA AAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>:

n685.pep

```

1  LFC RIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSP EPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLO PAFDKAATVG TLFEPTYEAL HRYNPQLVIT
151 GGP GAEAYEQ LAKNATTIDL TVDNGNIRTS GEKOMETLAR IFGKEARAAE
201 LKA QIDALFA QTREAAKKGK RGLVLSVTGN KVSAGTQSR LASWIHGDIG
251 LPP VDESRLN EGHGQPVSE YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNA LVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQ KAAFKKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

          10      20      30      40      50      60
m685.pep  LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPPEAAEKT
          ||||| : |||||
g685      LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPACSPPEAAEKT
          10      20      30      40      50      60

          70      80      90      100     110
m685.pep  VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
          |||| : | |||||
g685      VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTEPGVNVGATTAPVRV
          70      80      90      100     110     120

          120     130     140     150     160     170
m685.pep  DYLPQAFDKAATVGTLEFPDYEALHRYNPQLVITGGPGAAYEQLAKNATTIDLTVDNGN
          ||||| : |||||
g685      DYLPQAFDKAATVGTLEFPDCESLHRHNPQFVITGGPGAAYEQLAKNATTIDLTVDNGN
          130     140     150     160     170     180

          180     190     200     210     220     230
m685.pep  IRTSGEOMETLARIFGKEARAAELKAQIDALFAQTREAAKKGKRGVLVSVTGNKVSAGF
          ||||| : |||||
g685      IRTSGEOMETLSRIFGKEARVAELNAQIDALFAQKREAAKKGKRGVLVSVTGNKVSAGF
          190     200     210     220     230     240

          240     250     260     270     280     290
m685.pep  TQSRLASWIHGDIGLPPVDESRLNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAA
          |||||
g685      TQSRLASWIHGDIGLPPVDESRLNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAA
          250     260     270     280     290     300

          300     310     320     330     340     350
m685.pep  VEVLDNA LVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQKAAFKKAEPVAAAGKKX
          |||||
g685      VEVLDNA LVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQKAAFEKAEPVAAQX
          310     320     330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTGGCC GTATCGGGAA TTTGCGTGT TCGGGCGTGG TTTCTGCAGG
51  TTGTTTGCCT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCAC
101 CCGTGAAACC GCGTTTTAT TGGGAGCCT GCGCCGTCT GCTGACCGCC
151 TGTTCGCCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGCGCTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGA
351 TTATTTGCAG CTTGCATTG ACAAGCGCGC AACGTTGGGG ACGCTGTTCTG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCAATACC
451 GGCGGGCCGG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGGGAAAGC
551 AGATGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCCGCCAA
651 AGGCAAGGA CGCGGGCTGG TGCTGTCCGT TACGGGCAAC AAGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```

1100

```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGAAGCGCA AGCAAATCAT
951 CGTCATGCCT GCCGCGAAT ACATTGTCGC GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

```

a685.pep
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAARGKG RGLVLSVTGN KVSAGTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQ KEAFEKAEPV
351 AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

```

m685/a685    98.9% identity in 355 aa overlap

          10      20      30      40      50      60
m685.pep    LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
a685         LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
          10      20      30      40      50      60

          70      80      90     100     110     120
m685.pep    VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
a685         VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
          70      80      90     100     110     120

          130     140     150     160     170     180
m685.pep    PAFDKAATVGTLEFPDYEALHRYNPQLVITGGPGEAEYEQ LAKNATTIDLTVDNGNIRTS
a685         PAFDKAATVGTLEFPDYEALHRYNPQLVITGGPGEAEYEQ LAKNATTIDLTVDNGNIRTS
          130     140     150     160     170     180

          190     200     210     220     230     240
m685.pep    GEKQMETLARI FGKEARAAELKAQIDALFAQTREAARGKGRGLVLSVTGNKVSAGTQSR
a685         GEKQMETLARI FGKEARAAELKAQIDALFAQTREAARGKGRGLVLSVTGNKVSAGTQSR
          190     200     210     220     230     240

          250     260     270     280     290     300
m685.pep    LASWIHGDIGLPPVDESLRNEGHPVSFEYI KEKNPDWIFIIDRTAAIGQEGPAAVEVL
a685         LASWIHGDIGLPPVDESLRNEGHPVSFEYI KEKNPDWIFIIDRTAAIGQEGPAAVEVL
          250     260     270     280     290     300

          310     320     330     340     350
m685.pep    DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQKAAFKKAEFVAAGKKX
a685         DNALVRGTNAWKRKQIIVMPAANYIVAGGSRLIQAAEQKAAFKKAEFVAAGKEX
          310     320     330     340     350

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

```

g686.seq (partial)
1  ..AATTTCCTCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAGGCTTC ggcgGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCCTCAGCA TAGCGCCGGC
151 ATTGTGGAAG CGGTCGGCAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201 GGTGAGGCGG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686 >:

g686.pep (partial)

```

1  ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
51  IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPMVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

m686.seq..

```

1  ATGATGTTGA AAAAATTCGT ACTCGCGCGT ATTGCCGCAT TGGTTTTGGC
51  GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
101 TCCTCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA
151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
201 CGCGTTTGAA TCCGTCGCCT ACTCCTTGC TACGCATACT ACCGGCATTG
251 TGGAAACGGT CGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
401 TCGGCGGGAT GGTGTTGCTA TCCGTCCCAA TGGATGCGGT AAAGGCTAAA
451 TCCGTCAACG GGACTACCGG CTTTCATAGA ATCGGAATGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

m686.pep

```

1  MMLKKFVLGG IAAVLVLAACG GSEGGSGAXX XNFSACSADD VFNDICSAVE
51  GFGGIARVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGGMVFV SVPMDAVKAK
151 SVNGTTGFIR IGM*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

g686.pep				10	20	30
				NFSCRADDVFDDICSAVEGFGGIARSVQLG		
m686	LKKFVLGGIAALVLAACG	GGSEGGSGAXX	XNFSACSADDVFNDICSAVEGFGGIARSVQLG			
	10	20	30	40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYSLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
m686		AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
		70	80	90	100	110
g686.pep		100	110	120	130	
		GIAAALWPMVIAVGGMVFVSPMDAVKAESVNGTTGFVRIGMX				
m686		GIAAALWPMVIAVGGMVFVSPMDAVKAKSVNGTTGFIRIGMX				
		130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

a686.seq (partial)

```

1  ..AATTTCCTT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAAGCTTC GCGGCGATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGCTCAGCA TACTACCGGT
151 ATTGTGAAA CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201 GGTGAGGCG GATATTTTGG GCAACGCCCT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAGGCC
351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)

1102

```

1  ..NFSCRADDVF DDICSAVESF GGIARSVQLG AVSGGAFESV AYSLRQHTTG
51 I VETVDKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFIRIG M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. meningitidis*:

m686/a686 96.2% identity in 131 aa overlap

```

              10      20      30      40      50      60
m686.pep      LKKFVLGGIAALVLAACGGSEGGSGAXXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
a686              NFSCRADDVFDDICSAVESFSGGIARSVQLG
                      10      20      30

              70      80      90      100     110     120
m686.pep      AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
a686      AVSGGAFESVAYSLRQHTTGIVETVDKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
                      40      50      60      70      80      90

              130     140     150     160
m686.pep      GIAAALWPVIAVGGMVFVSVPMDAVKAESVNGTTGFIRIGMX
a686      GIAAALWPVIAVGGMVFVSVPMDAVKAESVNGTTGFIRIGMX
                      100     110     120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2279>

```

g687.seq
1  ATGAAATCCA GACACCTCGC CCTCGCCCTC GCGGTGCGG CCCTGTTCGC
51  CCTTGCCGCG TCGCAGACGA AGTCCAAAC CAGCGTCCCC GCCGACAGCG
101 CGCCTGCCGC TTCGGCAGCC GCCGCCCGG CAGGACTGGT CGAAGGGCAA
151 AACTACACCG TCCTTGCCAA CCGGATTCCC CAACAGCAGG CAGGCAAGGT
201 TGAAGTGTCT GAGTTTTCG GCTATTTTG TCCGCACTGC GCCCGCCTcg
251 AACCTGTTTT GAGCAAACAC GCCAAGTCTT TTAAGACGA TATGTACCTG
301 CGTACCGAAC ACGTCGTCTG GCAGAAAGAA ATGCTGCCCG TGGCACGCGc
351 cGCCGCCGCC GTCGATATGG CTGCCGCCGA AAGCAAAGAT GTGGCGAACA
401 GCCATATTTT CGATGCGATG GTCAACCAA AAATCAAGCT GCAAGAGCCG
451 GAAGTCCTCA AAAAATGGCT GGGCGAACAa ACcgctTTG ACGGCAAAAA
501 AGTCCTTGCC GCCTACGAAT CCCCCGAAAG TCAGGCGCGC GCcggcAAAA
551 TGCAGGAGCT GACCGAAACC TTCCAAATCG ACGGTACGCC CACGGTTATC
601 GTCGGCGGCA AATATAAAGT CGAATTTGCC GACTGGGAGT CCGGTATGAA
651 CACCATCGAC CTTTGGCGG ACAAAGTACG TGAAGAACAA AAAGCCGCGC
701 AGTAG

```

This corresponds to the amino acid sequence <2280 ID 724; ORF 687>:

```

g687.pep
1  MKSRHLALAL GVAALFALAA CDSKVQTSVP ADSAPAASAA AAPAGLVEGO
51  NYTVLANPIP QQQAGKVEVL EFFGYFCPHC ARLEPVLSKH AKSFKDDMYL
101 RTEHVWQKE MLPLARLAAA VDMAAASKD VANSIFDAM VNQIKLQEP
151 EVLKKWLGEQ TAFDGGKVL AYESPESQAR AGKMQLTET FQIDGTPTVI
201 VGGKYKVEFA DWESGMNTID LLADKVREEQ KAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2281>:

```

m687.seq
1  ATGAAATCCA GACACCTTGC CCTCGGCGTT GCCGCCCTGT TCGCCCTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAAGCGT CCCCGCCGAC AGCGCGCTG
101 CCGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCAAGG GCAAACTAT
151 ACCGTCTCTG CCAACCCGAT TCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAAA TCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT

```

```

501 TGC CGCCTAC GAGTCCCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGTAAATATA AAGTTGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAAAGCC GCGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2282; ORF 687>:

```

m687.pep
1  MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWQKEML TLARLAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNEV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQLTETTFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

```

m687/g687      97.0% identity in 234 aa overlap

              10      20      30      40      50
m687.pep      MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
              |||||
g687           MKSRHLALALGVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
              10      20      30      40      50      60

              60      70      80      90      100     110
m687.pep      QQQAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTHEHVWQKEMLTTLARLAAA
              |||||
g687           QQQAGKVEVLEFFGYFCPHCARLEPVLSKHAKSFKDDMYLRTHEHVWQKEMLPLARLAAA
              70      80      90      100     110     120

              120     130     140     150     160     170
m687.pep      VDMAAADSKDVANSHIFDAMVNQKIKLQNEVLLKKWLGEQTA FDGKKVLAAYESPESQAR
              |||||
g687           VDMAAAESKDVANSHIFDAMVNQKIKLQEPEVLLKKWLGEQTA FDGKKVLAAYESPESQAR
              130     140     150     160     170     180

              180     190     200     210     220     230
m687.pep      ADKMQLTETTFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
              |||||
g687           AGKMQLTETTFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

```

a687.seq
1  ATGAAATCCA AACACCTCGC CCTCGGCGTT GCCGCCCTGT TCGCACTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAGCGT CCCGCCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAACTAT
151 ACTGTCCTTG CCAACCCGAT TCCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTGCAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAATGCTG ACGCTCGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAGA GCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT
501 TGCCGCTTAC GAATCTCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGCAATATA AAGTCGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAAAGCC GCGCACTAA

```

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

```

a687.pep
1  MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWQKEML TLARLAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNEV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQLTETTFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N meningitidis*:

```
m687/a687      98.7% identity in 232 aa overlap

              10      20      30      40      50      60
m687.pep      MKSRHLALGVAALFALAACDSKVQTSVPADSAPASAAAAAPAGLVEGQNYTVLANPIPQQ
              |||:|||||
a687           MKSKHLALGVAALFALAACDSKVQTSVPADSAPASAAAAAPAGLVEGQNYTVLANPIPQQ
              10      20      30      40      50      60

              70      80      90     100     110     120
m687.pep      QAGKVEVLEFFGYFCPHCAHLEPVLSKHAJSFKDDMYLRTEHVWQREMLTLARLAAAVD
              |||:|||||
a687           QAGKVEVLEFFGYFCPHCAHLEPVLSKHAJSFKDDMYLRTEHVWQREMLTLARLAAAVD
              70      80      90     100     110     120

              130     140     150     160     170     180
m687.pep      MAAADSKDVANSHIFDAMVNQIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQARAD
              |||:|||||
a687           MAAADSKDVANSHIFDAMVNQIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQARAD
              130     140     150     160     170     180

              190     200     210     220     230
m687.pep      KMQELTETFDIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAOX
              |||:|||||
a687           KMQELTETFDIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAHX
              190     200     210     220     230
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

```
g688.seq
1  GTGCTACACT AGACATCCCG ATTTGCACAG AAAGTTCTC CCGTGAACAA
51 AACCTCATC CTGCCCCTTT CCGCCCTGTT CAGCCTGACC GCGTGCAGCG
101 TCGAACGCGT CTGCTGTTT CCCTCCTACA AACTCAAAAT CATCCAAGGC
151 AACGAACGCG AACCGCGCGC CGTTGCCGCC CTGCGCCCCG GCATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCTTTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGAACGCA GCAACCTGAC CGTCTATTT GAAACGCGC TACTCGTCCG
351 CACCGAAGGC GACGCCCTCC AAAATGCCGC CGAAGCCCTC CGCGCGAAAC
401 AAAACGCAGA CAAACAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688 >:

```
g688.pep
1  VLH*TSRFAQ KGSPVNKTLI LALSALFSLT ACSVERVSLF PSYKLKIIQG
51 NELEPRAVAA LRPGMTKDQV LLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KERSNLTVYF ENGVLRTEG DALQNAEAL RAKQNADKQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

```
m688.seq
1  GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATT CCGTGAACAA
51 AACCTCATC CTGCCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGTG
101 CCGAACGCGT TTCACTGTTT CCCTCGTACA AACTCAAAAT CATACAGGCG
151 AACGAACGCG AACCGCGCGC CGTTGCCGCC CTCCGCCCCG GCATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCTTTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGAACGCA GCAATCTGAC CGTCTATTT GAAACGCGC TACTCGTCCG
351 CACCGAAGGC GACGCTCCTGC AAAACGCTGC CGAAGCCCTC AAAGACCGCC
401 AAAACACAGA CAAACCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

```
m688.pep
1  VLHYPSRFAQ KGISVNKTLI LALSALLGLA ACSAERVSLF PSYKLKIIQG
51 NELEPRAVAA LRPGMTKDQV LLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KERSNLTVYF ENGVLRTEG DVLQNAEAL KDRQNTDKP*
```


Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

```
m688/g688      90.6% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep      VLHYPSTRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPYKLIQNELEPRVAA
              ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688           VLHXTSRFAQKGSPVNKTLILALSALFSLTACSVVERVSLFSPYKLIQNELEPRVAA
              10      20      30      40      50      60

              70      80      90     100     110     120
m688.pep      LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688           LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
              70      80      90     100     110     120

              130     140
m688.pep      DVLQNAAEALKDRQNTDKPX
              | : ||||| : |||
g688           DALQNAAEALRAKQNAQKQX
              130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

```
a688.seq
1  GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATT T CCGTGAACAA
51 AACCTCATC CTGCCCTTT CCGCCCTCT CCGCCTTGCC GCGTGCAGCG
101 TCGAACGCGT TTCCTGTTC CCCTCGTACA AACTCAAAAT CATACAGGGC
151 AACGAACTCG AACCTCGCGC CGTCGCCTCC CTCGCCCCG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTT GAAACGGCG TGCTCGTCCG
351 CACCGAAGGC AACGCCCTGC AAAATGCCG CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

```
a688.pep
1  VLHYPSTRFAQ KGISVNKTLI LALSALLGLA ACSVERVSLF PSYKLIQNE
51  LEPRVAVAS LRPGMTKDQV LLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KDRSNLT VYF ENGVLVRTEG NALQNAAEAL RVKQNAQKQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

```
m688/a688      93.5% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep      VLHYPSTRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPYKLIQNELEPRVAA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688           VLHYPSTRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPYKLIQNELEPRVAVAS
              10      20      30      40      50      60

              70      80      90     100     110     120
m688.pep      LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688           LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
              70      80      90     100     110     120

              130     140
m688.pep      DVLQNAAEALKDRQNTDKPX
              : : ||||| : |||
a688           NALQNAAEALRVKQNAQKQX
              130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

```

g689.seq (partial)
1  ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTTCAT CGATGCCTAC CTGCCCGCGA
101 T'TCCGAAAT GCGCGAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGTATTATGT CGGCACGCGG TTCGGGCAAG TGGCCGGCGG
201 CCGCGTGTCC GACATCAAAG GCGCAAACC CGTCGCCCTG ACCGGTTTGA
251 T'TGTATATTG CCTTGCCGTT GCCGCCATCG TATTGCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGCGG TTCGGCGCAG GCATGGCTGT
351 AGTCATCGTc ggtgcgatgg tgcgcgatTA TTATTCGGGA CGCAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCATCATTC TGATGTTGT GCCGCTGGCC
451 GCACCCATGG TCGCGCATT GTTGCAGGGA TTGGGCGGAT GCGGGGCGAT
501 TTTCTGTTTTT ttggcGgcgt ATTGCGCCGT GCTGCCCGGT TTGGTACAGT
551 A'TTTCCTGCC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTT
601 GGGCTGGTGG CGGGGCGGTT CAAGCGCGTA TTGAAAACCC GTGCCGCGAT
651 GGGTtatCTG TTTTTTCAGG CATTACAGTT CGGTCGATG TTCGCTTTC
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCACGT TACGCCGCAC
751 CCGGTACGCAT GGGTGTGTC ACTCAACATC ATCAGCATGA TGTTTTTCAG
801 CCGCGTTACC GCGTGGCGGC TTAAAACCGG CGCGCATCCG CAAAGCATCC
851 TGCTCGGGG GATTGTCGTC CAATTGCCG CCAACCCGTC CCAATCGCC
901 GCGGTGCTGT TTTTCGGGTT GCCCCCGTT TGGCTGCCGG TCGCGTGCCT
951 GATGTTTTTC GTCGGTACGC AGGGCCTGGT CGGTGCGGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAA GAAGAGGCGG GCAGCGCGAA CGCCGTGTCG
1051 GGTGTATTCC GGTCTTAAT CCGCGCGGGC GTGGTCATGG CGGCAACCGT
1101 GATGCGGCA ACCATGACCG CGTCCGCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGGAGGAAA ACGAAAAAA GCGAATACTT

```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689>:

```

g689.pep (partial)
1  ..SPPLPMSGK LMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51  SLSLFMFGTA FGQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
101 QLLNLRAVQA FGAGMAVVIV GAMVRDYSYSG RKAACMFALI GIILMVVPLA
151 APMVGALLQG LGGWRAIFVF LAAYSPVLPG LVQYFLPNPA VGGKIGRDVF
201 GLVAGRFKRV LKTRAAMGYL FFQAFSFGSM FAFLETSSFV YRQLYHVTPH
251 RYAWVFALNI ITMMFFSRVT AWRLKTGAHP QSILLRGIVV QFAANPSQLA
301 AVLFFGLPPF WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

```

m689.seq
1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCT GTTGTGCCG GTGTGTTAAA ATTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTGTGTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AACTGATGG CCGTTTTGAT
201 GGCGATGCTG GTTACGCTGA TGCCGTTTTT CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
301 CAGAGTTTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCGG
351 CGGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCCTTGCC GTTGCCGCCA TCGTATTGTT TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCCGGT GGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGC CGA TTATTATTCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGTT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCTT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG ACGGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAA CCCGTGCTGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTGCGTTCC ATGTTGCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCG TGTACGCCT
901 CATCAATACG CTGCGGCTT TGCATCAAC ATCATCACGA TGATGTTTTT
951 CAACCGCGTT ACCCGGTGGC GGCTCAAAAC CGGCGTGAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACCT GTCCCAACTC
1051 GCGCGCCGTC TGTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTGCGTGCA AACACGCAGG
1151 CGTGCTTTTAT GTCTTATTTT AAAGAAGAGG CGCGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGCGGAC
1251 CTTCTTGAC GACGGTTCGG CAACCGTGAT GCGCGCAACG ATGACCGCGT
1301 CCACCTCTTG CGGCATTGCG CTTCGTGGC TCTGCTCGCA TCGTCCGTG

```

1351 AAGAAACG GCGAAGCGA ATACCTTAA

This corresponds to the amino acid sequence <SEQ ID 2294; ORF 689>:

m689.pep
 1 LLIHYIVPVR PVLPGLLLP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
 51 PSAHYPEMSE KLMAVLMAML VTLMPFSDA YLPAIPEMAQ SLNADVHRIE
 101 QSLSLFMFGT AFGQVVGGSV SDIKGRKFA LTGLIVYCLA VAAIVFVSSA
 151 EQLLNLRVVQ AFGAGMTVVI VGAMVRDYS GRKAAQMFAL IGIILMVVPL
 201 VAPMVGALLQ GLGGWQAIQV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
 251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESSF VYQQLYRVTP
 301 HQYAWAFALN IITMMFFNRV TAWRLKTGVH PQSILLWGIV VQFAANLSQL
 351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
 401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
 451 KENGQSEYL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

m689.pep	30	40	50	60	70	80
	CAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSEKLMAVLMAMLVTLMPFSIDAY					
g689						
m689.pep	90	100	110	120	130	140
	LPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLA					
g689						
m689.pep	150	160	170	180	190	200
	AAIVFVSSAEQLLNLRVVQAFGAGMTVVI VGAMVRDYSSGRKAAQMFALIGIILMVVPLV					
g689						
m689.pep	210	220	230	240	250	260
	APMVGALLQGLGGWQAIQVFLAAYSLVLLGLVQYFLPKPAVGGKIGRDVFGVLVAGRFRKRV					
g689						
m689.pep	270	280	290	300	310	320
	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMMFFNRVT					
g689						
m689.pep	330	340	350	360	370	380
	AWRLKTGVHPQSILLRGIVVQFAANLSQLAAVLFFGLPPFWLLVACVMFVSVGTQGLVGAN					
g689						
m689.pep	390	400	410	420	430	440
	TQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLHDGSATVMAATMTASTSCGIAL					
g689						
m689.pep	450	460				
	LWLCSHRAWKENGQSEYLY					
g689						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

```
a689.seq
1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTCG CGGGGCTTTT
51  GTTGCCGCCT GTTTGTGCCG GTGTGTTAAA ATTTCCGTT TCCGCGTATT
101 GTGTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCC ATTATCCTGA AATGAGCGAA AAATGATGG CCGTTTTGAT
201 GGC GATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCAGC GCCTTCGGAC AGGTGGTCCG
351 CGGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGGCCGCTCA CTGCCTTGCC GTTGCCGCCA TCGTATTGTC TTCGAGTGCC
451 GAA CAGCTCC TCAACCTGCG CGTCGTGCG GCATTCGGTG CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGC CGA TTATTATCC GGACCAAAG
551 CCGCCAGATG GTTTCGCCCT ATCGGCATCA TTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTGGGCGC ATTGTTGCG GGCTTGGGTG GCTGGCAGGC
651 GATTTTGTG TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG CAGGGATGTG
751 TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAAA CCCGTGCCCG
801 GATGGGTAT CTGTTTTTTC AGGCATTGAG CTTCGGTTCG ATGTTCCGCT
851 TTC TGACCA ATCTTCTTC GTGTACCAGC AGCTCTACCA CGTTACGCGG
901 CACCAGTACG CTTGGGCGTT TGCACCAAC ATCATCAGCA TGATGTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAAC CGGCGTGCAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACCT GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTTCG GTTGCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTGCGGTGA AACACGCGAGG
1151 CGTGTTTTAT GTCCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTTGAC GACGGTTCGG CAACCGTGAT GCGGCAACC ATGACCGCGT
1301 CTACCTCTTG CGGCATTGCG CTTTGTGGC TCTGCTCGCA TCGTCCGTGG
1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

```
a689.pep
1  LLIHVIVPVR PVLPGLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPAV LTGLAVYCLA VAAIVFASSA
151 EQLNLNRVVO AFGAGMTVVI VGAMVRDYYS GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAIFV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGRFKR VLKTRAAMGY LFFQAFSFGS MFAELTESSF VYQQLYHVT
301 HOYAWAFALN IITMFFNRI TAWRLKTGVH PQSILLWGIV VQFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVEQSLIGA VGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
451 KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

m689/a689 99.1% identity in 459 aa overlap

```

      10      20      30      40      50      60
m689.pep  LLIHVIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
a689      LLIHVIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
      10      20      30      40      50      60
m689.pep  KLMAVLMAMLVTLMPSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
a689      KLMAVLMAMLVTLMPSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
      70      80      90     100     110     120
m689.pep  SDIKGRKPVALTGLIVYCLAVAAIVFSSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYYS
a689      SDIKGRKPVALTGLAVYCLAVAAIVFASSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYYS
      130     140     150     160     170     180
m689.pep  SDIKGRKPVALTGLIVYCLAVAAIVFSSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYYS
a689      SDIKGRKPVALTGLAVYCLAVAAIVFASSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYYS
      130     140     150     160     170     180
m689.pep  GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAIFVFLAAYSLVLLGLVQYFLPKP
a689      GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAIFVFLAAYSLVLLGLVQYFLPKP
```

```

a689      |||||
          GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAFVFLAAYSLLVLLGLVQYFLPKP
          190      200      210      220      230      240

          250      260      270      280      290      300
m689.pep  AVGGKIGRDVFGVLVAGRFRKRVLKTAAANGYLFQAFSFGSMFAFLTESSFVYQQLYRVTP
          |||||
a689      AVGGKIGRDVFGVLVAGRFRKRVLKTAAANGYLFQAFSFGSMFAFLTESSFVYQQLYHVT
          250      260      270      280      290      300

          310      320      330      340      350      360
m689.pep  HQYAWAFALNIITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFFGLPP
          |||||
a689      HQYAWAFALNIITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFFGLPP
          310      320      330      340      350      360

          370      380      390      400      410      420
m689.pep  FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMATFLH
          |||||
a689      FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMATFLH
          370      380      390      400      410      420

          430      440      450      460
m689.pep  DGSATVMAATMTASTSCGIALLWLC SHRAWKENGQSEYILX
          |||||
a689      DGSATVMAATMTASTSCGIALLWLC SHRAWKENGQSEYILX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

```

g690.seq (partial)
1  ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGC CGCGCGT TCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCGCGTTC GTCTTCCGCG TCATCGGCTT CTTCCCAAC CGATTGCAA
151 CCGCGCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCCTGC ACCCGCCGC CGGCATTGGC GATCTCATAC
251 AGCAAAATCGC CGAACACATC GACTCGGACT GTCTGTTGC CCTTTCCCAT
301 AACGAACTGG AAACCGTTT CGGCTTACCC GCGCGCGGCT ATGACAACAT
351 ACAGCGGctg CTgtttcccg ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGCcgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACC CGC GGAACAAGGCG
551 AGGAACCGAA ACGGCACGT TATTTTGAAG TTTCGGCAAC ATctgCctat
601 TTgaaccggc ACAACAacGG ACTTggcgGC AATTTCaAT ACATCGGCA
651 ATTGCCCGGC TATCTGAAA TGCACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCAGC CGTATTGTGC TTTACGAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

```

g690.pep (partial)
1  MKNKTSSLPL WLAAIMLAAR SPSKEDKKE NGASAASSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQIAEHI DSDCLFALSH
101 NELETRFGLP GGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSOKTR GQGEPEKRR YFEVSATSAY
201 LNRHNNGLGG NFQYIGQLPG YLKMHEMLE NQSLFRLSNR ERNPDKPFLD
251 IHFDENGKIT RIVVYERNIY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

```

m690.seq..
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACC CGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTGCAT
101 CCGCTGCTTC GTCTCCGCG TCATCAGCTC CTTCCCAAC CGATTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATTGC ACCAGCCTGC ACCCGCCAC CGGCATTGAC GATCTCATGC
251 AGCAAAATCGC CGAACACATT GACTCGGACT GTCTGTTGC CCTTTCCCAT
301 CACGAACTGG AAACCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAC GCGCAGGATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACCCGC GGACAAGGCG

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```

551 AGGAGCCGAA ACGCACGCGT TATTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTCCAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAA TACACGGAGA AATGCTTGA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTATAGC
751 ATCCATTTTG ACGAAATGG CAAATCACG CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCAATCCAA ACACGGGGCG AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
  1 MKNKTSLLLL WLTAIMLTAC SPSKDDKTKE VGASAASSSA SSAPSQTDLQ
 51 PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQIAEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDE DYHQIILAI EDLRYGKRTI
151 SRQAQNALME QERRLREATL LLIQGSQETR GQGEPEKRTY YFEVSATPAY
201 SSRHNNGLGG NFQYISQLPG YLKHGEMLE NQSLFRLSNR ERNPDKPFEL
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

```

m690/g690      89.3% identity in 408 aa overlap

      10      20      30      40      50      60
m690.pep      MKNKTSLLLLWLTAIMLTACSPSKDDKTKEVGASAASSSAAPSQTDLOPTASAPDNVK
      ||||| |||:||||:| |||:|||| ||||| ||||| |||||:|||||
g690           MKNKTSLLPLWLAAIMLAARSPSKEDKTENGASAASSSAAPSQTDLOPAASAPDNVK
      10      20      30      40      50      60

      70      80      90      100     110     120
m690.pep      QAESAPPSNCTSLHPATGIDDLMQIAEHIDSDCLFALSHHELETRFGLPDGGYDNIQRL
      ||||| |||:||||:| |||:|||| ||||| ||||| |||||:|||||
g690           QAESAPLXNCTGLHPAAGIGDLIQQIAEHIDSDCLFALSHNELETRFGLPGGGYDNIQRL
      70      80      90      100     110     120

      130     140     150     160     170     180
m690.pep      LFPDIRPEDPDYHQIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQETR
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g690           LFPDIRPEDPDYHQIMLAIEDLRYGTRTISRQAQDAIMEQERRLREATLMLTQGSQKTR
      130     140     150     160     170     180

      190     200     210     220     230     240
m690.pep      GQGEPEKRTRYFEVSATPAYSSRRHNNGLGGNFQYISQLPGYLKHGEMLENQSLFRLSNR
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g690           GQGEPEKRRARYFEVSATSAYLNRHNNGLGGNFQYIGQLPMHGMLENQSLFRLSNR
      190     200     210     220     230     240

      250     260     270     279
m690.pep      ERNPDKPFELDIHFDENGKITRIVVYEKNIYFNPNTGRIX
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g690           ERNPDKPFELDIHFDENGKITRIVVYEKNIY
      250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.seq
  1 ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
 51 GACCCGCGTG TCCCGGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCGCTC GTCCACGGCA TCCGCGGCTT CGTCTCCGC GCCCCAAACC
151 GATTTGCAAC CGGCGGCATC CGCCCTGAT AACGTCAAGC AGGCAGAAAG
201 CGTGCCGCGC TCAAATTGCA CCGACCTGCA CCGCGCCACC GGCATTGACG
251 ATCTCATGCA GCAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCCGTTTC GGCTTACCCG GCGGCGGCTA
351 TGACAACATA CAGCGGCTGC TGTTTCCCGA CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAATCATA CTGGCAATTG AAGACTTGC TACGGAAAG
451 CGCACGATCA GCCGGCAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CTTCCGAGAA GCGACGCTGT TGCTGATACA GGCAGTCAA GAAACCCGCG
551 GACAAGGCGA GGAGCCGAAA CGCACGCGTT ATTTGAAGT TTCGGCAACC
601 CTTGCCATT CGAGCCGGCA CAACAACGGA CTTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGGCT ATCTGAAAT ACACGGAGAA ATGCTTGAAA

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1111

701 ACCAATCACT CTTCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
 751 TTTTATAGACA TCCATTTGA CGAAATGGC AAAATCACGC GTATTGTCGT
 801 TTACGAAAA AACATCTACT TCAATCCAAA CTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep

1 MKNKTSLL WLAAMLTAC SPSKEDTKE NGASAASSTA SAASSAPQT
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMOQIA EHIDSDCLFA
 101 LSHHELETRF GLPGGYDNI QRLFPDIRP EDPDYHQKII LAIEDLRYGK
 151 RTISROAQDA LMEQERRLRE ATLLLIQGSQ ETRGQGEPEK RTRYFEVSAT
 201 PAYSSRHNN LGGNFQYIGQ LPGYLKIHGE MLENQSLFRL SNRERNPDKP
 251 FLDIHFDENG KITRIVVYEK NIYFNPNLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

m690.pep	10	20	30	40	50
a690	10	20	30	40	50
m690.pep	60	70	80	90	100
a690	60	70	80	90	100
m690.pep	120	130	140	150	160
a690	120	130	140	150	160
m690.pep	180	190	200	210	220
a690	180	190	200	210	220
m690.pep	240	250	260	270	279
a690	240	250	260	270	279

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq

1 GTGCCGCTGC CTGCTCCCTG CCGTTTGGC AACCTGCCG CCTCTTTT
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCCGAA CGATTTTCAA CCGAACTGCG ACATACGCC GCTCGGGCTG
 151 ACACAGGGTC AGCACAATGA GCTGCGTAAA ATCCGCGCCG CCTTCAAAAT
 201 GCGGGGCGAC AGGCGCGGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
 251 GCGGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG
 301 GCGGCGGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTGCGGT
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
 401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep

1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
 51 TOGQHNELRK IRAAFKMGD EARLKVHSE HSRRSVVEI ISSDVFNRE
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWS SCLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAT
201 GGC GGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
251 GCCGGTCTGT CGTCGAAATC ATTTCTCTCG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGA CGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACGCCAAC
401 AGCAGCAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQSQHNELRK IRTAFKMGD RARLKMVHSE HSRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691 97.2% identity in 144 aa overlap

      10      20      30      40      50      60
m691.pep VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQSQHNELRK
      |||
g691      VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQSQHNELRK
      10      20      30      40      50      60

      70      80      90     100     110     120
m691.pep IRTAFKMGDRARLKMVHSEHSRRRSVVEI ISSDVFNREARDYVESRYLSGMDFAVDEL
      |||
g691      IRTAFKMGDRARLKMVHSEHSRRRSVVEI ISSDVFNREARDYVESRYLSGMDFAVDEL
      70      80      90     100     110     120

      130     140
m691.pep EIQRFFHILTPQQQMWLS SCLKX
      |||
g691      EIQRFFHILTPQQQMWLS SCLKX
      130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCACCG CCTTCAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTTCTCTCG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACGCCAAC
401 AGCAGCAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQSQHNELRK IRTAFKMGD RARLKMVHSE HSRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

m691/a691 97.2% identity in 144 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID '2309>

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692>:

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2311>:

```
m692.seq
1 GTGTTGCACA CGCTTTGTCG CTGTTCCGAA TCGATACGCC GGATTCCGGC
51 GAATGGCAGG GAATGGCGGA TTAAGGACA AAAATGCCGT CTGAACACGG
101 ATACAGTTCA GACGGCATCA TTTTATACGA CTGCCATTAT TGGCTGCGCT
151 TTCATTCCAT CGCGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCCGGCGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTCGCGTCAG CTTCTAGCCG CTGCTTTATG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CTTCGCGCGC GTACGCGGG
```

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```

401 AGTTCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCGCGC
451 GATGTCGCTC TTGGATGCGG TCAACGGATT GATGCCGCTC TTGAGTTTGA
501 TCCAAACCCAG TTCGTCGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTGCGCACT TGGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGTACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCACTCGGC TTGGATTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGCGGGCG CGCTGTCTT TTGACCGCG CAGGCGGCGA
951 GGAAGAGCGC GAGTGGGCG GCGGAAAGG TTTGAAGAA GGTTCATATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2312; ORF 692>:

```

m692.pep
1  VLHTLCRCSE SIRRIIRNGR EWRIKQKCR LNTDTVQTAS FYTTALFGCA
51  FIPCGRGFVA LEAFVRVGF EYGVIGLYV FKPLAVFVGG FDGRFPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVLG
151 DVREFGCGRI DAVFEFDPQ FVEHHQDAGE VGRVVGGRYG AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFEVVK IGFVLEDVDV QLALSQCQIR
251 AYIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVG
301 RSGCGGRAVF LTAAGGEDER ECGGKGFE GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

```

m692/g692    91.1% identity in 338 aa overlap

          10      20      30      40      50      60
m692.pep    VLHTLCRCSESIRRIIRNGREWRIKQKCR LNTDTVQTASFYTTALFGCA FIPCGRGFVA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692         VSHTRCRCSESIRRIWRNGREWRIKQKCR LNTDAVQTASFYTTALFGCA FIPCGRVFVA
          10      20      30      40      50      60

          70      80      90     100     110     120
m692.pep    LEAFVRVGFERVGVIGLYVFKPLAVFVGFDGRFPVDIGKARFLEQGFQ LHAAYGVVA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692         LEAFVRVGFERVGVIGLYVFKPLAVFVGFDGRFPVDIGKARLLEQGFQ LHAAYGVVA
          70      80      90     100     110     120

          130     140     150     160     170     180
m692.pep    VDDGKIHVGAATRQLRGFKLDDFVQVLGDVRFGCGQRIDAVFEFDPQ FVEHHQDAGE
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692         VDDGKIHVGAARQLCGFKLDDFVQVFRDVGFGCGQRIDAVFEFDPQ FVQHHQGACE
          130     140     150     160     170     180

          190     200     210     220     230     240
m692.pep    VGRVVGGRYGAAVDFDFQRFQQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692         VGRVVGGRYGAAVDFDFQRFQFARIQSQRGRHLEGFQVQVFFFEIVKIGFVLEDVDV
          190     200     210     220     230     240

          250     260     270     280     290
m692.pep    QLALSQCQIRAYIVGKLDQFDGVAFFLQLGLDLFFDHIAEVADGRAEDDF FFRRAVVG--
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692         QLALRQCQIRAHIVGKFDQFDGVAFFLQLGLDLFFDHIAEVAGRAEDDF FFRRAVIGRR
          250     260     270     280     290     300

          300     310     320     330
m692.pep    GGRSGCGGRAVFLTAAGGEDERECGGGKGFE EGFHIFSX
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692         GGRGCGG-RAVFLTAAGCEDERECGGGKGFE EGFHIFSX
          310     320     330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2313>

```

a692.seq
1  GTGTTGCACA CGCTTTGTCG CTGTTGCGAA TCGATACGCC GGATTCGGCG

```

```

51  GAATGGCAGG GAATGGCAGG TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCAATCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGCTGTCTT TGTGCGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTCTT TGAACAGGG CTTGCGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCGGC
451 AATGTCGCGT TTGGATGCGG TCAGCGGATT GATGCCGCTT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGCGGAA GTTGACGGG
551 TCCTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGTACAGTC CCAAAGGCGC GGTGCGCACT TGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGTTTGA
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGCACATAG TCGGTAAACT CGACCAAGTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGG TTGGATTGTG TCTTTGACCA TATCGCCGAA GTCGCGGACG
851 GTCGTGCGGA AGACGATTTT TTTTTCGCC GCGCGGTGT CGGCGCGGCG
901 AGAAGCGGAT GCGCGGGGCG CGCTATCTTT TTGACGCGCG CAGGCGGCGA
951 GAGATGAGCG GAGTGCGGCG GCGGAAGGG TTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

```

a692.pep
1: VLHTLCRCSE SIRRIIRNGR EWRIGQKCR LNTDTVQTAS FYTTALFGCA
51: FIPCGRGFVA LEAFVRVGFE RVGVIGLYV FKPLAVFVGG FDGRPVDIGK
101: ARFLEQGFQG LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQFVFG
151: NVRFQCGQRI DAVFEFDPQ FVEHHQDAGE VGRVVRGGRY AAVFDFFORF
201: QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251: AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRAVVGGG
301: RSGCGGRAIF LTAAGGEDER ECGGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

```

m692/a692 98.8% identity in 336 aa overlap

      10      20      30      40      50      60
m692.pep VLHTLCRCSESIRRIIRNGREWRIKQKRLNTDTVQTASFYTTALFGCAFI PCGRGFVA
a692      VLHTLCRCSESIRRIIRNGREWRIKQKRLNTDTVQTASFYTTALFGCAFI PCGRGFVA
      10      20      30      40      50      60

      70      80      90     100     110     120
m692.pep LEAFVRVGFERVGVIGLYVFKPLAVFVGGFDGRPVDIGKARFLEQGFQGLHAAAYGVVA
a692      LEAFVRVGFERVGVIGLYVFKPLAVFVGGFDGRPVDIGKARFLEQGFQGLHAAAYGVVA
      70      80      90     100     110     120

      130     140     150     160     170     180
m692.pep VDDGKIHVGAAATRLRGFKLDDFDVQVGLDVRFGCGQRIDAVFEFDPQFVEHHQDAGE
a692      VDDGKIHVGAAATRLRGFKLDDFDVQVGNVRFQCGQRIDAVFEFDPQFVEHHQDAGE
      130     140     150     160     170     180

      190     200     210     220     230     240
m692.pep VGRVVRGGRYGAAVDFDFQRFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
a692      VGRVVRGGRYGAAVDFDFQRFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
      190     200     210     220     230     240

      250     260     270     280     290     300
m692.pep QLALSQCQIRAHIVGKLDQFDGVAFFLQLGLDLFFDHIAE VADGRAEDDFFFRAVVGGG
a692      QLALSQCQIRAHIVGKLDQFDGVAFFLQLGLDLFFDHIAE VADGRAEDDFFFRAVVGGG
      250     260     270     280     290     300

      310     320     330
m692.pep RSGCGGRAIFLTAAGGEDERECGGGKGFEFGFHIFSX
a692      RSGCGGRAIFLTAAGGEDERECGGGKGFEFGFHIFSX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

```
g694.seq
1   TCGGCATTG  TGTGCCCCA  ACATCCGATG  CCTGCGTTAA  CGCCTGCGTC
51  AACGTTTGA  CAAATCGGGT  TTGGTTTCGC  CCTCGCGGCG  CAGCTCCTTG
101 GGCAGGACGA  ACACGATGCT  TTCTTCCGCG  CCCCCCCTT  CGCGCACGGT
151 TTCATGCCCC  CATCCGCGTA  TGGTTGCCAA  TACTTCCCGC  ACCAACACTT
201 CGGGCGCGGA  CGCGCCTGCC  GTTACGCCGA  CTTTGCTTTT  GCCTTCAAAC
251 CACGTGCGTT  GCaggTAGGA  CGCGTTGTCC  ACCATATACG  CATCGATTCC
301 GCGCGATGCC  GCCACTTCGC  GCAGGCGGTT  GCTGTTGGAC  GAATTGGGCG
351 AACCGACCAC  AATCACGATG  TCGCACTGTT  CCGCCAGCTC  TTTGACGGCG
401 GTTTGCCGGT  TGGTCGTCGC  ATAGCAGATG  TCTTCTTGT  GCGGATTGCG
451 GATATTGGGG  AAACGCGCGT  TCAGCGCGGC  GATGATGTCT  TTGGTTTCAT
501 GCACCGAGAG  CGTGGTTTGG  CTGACATAGG  CGAGTTTGTC  GGGGTTTCTG
551 ACTTCGAGTT  TTGCCACATC  TCCGACCGTT  TCGACCAAAA  GCATTTTGCC
601 CGGTGCAAGC  TGCCCCATCG  TGCCTTCGAC  CTCGGCGTGC  CCCTTATGCC
651 CGATCATGAT  GATTTCACAG  TCTTGGGCAT  CCAGTCGGGC  GACTTCCTTA
701 TGCACTTTCG  TCACCAGCGG  GCAAGTCGCA  TCAAATACCC  GGAAACCGCG
751 CTCGCGCGCT  TCCTGCTGCA  CCGCCTTCGA  TACGCGGTGT  GCCGAATAAA
801 CCAAGTGTGC  GCCCGCGGCG  ACTTCCGCCA  AGTCTTCGAT  AAACACCGCG
851 CCTTTTTCGC  GCAGGTTGTC  CACGACGAAT  TTGTTGTGGA  CGACTTCGTG
901 GCGCACATAA  ACCGGCGCGC  CGAATCTTTC  CAAAGCAGCT  TCGACAATAC
951 TGATTGCCCC  ATCCACACCG  GCGCAGAAGC  CGCGCGGATT  GGCAAGGATG
1001 ATGGTTTTTC  CGTTCATAAG  TTTTGCAATC  CGTGTTCAGA  CGGCATTAC
1051 GTTTTTTTCG  TNNATCTTTG  CGATGGACGA  TATTGTCAAG  CACCGCCAAC
1101 ACCGCACCGA  CGCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694>:

```
g694.pep (partial)
1   SAFVLKHPM  PALTPASTFA  QIGFGFALAA  QLLGQDEHDA  FFRAPPPFANG
51  FMPPPSAYGC  YFPQHFGRR  RACRYADFAF  AFKPRALQVG  RVVHHIRIDS
101 ARCRHFAQAV  AVGRIGRTDH  NHDVALFRQL  FDGGLPVGRR  IADVFLVRIA
151 DIGETRVRQG  DDVFGFIDRE  RGLADIGEFV  GVSDFEFCHI  SDRFDQKHFA
201 RCKLPHRAFD  LGVPLMPDHD  DFTVLGIQSG  DFLMHRHQXR  ASRIKYPETA
251 LRRFLLHRLR  YAVCRINQCR  ARRHFRQVFD  KHRAFFAQVV  HDEFVDDFV
301 AHINRRAEFF  QSTFDNTDCP  IHTGAEAAAI  GKDDGFSVHK  FCIPCSDGII
351 VFLLXLCDDR  YCQAPPTPHR  RR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

```
m694.seq
1   TTGGTTTCCG  CATCCGGCAC  ACGGCAAAAA  TGCCGTCTGA  AGCCTGTTCA
51  GACGGCATT  GTGTTGCCCA  AACATTCAAC  GCCTGCGTCA  ACGTTTCAC
101 AAATCGGGTT  TGGTTTCGCC  CTCGCGGCGC  AACTCTTTGG  GCAGGACGAA
151 CACAATGCTT  TCTTCCGCAC  CCTCGCCTTC  GCGTACGGTT  TCGTGCCCCC
201 ATCCGCGTAT  GGTGCCAGT  ACTTCCCGCA  CCAACACTTC  GGGCGCGGAC
251 GCGCCTGCGG  TTACGCCGAC  TTTGTTTTTG  CCCTCAAACC  ATGCGCGTTG
301 CAGGTAGCCT  GCATTATCCA  CCATATACGC  ATCGATTCCG  CGCGATGCCG
351 CCACTTCGCG  CAAGCGGTTG  CTGTTGGACG  AATTGGGCGA  ACCGACCACA
401 ATCAGATGT  GCACTGTTC  TGCCAACTCT  TTGACGGCGG  TTTGCCGGTT
451 GGTCGTCGCA  TAGCAGATAT  CTTCTTGTG  CGGATTGCGG  ATATTGGGGA
501 AACGCGCGTT  CAGCGCGGCG  ATGATGTCTT  TGGTTTCATC  GACCGAGAGC
551 GTGGTTTGGC  TGACATAGGC  GAGTTTGTGC  GGGTTTCTGA  CTTGAGTTT
601 TGCCACATCT  CCGACCGTTT  CGACCAAAAG  CATTTTGCCC  GGCGCAAGCT
651 GCCCCATCGT  TCCTTCGACC  TCGACGTGCC  CCTTATGCCC  GATCATGATG
701 ATTTACAGAT  CTTGGGCATC  CAGTCGGGCG  ACTTCCTTAT  GCACTTTCGT
751 CACCAGCGGG  CAAGTCGCAT  CAAACACGCG  GAAACCGGc  TCCGCCGCTT
801 CTTGCCGCAC  CGCCTTCGAT  ACGCCGTGTG  CCGAATAAAC  CAGTGTCCGG
851 CCGGGCGGCA  CTTCCGCCAA  GTCTTCAATA  AACACCGCAC  CTTTTCACG
901 CAGGTTGTCC  ACGACGAATT  TGTGTGAAC  GACTTCGTGG  CGCACATAAA
951 TCGGCGCGCC  GAACTCTTCC  AAAGCACGTT  CGACAATACT  GATT GCCCGA
1001 TCCACACCAG  CGCAGAAGCC  GCGCGGATTG  GCAAGGATGA  TGGTTTTCTC
1051 GTTCATAAGC  CCGGTATTTC  GTTTTCAGAC  GGCATCAATA  TTTTCTTCT
1101 TGGGTTTTAC  GGTGGACGAT  GTTGTCACAC  ACCGCCAACA  CCGCACCAGC
1151 GCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

```
m694.pep
1   LVSASGTROK  CRLKPVOTAF  VLPKHSTPAS  TFAQIGFGFA  LAAQLFGQDE
51  HNAFFRTLAF  AYGFVPPSAY  GCQYFPHQHF  GRGRACRYAD  FVFALKPCAL
101 QVACIIHHR  IDSARCRHFA  QAVAVGRIGR  TDHNDHVALF  CQLFDGGLPV
```

```

151 GRRIADIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVNV DFVAHINRRA ELFQSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

```

m694/g694      86.8% identity in 372 aa overlap

          10      20      30      40      50
m694.pep      LVASAGTRQKCR LKPVQTAFVLPKHS----TPASTFAQIGFGFALAAQLFGQDEHNAFFR
g694           :||||| :||||| :||||| :||||| :|||||
                SAFVLPKHPMPALTPASTFAQIGFGFALAAQLLGQDEHDAFFR
                10      20      30      40

          60      70      80      90     100     110
m694.pep      TLAFAYGFVPPSAYGCQYFPHQHFGGRGRACRYADFVFAKPCALQVACIIHHIRIDSARC
g694           : |||:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
                APPFAHGFMPPSAYGCQYFPHQHFGGRGRACRYADFAFAFKPRALQVGRVVHHIRIDSARC
                50      60      70      80      90     100

          120     130     140     150     160     170
m694.pep      RHFAQAVAVGRIGRTHNHHDVALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDV
g694           :|:|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
                RHFAQAVAVGRIGRTHNHHDVALFRQLFDGGLPVGRRRIADVFLVRIADIGETRVQRGDDV
                110     120     130     140     150     160

          180     190     200     210     220     230
m694.pep      FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPHRSFDLDVPLMPDHDDFT
g694           :|:|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
                FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPHRAFDLGVPLMPDHDDFT
                170     180     190     200     210     220

          240     250     260     270     280     290
m694.pep      VLGIQSGDFLMHFRHQASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHR
g694           :|:|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
                VLGIQSGDFLMHFRHQASRIKYPETALRRFLHLRLRYAVCRINQCRARRHFRQVFDKHR
                230     240     250     260     270     280

          300     310     320     330     340     350
m694.pep      TFFTQVVHDEFVNVDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGI
g694           :|:|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
                AFFAQVVHDEFVNVDFVAHINRRAELFQSTFDNTDCPIHTGAEAARIGKDDGFSVHKFCI
                290     300     310     320     330     340

          360     370     380
m694.pep      SFSDDGINIFLLGFYGGRCCTPTPTPHRRRX
g694           :|:|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
                PCSDDGIHVFLXXLCDGRYQAPPTPHRRRX
                350     360     370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

```

a694.seq
1   TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51  GACGGCATT  GTGTTGCCA AACATTCAAC GCCTGCGTCA ACGTTTGAC
101 AAATCGGGT  TGTTTCGCC CTCGCGGCGC AACTCTTGG GCAGGACGAA
151 CACAATGCT  TCTTCGCAC CCTCGCCTC GCGTACGGT TCGTGCCCCC
201 ATCCGCGTAT GGTGCCAGT ACTTCCGCA CCAACTTC GGGCGCGGAC
251 GCGCCTGCC  TTACGCGGAC TTTGTTTTG CCTCAAAC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGGATGCCG
351 CCACCTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCAGGATG  CGCACTGTT TGCCAACCT TTGACGGCGG TTTGCCGTT
451 GGTCTGCGCA TAGCAGATAT CTTCTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGG  TGACATAGG GAGTTTGTG GGGTTTCTGA CTTCGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAG CATTTTGCCG GCGCAAGCT
651 GCCCATCTGT TCCTTCGACC TCGACGTGCC CTTATGCCC GATCATGATG

```

1118

```

701 ATTTTCACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CAC CAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACCTTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCA GCGAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTCCAAC ACCGCCAACA CCGCACCAGC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

```

a694.pep
1  LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDHVALF CQLFDGGLPV
151 GRRADIIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHI SDRFDQK HFARRKLPFR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVFN DFVAHINRRA ELFQSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

```

m694/a694    100.0% identity in 385 aa overlap

          10      20      30      40      50      60
m694.pep    LVSASGTRQKRLKPVQTAFVLPKHSTPASTFAQIGFGFALAAQLFGQDEHNAFFRTLAF
a694         LVSASGTRQKRLKPVQTAFVLPKHSTPASTFAQIGFGFALAAQLFGQDEHNAFFRTLAF
          10      20      30      40      50      60

          70      80      90     100     110     120
m694.pep    AYGFVPPSAYGCQYFPHQHFGRGRACRYADVFALKPCALQVACIIHHIRIDSARCRHFA
a694         AYGFVPPSAYGCQYFPHQHFGRGRACRYADVFALKPCALQVACIIHHIRIDSARCRHFA
          70      80      90     100     110     120

          130     140     150     160     170     180
m694.pep    QAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRRIADIIFLVRIADIGETRVQRGDDVFGFI
a694         QAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRRIADIIFLVRIADIGETRVQRGDDVFGFI
          130     140     150     160     170     180

          190     200     210     220     230     240
m694.pep    DRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPFRSFDLDVPLMPDHDDFTVLGI
a694         DRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPFRSFDLDVPLMPDHDDFTVLGI
          190     200     210     220     230     240

          250     260     270     280     290     300
m694.pep    QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT
a694         QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT
          250     260     270     280     290     300

          310     320     330     340     350     360
m694.pep    QVVHDEFVFNDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGISFSD
a694         QVVHDEFVFNDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGISFSD
          310     320     330     340     350     360

          370     380
m694.pep    GINIFLLGFYGGGCCPTPPTPHRRRX
a694         GINIFLLGFYGGGCCPTPPTPHRRRX
          370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```

g695.seq
1   TTGCTCTCAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGT TGAACGG AAGGGTGATG CGCGAAGCGG CTTTGTGATG GCCGCCCAGT
101 GTC AAAAATC TCAAAGATT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGT CCCCATC ACCCTGCCCG TCGGCGACGG TTGACCCCTG CTTCTGAAAA
201 AAT AATGAAG ACCAAATTAC CGCTTTTAT CATTGGGCTG TCTGTGTCTG
251 CCT CCTGTGC TTCCGTTTCA CCCGTTCCGG AGGGCAGCCG AACCGAAATG
301 CCG ACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACTCT
351 GCA AGACCGT TTGGACTATC TGGAAGGCAA AATCGTCCGG CTGTGGAACG
401 AAG TGGAAAT GTTAAACGGG AAAGTCAAAG CATTGGAGCA TACGAAAAATA
451 CAC CTTCCG GCAGGCATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGA GCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAA CCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAACCGGC
601 AGG TTTTCTG CCGCAGCCGC CTTGTTGAAG GGGGCGGACG GCGGAGACGG
651 CGG CAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTA TGGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGT TTCAAAG ACAGCCCAAC CGGCCCCGAA GTCATATTCA AAATCGGCGA
801 ATG CCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCC TGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG GCCTGCCGCA
901 GCC GTACGCA AACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```

g695.pep
1   LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCONSQRF QSKPAERYAD
51  CPHPHPARRR FDPASEKIMK TKLPLFIWL SVSASCASVL PVPEGSRTM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRTYVQK LDDRKLKEHY LNTEGGSASA HTVETAONLY NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLLO SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQOKDIARA TWRSLIQTPY GSPAARKRAA
301 AVRKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```

m695.seq
1   TTGCTCTCAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGCTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGT CCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCCCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTGGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGGAAGGCAA AATCGTCCGG CTGTGGAACG
401 AAGTGGAAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCTTCCG GCAGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCTG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAGCGGC
601 AAGTTTTCTG CCGCTGCCTC CTTGTTGAAA GCGCGGACG GAGGCGACGG
651 CGG CAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG GCCTGCCGCA
901 GCC GTGCGCA AACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```

m695.pep
1   LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRHPQRF QSKPAERPAP
51  RPHHPARRRR LDPASEKIMK IKLPLFIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHART
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAONLY NQALKHYKSG
201 KFSAAAALLK GADGGDGGSI AQRSMYLLLO SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQOKDIARA TWRSLIQTPY GSPAARKRAA
301 AVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

m695/g695 90.8% identity in 305 aa overlap

	10	20	30	40	50	60
m695.pep	L.PQTRPSRRHRHROQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR					
	: : : : :					
g695	L.PQTRPARRHRHROQYFVERKGDARSGFXCAAQCNQSFQSKPAERYADCPHHPARRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m695.pep	L.DPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR					
	:					
g695	F'DPASEKIMKTKLPLFIIWLSVSASCASVLPVPEGSRTemptQENASDGIPYPVPTLQDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m695.pep	L.DYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTEGGSASA					
g695	L.DYLEGKIVRLSNEVEMLNGKVKALEHTKIHPGRTYVQKLDLDRKLKEHYLNTEGGSASA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m695.pep	HTVETAQNLNQAALKHYKSGKFSAAAALLKGADGGDGGSIQSRSMYLLQLSRARMGNCS					
g695	HTVETAQNLNQAALKHYQNGRFSAAAALLKGADGGDGGSIQSRSMYLLQLSRARMGNCS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m695.pep	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAARKAAA					
g695	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQOKDIARATWRSLIQTYPGSPAARKAAA					
	250	260	270	280	290	300
m695.pep	AVRKRKX					
g695	AVRKRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

a695.seq

```

1  TTGCTCAAG CTTGTCCGGC AAGGCGGCAT CATTGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTCGGATGC GCCGCCGAGC
101  GTCGGCATCC TCAAAGATT TAAACAAAC CTGCCGAACG ATACGCGGAT
151  TGTCCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCTG CTTCTGAAAA
201  AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCCGTATCCG
251  CCGCTGTGTC TTCCCTGTGT TCCCGCAATA TTCAGGATAT CGCGCTCGAA
301  CCGCAGGCAG AGGCAGGTAG TTCGGACGCT ATTCCCTATC CCGTTCCAC
351  TCTGCAAGAC CGTTGGATT ATCTGGAAGG CACACTCGTC CGCCTGTCTG
401  ACGAAGTGGA AACCTTAAAC GGCAAAGTCA AAGCACTGGA GCATGCGAAA
451  ACACACCCCT CCAGCAGGCG ATACGTCCAA AACTCGACG ACCGCAAGTT
501  GAAAGAGCAT TACCTCAATA CCGAAGGCGG CAGCGCATCC GCACATACCG
551  TCGAAACCGC ACAAAACCTC TACAATCAGG CACTCAAACA CTATAAAAGC
601  GGCAGGTTTT CTGCCGCTGC CTCCTGTGTG AAAGGCGCGG ACGGAGGCGA
651  CGGCGGCGAG ATCGCGCAAC GCAGTATGTA CCTGTTGCTG CAAAGCAGGG
701  CGCGTATGGG CAACTGCGAA TCCGTCATCG AAATCGGAGG GCGTTACGCC
751  AACC GTTCA AAGACAGCCC AACC GCGCCT GAAGCCATGT TCAAAATCGG
801  CGAATGCCAA TACAGGCTTC AGCAAAAAGA CATTGCAAGG GCGACTTGGC
851  GCAGCCTGAT ACAGACCTAT CCCGGCAGCC CGGCGGCAAA ACGCGCCGCC
901  GCAGCGTGC GCAACGATA G

```

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

a695.pep

```

1  LPQACPARRH HCHROQYFVER KGDARSGFRC AAQRRHPQRF *SKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIIWL SVSAACSSPV SRNIQDMRLE
101  PQAEAGSSDA IPYPVPTLQD RLDYLEGLTV RLSNEVETLN GKVKALEHAK
151  THPSSRAYVQ KLDDRKLKEH YLNTEGGSAS AHTVETAQNL YNQALKHYKS
201  GRFSAAAALL KGADGGDGGG IAQRSMYLLL QSRARMGNCE SVIEIGGRYA
251  NRFKDSPTAP EAMFKIGECQ YRLQOKDIAR ATWRSLIQTY PGSPAARKAA
301  AAVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

m695/a695 88.3% identity in 308 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:

1122

```

1   TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAAT
51  ATT'TGGCGGC ATCTTTCATT TTGCTGCGC CTTCCTGAGT CGCGTCGGCA
101 GCT'TTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGT'TACAGCT TCCTCGGCAC TTGCCTTTC ATCAGCCGCA GCATCTTTGA
201 CTT'GGTCTTT CGCTTCTTCG ACGGCAGAA GCGCAGACTC GGCGGCAGAA
251 GCC'GCAGTGT CTTTAACATC GGACTCAACG GCTTGAACCG CTTCTTAAC
301 CTC'CTGTTTG GCTTCTTTCG AACAAAGCTG CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

```

a696.pep
1   LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
101 LLFGFLRTSC QGSRHHCNGQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

```

m696/a696      100.0% identity in 120 aa overlap

                10      20      30      40      50      60
m696.pep      LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFYSFLGTCLC
a696           LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFYSFLGTCLC
                10      20      30      40      50      60

                70      80      90      100     110     120
m696.pep      ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRFLNLLFGFLRTSCQSRHHCNGQ
a696           ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRFLNLLFGFLRTSCQSRHHCNGQ
                70      80      90      100     110     120

m696.pep      X
                |
a696           X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

```

g700.seq
1   ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTGCCGG
51  ATTTTTTATC CGTGTTCCCA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTCG
151 CGCGTGGAGG ATTTGGGTTT GCGGTGGGCG GATATGGCGT TGACGGTTCT
201 TTGGCTGTTT GTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 GTGGAAAGTT GTCCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTC CTTAACCGGC GGGGCATCCG
501 GCTGTCCGTT TGGTTTATAT TGTCTCTCTT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGATGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTAATGACCG AGGCTTACGG
651 GGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTCC GGATGCGGCG
751 GTGGGGGTCT GCGCGCGGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGCGGGC GGTTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGCGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTTTC CACGCTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

```

g700.pep
1   MSSLMTLFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRIG DMALTVLWLF VCTVGANLLA LAVLGKLSPW RIGGKKGVS
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMPs ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRRGIRLSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```

201 G FGWYSLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPIQGAG GLEVVPVAVS FGVVVNIAAP FLMVVFSTLG
 301 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2333>:

m700.seq

1 A TGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
 51 A TTTTATC CGTGTGCCA AGCCTTACCT GCCCGCTTG GATAAGGTGC
 101 T ATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCTG
 151 C GCGTGGAGG ATTTGGGTTT GCGGTTGGAC GATATGGCGT TGACGGTTCT
 201 G TGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
 251 T GGGAAAGTT ATTCCTGTTG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
 301 G TCGGCGTGT CCGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
 351 T GCATTCGGC AAACGTATGC GCGATATTG GATGCCGTCT GAAAGCGCGG
 401 G CATGTATTG TCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAA
 451 A GCAGCGGCG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTTCG
 501 G TTGTCGGTC TGGTTTATGC TTTCATCTCT TTCGGGCGGG CTGCTGTTTG
 551 C CGCATCGAC AGACGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
 601 G GCTTCGGTT GGTATCCCT CTCGGGTTTG GTCATGACCG AGGCTTACGG
 651 C GCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
 701 T TCACTGCG ATTTATCCCG CTGCTGATGA AGCGTTTTC AGATGCGGCG
 751 G TGGGGGTTG GCGGTGCGAC CAGTATGGAT TTTACATTGC CCGTGATTCA
 801 G GGTGCGGGC GGTTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
 851 T GGTCAATAT CGCCGCCCG TTTCTGATGG TGGTGTTC CGCTTTGGGT
 901 TGA

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>:

m700.pep

1 MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSL
 51 RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLPW RIKGKKGVS
 101 VGVSGSVGQL GCVLLGFAGF KLMRDIWMP ESAGMYCLML LVFLIGVQLK
 151 SSGVSLRQVL VNRRGIRLSV WEMLSLSSGG LLFAASTDGV SWTKGLAMAS
 201 GFGWYSLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPIQGAG GLEVVPVAVS FGVVVNIAAP FLMVVFSA
 301 *

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

m700/g700

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
g700	MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLLIGVSLSRVEDLGSRLG					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKKGKGVSVGVSGSVGQLGCVLLGFAGF					
g700	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKKGKGVSVGVSGSVRQLGCVLLGFVSG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWEMLSLSSGG					
g700	KLMCDIWMPSENAGMYCLMLLVFLIGVQLKSSGVSLRQVLNRRGIRLSVWFILSSLSGG					
	130	140	150	160	170	180
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYSLSGLVMTAYGAVWGSIMLLNDLARELFALAFIP					
g700	LLFAASADGVSWTKGLAMASGFGWYSLSGLVMTAYGAVWGSIMLLNDLARELFALAFIP					
	190	200	210	220	230	240

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	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFLTPVIQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
g700	LLMKRFPDAAVGVGGATSMDFLTPVIQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
g700	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

a700.seq

```

1   ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51  ATTTTATATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCT
151 CGCGTGGAGG ATTTGGGTTT GCGGTGGGAC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTGTACGCG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
301 GTCGGTGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCATCCGGC AAACGTATGC GCGATATTTG GATGCCGCTC GAAAACGCGG
401 GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTTG GTCAACCGCA GGGGTATTCT
501 GTTGTCGGTC TGGTTTATGC TTTTCTCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGACGGTGTG TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATCCCTT CTCGGGTTTG GTGATGACCG AGGCTTACCG
651 CGCGGTATGG GGCAGTATCG CGCTTTTGAA CGATTTGGCA CGAGAGCTGT
701 TCGCGTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTCG CGATGCGGCA
751 GTGGGGGTCG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTCT
801 GGGTGCGGGC GGCTTGGAAG CCGTACCGGT AGCGGTGAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCTCCG TTTCTGATGG TGGTGTTCCT CGCTTTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

a700.pep

```

1   MDSIMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLPFW RIKGKGKGV
101 VGVSGSVGQL GCVLLGFASG KLMRDIWMP ENAGMYCLML LVLXIGVQLK
151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASADGV SWVKGLAMAS
201 GFGWYSLSGL VMTEAYGAVW GSIALNLNLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSMDF LTPVIRGAG GLEAVPVAVS FGVVVNIAAP FLMVVFSALG
301 *

```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSIMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
a700	MDSIMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKGKGKGVSVGVSGSVGQLGCVLLGFASG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKGKGKGVSVGVSGSVGQLGCVLLGFASG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180

q701.seq

1	ATGTCCTTGCC	ACATATTCCA	AGTTGCAGGG	ATACCGACCG	CTTCGATGGC
51	ACAATCTACG	CCGTCCTCGC	CGACGATGCG	GAAAACTTGT	TTGGAGACGT
101	CGCCCGGAAG	GGGGCTGATG	GTATGGGTGC	CGCCCAACTC	TTTCGCGCGT
151	TTCAAACGGT	TTTCGTCGAT	ATCGCACACG	ATAATGGCCG	CAGGGCTATA
201	CAGTTGGGCG	GTCAACAAGG	CGGACATACC	GACAGGGCCG	GCACCTGCGA
251	TGAATACGGT	ATCGCCGGGT	TTCACATCGC	CGTATTGTCAC	GCCGATTTCG
301	TGGGCGGTGC	GTAAGCGCTC	GCTCAACAGC	AGGGCGGATT	CTTCGTTGAC
351	GTTGTCTGTC	GTAAGCACGA	GCTGTGTTGC	GGCATAA	

g701.pap

1 MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VVWAPNSFAG
51 FKRFSsisHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
101 WAVGKASLNS RAISsLTISC GGTRLLSA*

m701.seq

1	ATGTCCTTGCC	ACATATTCCA	TGTAGCAGGG	ATACCGACGG	CTTCGATGGC
51	GCAATCCACG	CCGTTCTTCG	CGACGATGCG	AAAGACTTGT	TTGGATACTT
101	CGCCGGAAGC	AGGGTTTAATG	GTATGGGTGC	CACCAATTC	TTTCGCGCAGT
151	TTCAAACGGT	TTTCGTTCCAT	ATCGCAAACG	ATCATGGCGG	CGGGACTGTA
201	CAGTTGGGCG	GTCACAGGG	CGGACATACC	GACAGGGCCT	GCCCCAGCGA
251	TGAATACCGT	GTCGCGGGT	TTGACATCGC	CGTATTGCAC	GCCGATTTCG
301	TGGCGGTGCG	GCAAAGCGTC	GCTCAACAAC	AGGGCGATTT	CTTCGTTGAC
351	ATTATCGGGC	AGCGGAACGA	GGCTGTTGTC	GGCATAA	

m701.pap

1 MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSPEAGLM VVWAPNSFAS
51 FKRFFSSISQT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS
101 WAVGKASLNN RAISSLTLSG SGTLLISA*

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

m701/g701

```

      10      20      30      40      50      60
m701.pep  MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSISQT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g701      MSWHIFQVAGIPTASMAQSTPSSPTMAKTCLETSPEAGLMVWVAPNSFAGFKRFSISHT

```

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	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	: : : : :					
g701	IMAAGLYSWAVNKADIPTGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISSLTLSG					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
	:
g701	GGTRLLSAX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACGG CTTCGATCGC
51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTTG CGCCCAACTC TTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201 CAGTTGGGCG GTCCGCCAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGTGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351 GTTGTCGGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VVWAPNSFAS
51  FKRFSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101 CAVGKASLNN RATSSLTSLG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVVWAPNSFASFKRFSISQT					
	: : :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPPEAGLMVVWAPNSFASFKRFSISQT					
	10	20	30	40	50	60

	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	: : : : :					
a701	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTSLG					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
a701	SGTRLLSAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
1  ATGCCGTGtT ccaAAGCCAG TTGGAATTCC CCCGGAGtgg cAACGCCGGG
51  AATCAGGGGA ATGCCGCTGT TGCGGCCGGC TCTGGCGAGG GATTCTGCA
101 AACCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGAT TGTTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTC
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTGAGGGT GGGGATGCCG CCTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAAt cgCCATCACA GGCACAAC TG CGCCGGCGGT
351 CAGGATTTCC cggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

1127

```

1  MPCSASWTS PGVATPGIRG MPLLRLPALR DSCKPGLMAK TAPASSTALS
51  C SGLVTPAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRARDKST
101 AVLKSSIAIT GTTAPAVRIS RGV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

m702.seq

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAAC TG CGCCGGCGGT
351 CAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTC TC CGGGTGGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

m702.pep

```

1  MPCSASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  C SGLVTPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

m702/g702

	10	20	30	40	50	60
m702.pep	MPCSASWISPGVATPGIRGMPELLWPALARDSCSPGLMAKTAPASSTALSCSGLVTPAP					
g702	MPCSASWISPGVATPGIRGMPELLRPALARDSCKPGLMAKTAPASSTALSCSGLVTPAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m702.pep	TMALGTSIAIRRMASRPTGVRRVISRVGMPPSTRAWDKSM AVLKSSIAIT GTTAPAVKIS					
g702	MMALGISLAIRRMASPTGVRRVISRVGMPPSTRARDKST AVLKSSIAIT GTTAPAVRIS					
	70	80	90	100	110	120
	130	140				
m702.pep	RGVSLDISVL RVEWGILLRW DRLX					
g702	RGVSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

a702.seq

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAAC TG CGCCGGCGGT
351 CAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTC TC CGGGTGGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

a702.pep

```

1  MPCSASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  C SGLVTPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

1128

```

m702.pep  MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPPAP
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702      MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPPAP
          10      20      30      40      50      60

          70      80      90      100     110     120
m702.pep  TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702      TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
          70      80      90      100     110     120

          130     140
m702.pep  RGVSLDISVLRVEWGILLRWDR LX
          ||||||||||||||||||
a702      RGVSLDISVLRVEWGILLRWDR LX
          130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

```

g703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTGCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAAACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAGGCC GTTTACGACA ATATCAGCGG TTTTATATAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCGAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTTGGAA CAGGTTGTTC CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCCTT CTTTGTACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GCGGAACGG ATTGACCGTG CCGTctgTgc gcTGTgggt aaggCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

```

g703.pep
1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51 EDTPQLRQSL LENEVNTVV AQEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
201 DGYVPLKLE QGVPLYQAI KDLKKGEFTA TPLKNGDFYV VYYVNSDREV
251 KVPSFDEMKG QIAGNLQAE R IDRAVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

```

m703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTGCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAAACG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAGGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTTGGAA CAGGTTGTTC CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```


701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
 801 GCGGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

1 MKAKILTSVA LLACSGSLFA QTLATVNGOK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
 201 VGYVPLKDLE QGVPPPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
 251 KVPSEDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGOKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGOKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVNTTVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVNTTVVAQEVKRLKLDRAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
g703	EAYALHIAKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNSREVKVPSEDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703	VYYVNSREVKVPSEDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

1 ATGAAAGCAA AAATCCTGAC TTCGTTGCA CTGCTTGCCT GTTCCGGCAG
 51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CCGTCAGAAA ATCGACAGTT
 101 CCGTCATTGA TGCAGAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
 151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAAACG AAGTGGTCAA
 201 CACCGTGGTC GCACAGGAAG TGAACGCCT GAAACTCGAC CCGTCGGCAG
 251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
 301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGG
 351 CTGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT
 401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
 451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
 501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
 551 TCTTGAAACA ATATCCCTC AACGACCGTA CCAACAGAC CCGTGCGCCG
 601 GTCGGATATG TGCCGCTGAA AGATTGGGAA CAGGGTGTTT CGCCGCTTTA
 651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

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701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
 801 GGCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

a703.pep
 1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
 201 VGYVPLKDLE QGVPPPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
 251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

m703/a703 100.0% identity in 288 aa overlap

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
a703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVNTTVVAQEVKRLKLDLSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
a703	LENEVNTTVVAQEVKRLKLDLSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
a703	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
a703	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNSREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
a703	VYYVNSREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

a704.seq
 1 ATGAAAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA
 51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT
 101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC
 151 AAACAACGCA CCGCCGACGC GCAAAAACC GAGCTGCCG CCCAAGAAAT
 201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG
 251 TGGAAACCCA CGGCGGCACG CGCGAGGCGG TTTTAATGCT CGGCGGCATC
 301 ACCTGCGCCG CCTGCGTCTG GCTGATCGAA CAGCAGCTTT TGCGTACAGA
 351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG
 401 TCTGGGACGA CGGCAAAATC CGCCTTTCCG ACATTCTGTT GAAAATCAGG
 451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCGC
 501 CAACCAAAAA GAACGCAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC
 551 TGGGGATGAT GCAGACGATG ATGTTTCGCGC TGCCGACCTA CCTTTACGGC
 601 GGCGACATCG AACCCGATTT CCTGCAAATC CTCCATTGGG GCGGCTTTTT
 651 AATGGTGCTG CCCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGGCG
 701 CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
 751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA

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801 TGCAGGGCAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851 TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCCGCCGAGA GGCTGGTGAA GCTGATTCTT GCGTTTTGCC ATCATATGCC
951 CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATGTA
1001 AGCGGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCCTTGAC
1051 GGCACGGTGC TGGAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGGCGGC
1201 GGCACGCGAC TGTGCGACAT CGTCCGCTG CTGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCCGTCT TCATCGGCTG GACGCTGTAC
1351 GCCGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCCCTG GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GGCAGCGCAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCTCG CCCAAACCA CACATCATC TTCGACAAA CCGGCACGCT
1551 GACCCAAGGC AAACCGCCG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTCTCGCG GTGGCGCAGG CTTAGAACA ACAGTCCGAA
1651 CATCCCCCTG CCCGCCCAT CCTCAACTGC CGCATTTTCA ACGGCAGCGT
1701 CCCCACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GCGGAAACAC AGGTTTGGGC ATTGGGCAGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAA GAACCGCAA CAGAAGGCGG
1851 CCGCAGCGCG GTTACCTCG GCAGTCAAAG CGGTTTCCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCG CGGAGGCGGT GCGGCAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCCTGGGTGT CGGCACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCG CCGTTTGGC
2151 GCAGGCAGAC GTATCCGCCG CCGCAGCGGG CGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATGTGTGTA TTGAACGAAG ATTTGCGTAC CGTCCCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCCGCCAT ATTATCCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCAAAA CGGGGAAAA TGCAGTCTGA
2451 AAAAATGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```

a704.pep
1 MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAS IIDAGLSY
51 KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLE QQLLRTDGIV RIDLNYSTHR CRVWDDGKI RLSDILLKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMQTM MFALPTYLYG
201 GDIEPDLQI LHWGGFLMVL PVVFCAPVF YQALRDLKN RRVGMDPTPT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPETIPVD
351 GTVLEGSsav NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAELAEQYAS SFI FGELLLA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTTDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPOTEGGSA VYLSQSGFQ AVFYLDQPLK DSAAEAVRQL
651 AGKNLTLHLI SGDRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAAAGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRQLIWAG AYNIIAVPLA VLGYPWPWIA ALGMSFSSLA
801 VLGNALRLHK RGKMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

      10      20      30      40      50      60
m704.pep MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLSYKQRTADAQKT
          |||
a704      MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLSYKQRTADAQKT
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
m704.pep ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLEQQQLLRTDGIV
          |||
a704      ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLEQQQLLRTDGIV
          |||

```

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	70	80	90	100	110	120
m704.pep	130	140	150	160	170	180
a704	RIDLNYSTHRCRVVWDDGKIRLS	DILLKIRQIGYTAAPYDAQKIEA	ANQKQYIVRLA			
	130	140	150	160	170	180
m704.pep	190	200	210	220	230	240
a704	VAGLGMQTMFALPTYLYGGDIEP	DFLQILHWGGFLMVL	PVVFYCAVPF	FYQGALRDLKN		
	190	200	210	220	230	240
m704.pep	250	260	270	280	290	300
a704	RRVGMDTPITVAIIMTFIAGV	YSLATNAGQGM	YFESIAML	LLFFLLGGRFMEHI	ARRKAGD	
	250	260	270	280	290	300
m704.pep	310	320	330	340	350	360
a704	AAERLVKLIPAFCHHMPDYP	DTQETCEAAV	VKLKAGDIV	LVKPGETIP	VDGTVLEGSSAV	
	310	320	330	340	350	360
m704.pep	370	380	390	400	410	420
a704	NESMLTGESLPVAKMPSEK	VTAGTLNTQSP	LIIRTDRTGG	TRL	SHIVRL	LDRALAQKPR
	370	380	390	400	410	420
m704.pep	430	440	450	460	470	480
a704	TAELAEQYASSFIFGELL	LAVPVFIGW	TLYADAHTAL	WITVALL	VITCPCAL	SLATPTAL
	430	440	450	460	470	480
m704.pep	490	500	510	520	530	540
a704	AASTGTLAREGILIGGQ	AIETLAQTTD	IIFDKTG	TLTGKPAV	RRISLL	RGTDEAFVLA
	490	500	510	520	530	540
m704.pep	550	560	570	580	590	600
a704	VAQALEQQSEHPLARAIL	NCRISDGSVP	DIKQRLNR	IGEGVGAQ	LT	VNGETQVWALGR
	550	560	570	580	590	600
m704.pep	610	620	630	640	650	660
a704	ASYVVAEISGKEPQTEG	GSASVYLG	SGSQFQAV	FYLDPLK	DSAAEAVR	QLAGKNLTLHIL
	610	620	630	640	650	660
m704.pep	670	680	690	700	710	720
a704	SGDRETAETAARALG	VAHYRAQAMP	EDKLEYV	KALQKEGK	VLMIGD	GINDAPVLAQAD
	670	680	690	700	710	720
m704.pep	730	740	750	760	770	780
a704	VSAAAAGGTDIARDG	ADIVLLNED	LRTVAHLL	DQARRTR	HHIIRQ	NLIWAGAYNIIAVPLA
	730	740	750	760	770	780
m704.pep	790	800	810	820		
a704	VLGYVQPWIAALGMS	FS	SLAVLG	NALRLH	KRGKMQ	SEKMPSEQX
	790	800	810	820		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2357>:

```

g705.seq
1  GTGTTCAATA ATTTCTtgc CTCTCTGCCG TTTATGACGG AAACACGCGC
51  TGATATGCTC ATCAGCGCGT TTTGGCCCAT GGTAAAGCC GGCTTTACAG
101 TGTCCTTgcC TTGGCGGATC GCTTCTTTTCG TTATCGGCAT GATTATTGCC
151 GTAGCCGTTG CTTTGGTAAG AATCATGCCT TCCGGCGGTA TTTTCCAAAA
201 ATGCTTGTGT AAGCTGGTGG AATTTTATAT TTCCGTCGTT CGCGGTACGC
251 CGCTGTGGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC GTCCGTCGGC
301 ATCTATATCA ATCCGATTCC CGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAC GCTTCCGAAA CCATACGCGC GCGATTTTG TCCGTGCCGA
401 AAGGCGAGTG GGAAGCAGGT TTCTCCATCG GTATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCACC GCAGGCATTC CGCGTCGCGG TTCCGCCGTT
501 GAGCAACGAG TTTATCGGCT TGTTCAAAAA CACCTCGCTT GCCGCCGTGG
551 TAACGGTAAC GGAGCTTTTC CGTGTCGCAC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCTGTCTA TATCGAAGCT GCATTGGTTT ATTGGTGTTC
651 CTGTAAAGTG CTGTTTTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GTTATGTCCG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

```

g705.pep
1  VFNNFLASLP FMTETRADML ISAFWPMVKA GFTVSLPLAI ASFVIGMIIA
51  VAVALVRIMP SGGIFQKCLL KLVEFYISV RGTPLLVLV IVFYGLPSVG
101 IYINPIPAAI IGFSLVNGAY ASETIRAAIL SVPRGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVK LFLIQARLEK RFDYRVAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

```

m705.seq
1  GTGTTCAATA ATTTCTTGC TTCGTCGCCG TTTATGACGG AAACACGCGC
51  CGATATGATT GTCAGCGCGT TTTTGCCATAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGCG GATTATGCCC GCCGGCGGCA TCGTGGCGAA
201 AATCCTGCTG AAATGGTGG AATTTTATAT TTCCGTCAAT CGCGGTACGC
251 CGCTGTGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCCGTGCGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAC GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCTA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TTGTCGCGCC GCAGGCATTC CGCGTTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGTTC
651 TTGTAAAGTG CTGTTCTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

```

m705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLV IVFYGLPSVG
101 IYIDPIPAAI IGFSLVNGAY ASETIRAAIL SVPRGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVK LFLIQARLEK RFDYRVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

```

m705/g705    95.0% identity in 238 aa overlap

          10      20      30      40      50      60
m705.pep    VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
              |||||
g705         VFNNFLASLPFMTETRADMLISAFWPMVKAGFTVSLPLAIASFVIGMIIAVALVRIMP
              |||||

          70      80      90     100     110     120
m705.pep    AGGIVRKILLKLVEFYISVIRGTPPLLVLVIVFYGLPSVGIYIDPIPAIIGFSLVNGAY
              :||| :| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```
a705.seq
1      GTGTTC AATA ATTTCC TTGC TTCGCTGCCG TTTATGACGG AAACACGCCG
51     CGATATGATT GTCAGCGCGT TTTTGCCATAT GGTCAAAGCC GGCTTCGCGG
101    TCTCTCTGCC TTTGGCGGCA GCTTCTTTTCG TTATCGGTAT GATGATTGCG
151    GTAGCCGTTG CTTTGGTGCG GATTATGCCC GCGCGCGGCA TCGTGCGGAA
201    AATCCCTGTG AAATTTGGTG AATTTATAT TTTCCGTGAT CGCGGTACGC
251    CGCTGTTGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCGCTCGGC
301    ATCTATATCG ACCGCAATCC TCGCGGCATC ATCGGCTTTT CGCTCAATGT
351    CGCGGCATAT GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGATACGA
401    AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451    TTCCGCCGCA TCGTGCGCCC CGAGGCATTT CGCGTTCGCC TGCCCGCTTT
501    GAGCAAGCAG TTTATCGGTT TGTTTAAAAA CACTCTGCTC GCGCGCATCG
551    TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601    TATGATATTT TGCCCGCTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGTT
651    TTGTAAAGTT CTGTTCTCTGA TTCAGCGCGC TTTGAAAAA CGTTTCGACC
701    GCTACGTCGC CAAATAA
```

a705.pap

1	VFNNFLASLP	FMETETRADMI	VSAFLPMVKA	GFAVSLPLAA	ASFVIGMMIA
51	VAVALVRMP	AGGIVRKILL	KLVEFYISVI	RGTPLLVLQVL	IVFYGLPSVG
101	<u>IYIDP</u> IPAAI	IGFSLNVGAY	ASETIRAAIL	SVPKGQWEAG	FSIGHTYMQT
151	FRRI VAPQAF	RVAVPPLSNE	FIGLFKNTSL	AAVTVTVEL	RVAQETANRT
201	YDFLEVPYIEA	KLAVYQCFCKV	LFGLIARLEK	RFDRVYAK*	

Homology with a predicted ORF from *N meningitidis*

a705/m705 100.0% identity in 238 aa overlap

	10	20	30	40	50	60
a705.pep	VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP					
m705	VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP					
	10	20	30	40	50	60
a705.pep	AGGIVRKILLKLVEFYISVIRGTPLLVLQLVIVFYGLPSVGIIYDPIAAIIGFSLNVGAY					
m705	AGGIVRKILLKLVEFYISVIRGTPLLVLQLVIVFYGLPSVGIIYDPIAAIIGFSLNVGAY					
	70	80	90	100	110	120
a705.pep	ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL					
m705	ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL					
	130	140	150	160	170	180
a705.pep	AAVVTVTTELFRVAQETANRITYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX					
m705	AAVVTVTTELFRVAQETANRITYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX					
	190	200	210	220	230	239

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq
 1 ATGAACCTCT CGCAACGCAA ACGCCTTTC GgcccGCTGGC TCAACTCCTA
 51 CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCGgaa
 101 ccgTcCTGTT CGCCACCGCA CTCGCCGgc tACTCCACCT CCAacacggc
 151 gAATGGATAG GGATgACCGT CTTGTCGTC CTCGGCATGC TCCAGTTCCA
 201 AGGCGcgatt tActccaacg cgggtGAacg taTGctcggt acggtcatcg
 251 ggCtgGGCGC GGGTTGGGc gTTTTATGGC TGAACCAGCA TTAttccac
 301 ggCaacTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
 351 ctGGGCGCGC GTCGGCAAAA acggctacgt ccttatgctg GCGGGGctgA
 401 CGATGTGTCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
 451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATGCGCGC
 501 CGC CAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
 551 CCGACAACCT GGGCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
 601 AGGCGTATGA CGCGCGAACG TTGGAGCAG AATATGGTCA AAATGCGCCA
 651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCACCTCGCC GCCACATCGG
 701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
 751 CGC AAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCAAGCT
 801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
 851 TCACACTGCT CCAAAACGAC CTGCAACAAA CCGCCGCCCT CATCAACGGC
 901 AGACACGCCC GCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
 951 AGC CCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
 1001 GCA CCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
 1051 ACC CGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAG
 1101 CCTGCTTGA ACACGGGAAC ACGGCTGA

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep
 1 MNS SQRKRLS GRWLNSYERY RHRRLIHAVR LGTVLFATA LARLLHLQHG
 51 EWI GMTVFVV LGMLQFQAI YSNAVERMLG TVIGLGAGLG VLWLNQHYFH
 101 GNLLFYLTIG TASALAGWAA VGKNGYVPLM AGLTMCMLIG DNGSEWLD SG
 151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
 201 RRMTRERLEQ NMVKMRQINA RMVKSRSRLA ATSGESRISP SMMEAMQHAH
 251 RKI VNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTAAALING
 301 RHARRRIDT AINPELEALA EHLHYQWQGF LWLSTNMROE ISALVILLQR
 351 TRRKWLDAHE ROHLRQSILE TREHG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq
 1 ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
 51 CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
 101 CCGTCTCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
 151 GAGTGGATAG GGATGACCGT CTTGTCGTC CTCGGCATGC TCCAGTTTCA
 201 AGGGGCGATT TACTCCAAGG CCGTGGAACG TATGCTCGGC ACGGTCATCG
 251 GGC TGGGCGC GGGTTGGGc GTTTTATGGC TGAACCAGCA TTATTTCAC
 301 GGC AACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
 351 CTGGGCGGGC GTCGGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA
 401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
 451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATGCGCGC
 501 CGC CAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
 551 CCGACAACCT GGGCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
 601 AGGCGCATGA CCGCGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
 651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCATCTCGCC GCCACATCGG
 701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
 751 CGT AAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCAAGCT
 801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
 851 TCACACTGCT CCAAAACGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
 901 AGACACGCCC GCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
 951 AGC CCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
 1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
 1051 ACC CGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAG
 1101 CCTGCTTGA ACACGGGAAC ACGGCTGA

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep
 1 MNT SQRNRLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
 51 EWI GMTVFVV LGMLQFQAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
 101 GNLLFYLTIVG TASALAGWAA VGKNGYVPLM AGLTMCMLIG DNGSEWLD SG
 151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
 201 RRMTRERLEE NMAKMRQINA RMVKSRSRLA ATSGESRISP ANMEAMQHAH
 251 RKI VNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTVALING

1136

301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMQR E ISALVILLQR
 351 TRRKWLDAHE RQHLRQSLLE TREHG*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQRNRLVSRWLN	SYERYRYRRLIHAVRLGGAVLFATASARILLHLQHGEWIGMTVFVV				
g706	MNSSQRKRLSGRWLN	SYERYRHRRLIHAVRLGGTVLFATALARILLHLQHGEWIGMTVFVV				
	10	20	30	40	50	60
	70	80	90	100	110	120
m706.pep	LGMLQFQGAIYSKAVERMLGT	VIGLGAGLGVLWLNQHYFHGNLLFYLT	VTG	TAS	ALAGWAA	
g706	LGMLQFQGAIYSNAVERMLGT	VIGLGAGLGVLWLNQHYFHGNLLFYLT	IGT	TAS	ALAGWAA	
	70	80	90	100	110	120
	130	140	150	160	170	180
m706.pep	VGKNGYVPMLAGLTMCLIGDNGSEWLD	SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR				
g706	VGKNGYVPMLAGLTMCLIGDNGSEWLD	SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR				
	130	140	150	160	170	180
	190	200	210	220	230	240
m706.pep	FMLADNLADCSKMAEISNGRRMT	RERLEENMAKMRQINARMVKS	RSHLAATS	GESRISP		
g706	FMLADNLADCSKMAEISNGRRMT	RERLEQNVMKMRQINARMVKS	RSHLAATS	GESRISP		
	190	200	210	220	230	240
	250	260	270	280	290	300
m706.pep	AMMEAMQHAHRKIVNTTELLLT	TAAKLQSPKLNSEIRLLDRHFTLLQTD	LQQT	VALING		
g706	SMMEAMQHAHRKIVNTTELLLT	TAAKLQSPKLNSEIRLLDRHFTLLQTD	LQQT	AALING		
	250	260	270	280	290	300
	310	320	330	340	350	360
m706.pep	RHARRIRIDTAINPELEALA	EHLHYQWQGF	LWLSTNMQR	EISALVILLQ	TRRKWLDAHE	
g706	RHARRIRIDTAINPELEALA	EHLHYQWQGF	LWLSTNMQR	EISALVILLQ	TRRKWLDAHE	
	310	320	330	340	350	360
	370					
m706.pep	RQHLRQSLLE	TREHG				
g706	RQHLRQSLLE	TREHG				
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

1	ATGAACACCT	CGCAACGCAA	CCGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGCTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGGG
101	CCGTCTGT	CGCCACCGCC	TCCGCCCGGC	TGCTCCACCT	CCAACACGGC
151	GAGTGGATAG	GGATGACCGT	CTTCGTCGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGGTTTGCGC	GTTTATGGC	TGAACCAGCA	TTATTTCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CACTGGCCGG
351	CTGGGCGGCG	GTCGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GCTCATCGGC	GACAACGGCA	GCGAATGGTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCCAAACTG	CTGCCGCTGA	AATCCACACT	GATGTGGCGT	TTCATGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGGCGCATGA	CCCGCGAACG	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGCAG	CCACCTCGCC	GCCACATCGG
701	GCGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCCAC
751	CGTAAAATTG	TCAACACCAC	CGAGCTGCTC	CTGACCACCG	CCGCCAAGCT
801	GCAATCTCCC	AAACTCAACG	GCAGCGAAAT	CCGGCTGCTT	GACCGCCACT
851	TCACACTGCT	CCAAACCGAC	CTGCAACAAA	CCGTCGCCCT	TATCAACGGC


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9 01 AGACACGCC CCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
9 51 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
10 01 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
10 51 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAG
11 01 CCTGCTTGAA ACACGGGAAC ACAGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

```

a706.pep
1  MNTSQRNRLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51 EWIGMTVFVV LGMLQFQGA IYKKAVERMLG TVIGLGAGLG VLWLNQHYFH
1 01 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWFD SG
1 51 LMRAMNVLI GAAIAIAAKL LPLKSTLMWR FMLADNLTDC SKMIAEISNG
2 01 RRMTRERLEE NMAKMRQINA RMVKSRSHLA ATSGESRISP AMMEAMQH AH
2 51 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
3 01 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMROE ISALVILLQR
3 51 TRRKWLDAHE RQHLRQSLE TREHS*

```

a706/m706 99.5% identity in 374 aa overlap

	10	20	30	40	50	60
a706.pep	MNTSQRNRLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG EWIGMTVFVV					
m706	MNTSQRNRLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG EWIGMTVFVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a706.pep	LGMLQFQGA IYKKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
m706	LGMLQFQGA IYKKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
a706.pep	VGKNGYVPM LAGLTMCLIGDNGSEWFD SGLMRAMNVLI GAAIAIAAKL LPLKSTLMWR					
m706	VGKNGYVPM LAGLTMCLIGDNGSEWLD SGLMRAMNVLI GAAIAIAAKL LPLKSTLMWR					
	130	140	150	160	170	180
	190	200	210	220	230	240
a706.pep	FMLADNLTDC SKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRSHLA ATSGESRISP					
m706	FMLADNLADCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRSHLA ATSGESRISP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a706.pep	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD LQQTVALING					
m706	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD LQQTVALING					
	250	260	270	280	290	300
	310	320	330	340	350	360
a706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMROEISALVILLQRTTRRKWLDAHE					
m706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMROEISALVILLQRTTRRKWLDAHE					
	310	320	330	340	350	360
	370					
a706.pep	RQHLRQSLE TREHSX					
m706	RQHLRQSLE TREHGX					
	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

m707.seq

```

1 ATCGAAATTA TTAACGATGC AGAACTTATC CGTTCATGC AGCGTCAGCA
51 GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTTGGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTCTTT
201 TCTTCCTTCT GTGCTCATGA AAGAAACAGC TTTTAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCTGCGGTG GCTACCTCAC TTCCCAAGCT ATTATCCAAC CACAGAATAT
351 GGATTCCGGGA ATTCTGAAAT TACGGGTATC AGCAGCGGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAATTTC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGCCG AGTGTTAAAA
551 CAGATATCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTTACAG
601 ATCAAATGCG AGCAGAATAA ACCCATAACG TTCAGTATCG GTATAGATGA
651 TCGGGCGCGC AAAACGACCG GCAAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTGT TTTATGTTT ATATGGACGC
751 GGTTTGGCGC ACAAACGGA CTTGACTGAT GCCACCGGTA CGGAAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCATTA TTCGGTGCCC GTAAAAAAT
851 GGCCTGTTTC TTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
901 GGCATTCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GCGCGCCGAG CGCATGCTTT GCGTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAAATGAAAT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCGC CTCTGCAGCG TGGGAAGCCG AATTGCCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 GCGGGACCGG CATGCGCCAA AGTATGCCTG CACCGGAAGA AAACGCGCGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGA
1251 CGCAGCCGCC CCATTATTT TAGGCAACA GCAGTTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCCA AGATAAATTG
1351 TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGGG AGCAGAGTCT
1401 TTTCGGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTT
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGCGG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCGG
1551 CTTCAGAGGA GGGCATAAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTG
1601 CCGGCAAGCC GCTTCATAAA CCCAAAGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```

1 MEIINDAELI RSMRQOHID AELLTDANVR FEQPLEKNY VISEDETPCT
51 RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQOIL
101 IVRGYLTSAQ IIQPNMDSG ILKLRSAGE IGDRIYEER DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE OGLENLRLRP SVKTDIQUIP SEEEGKSDLQ
201 IKWQONKPIR FSIGIDDAGG KTKGYQGNV ALSFDNPLGL SDFYVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGHRYHEATE
301 GYSVNYDYG KQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAE LRHRAY LNRWLDGKL SYKRGTMGRQ SMPAPEENG
401 DILPGTSRMK IITASLDAAA PFILGKQOFF YATAIQAWN KPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYQNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGKQ LMGAVVGFRG GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```

1 NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51 GAGCAGGCTA CAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTG GGGAATTCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCAATC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGAAGAAC TCGCTCGTTT GCCGAGTGTT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATTG ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTTCACT ATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NNTAAGCGAT TNGTTTTATG TTTTATATGG ACGCGGTTTG GTGCACAAAA
551 CGGACTTGAC TNGTGCCACC GGTACGGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

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751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAAGTATG CCGCACCTG AAGAAAACGG CCGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACOGCCATTC AAGCTCAATG
1101 GAACAAAACG CCTTTGGTGT CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTCG CGGATTTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
1  XKETAFTKGM CLGSNNLSRL QKAAQILIV RGYLTSQAI QPONMDSGIL
51  KLRVSAGEIG DIRYEEKRD KSAEGSISAF NNXKPLYRNK ILNLRDVEQG
101 LENLRLPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDNGKQ YQSSLAER
251 LWXXXFXXTS VXMKLWTRQ KYIDDAEIE VQRRSAGWE AELRHAYLX
301 RWQLDGKLSY KRGTMGRQSM PAPEENGSGT IPXXSRMKII TAGLDAAAPX
351 MLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

a707/m707 95.3% identity in 486 aa overlap

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a707.pep                                     10      20      30
                                         XKETAFTKGMCLGSNNLSRLQKAAQILIVR
m707                                     |||||
EDETPTCRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQILIVR
      50      60      70      80      90     100

a707.pep      40      50      60      70      80      90
GYLTSQAIQPONMDSGILKLRVSAGEIGDIRYEEKRDKSAEGSISAFNNKXPLYRNKI
|||||
m707      110     120     130     140     150     160
GYLTSQAIQPONMDSGILKLRVSAGEIGDIRYEEKRDGKSAEGSISAFNNKFPYRNKI

a707.pep      100     110     120     130     140     150
LNLRDVEQGLLENLRLPSVKTDIQIIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
|||||
m707      170     180     190     200     210     220
LNLRDVEQGLLENLRLPSVKTDIQIIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT

a707.pep      160     170     180     190     200     210
GKYQGNVALSXDNPGLGLSDXFYVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK
|||||
m707      230     240     250     260     270     280
GKYQGNVALSFDNPGLGLSDLFYVSYGRGLAHTDLTDATGTETESGSRYSVHYSVPVKK

a707.pep      220     230     240     250     260     270
WLFNFHNGHRYHEATEGYSVNYDNGKQYQSSLAERMLWXXXFXXTSVXMKLWTRQTY
|||||
m707      290     300     310     320     330     340
WLFNFHNGHRYHEATEGYSVNYDNGKQYQSSLAERMLWRNRLHKTSGVMKLWTRQTY

a707.pep      280     290     300     310     320     330
KYIDDAEIEVQRRRSAGWEAELRHAYLXRWQLDGKLSYKRGTMGRQSMPEENGSGTII
|||||
m707      350     360     370     380     390     400
KYIDDAEIEVQRRRSAGWEAELRHAYLNRWQLDGKLSYKRGTMGRQSMPEENGSGDIL

```

1140

	340	350	360	370	380	390
a707.pép	PXXSRMKIITAGLDAAAPXMLGKQOFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG					
m707	PGTSRMKIITASLDAAAPFILGKQOFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG					
	410	420	430	440	450	460
	400	410	420	430	440	450
a707.pép	EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK					
m707	EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK					
	470	480	490	500	510	520
	460	470	480			
a707.pép	VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX					
m707	VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX					
	530	540	550	560		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2373>:

g708.seq

```

1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCCTGA AATCGAACCC
201 TAAAAACGAA CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTGTC TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGTGCA GCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2374; ORF 708.ng>:

g708.pép

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSNPKNE LAWLVRAEIY QYLVNDKAO ESFRQALSIR
101 PDSAEINNNY GWFLCGRINR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPFAFKE LARTKMLAGQ LGDADYIFRK
201 YQSRVEVLQA DDLILGWKIA KALGNVQAAY EYEAQLQANF PYSEELQTVL
251 TQO*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2375>:

m708.seq

```

1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGTGGTTTCC TATGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTGTC TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2376; ORF 708>:

m708.pép

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAO ESFRQALSIK
101 PDSAEINNNY GWFLCGRLLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPAPFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

      10      20      30      40      50      60
m708.pep MPFKPSKRISLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
|||||
g708      MPFKPSKRISLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
      10      20      30      40      50      60

      70      80      90     100     110     120
m708.pep DALKSDPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSEINNNYGWFLCGRLLNR
|||||
g708      DALKSNPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSEINNNYGWFLCGRLLNR
      70      80      90     100     110     120

      130     140     150     160     170     180
m708.pep PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE
|||||
g708      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE
      130     140     150     160     170     180

      190     200     210     220     230     240
m708.pep LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNAQAAYEYEAQLQANF
|||||
g708      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNVQAAYEYEAQLQANF
      190     200     210     220     230     240

      250
m708.pep PYSEELQTVLTGQX
|||||
g708      PYSEELQTVLTGQX
      250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAAATATAT GCGCGGTCAG
151 GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTGACAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCGAG TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAO ESFRQXLSIK
101 PDSAEINNNY XWFLCGRLLNR PAESMAYFDK ALADPTYXPX YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPAPFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDPKNELAWLVRAEIQYLKVNDKAQESFRQXLSIKPDSAEINNXYWFLCGRLNR					
m708	DALKSDPKNELAWLVRAEIQYLKVNDKAQESFRQALSIPKPSAEINNXYWFLCGRLNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
m708	PAESMAYFDKALADPTYTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

1	ATGTTTGCTT	TCAAATCCTT	ACTCGATATG	CCGCGCGGTG	AGGCACTTGC
51	CGTCGTGCTC	GCTCTGATTG	CCGCAATGGG	CTATACCATC	ATTTCATTGG
101	AGTGGCTGCC	GCATATGTCC	ATTATTGCCG	CCATCGTCGT	GCTGATTTTG
151	TACGGCTTGG	CGCGCGGTTT	GAAATACAAC	GATATGCAGG	CAGGGATGAT
201	AGGCGCGTTG	AATCAGGCTA	TGGCGCGGCT	TTACCTGTTT	TTCTTCATCG
251	GGCTGATGGT	CAGCGCGCTG	ATGATGAGCG	GCGCGATTCC	GACGCTGATG
301	TATTACGGTT	TCGGGCTGAT	TTCCCGGACT	TATTTTATT	TTCCGCGCTT
351	CGCGCTGTGT	TCCGTCATCG	GCGTGTCCAT	CGGCAGCAGC	CTGACCGCCT
401	GCGCCACTGT	CGCGGTTGCC	TTTATGGGGA	TGGCGGCGGC	GTTTCAGGCC
451	GATATGGCGA	TGACGgcggg	cgcgattgTT	tccggTGTGT	TTTTCGGCGA
501	TAAATGTCC	CCGCTTTCGG	ACACCACGGG	CATTTCGCGG	TCCATCGTCG
551	GTATCGACCT	GTTTGAACAC	ATCAAAAACA	TGATGTACAC	CACCATCCCT
601	CGGTGGCTTA	TCAGCGCGGC	ACTGATGCTT	TGGCTTCTTC	CCAGCGTCGC
651	CGCGCAGGAT	TTGAACAGCG	TCGAATCCTT	CCGCAGCCAG	CTTGAAGCCA
701	CGGGATTGGT	GCACGGCTAT	TCGCTGATTC	CGTTTGCAT	GTTGGTCGTT
751	TTGGCATTGA	TGCGCGTCAA	TGCGGTGGTC	GCCATGCTCT	TTACCGTCAT
801	TGCCGCCGTT	GCCGTAACTG	ATCTGCACAG	CACGCCCGAT	CTGCGTCAGC
851	TCGGCGCGTG	GTTTTATGGC	GGCTACAAAC	TCGAAGGCGA	AGCGTTTAAA
901	GACATTGCCA	AACTGATTTC	GCGCGGCGGC	TTGGAGAGTA	TGTTCTTTAC
951	GCAGACCATC	GTTATCCTCG	GTATGAGTTT	GGGCGGGCTG	CTGTTTGGCG
1001	TCGGTGTGAT	TCCTTCCTTG	CTGGAGGCCG	TCCGTACCTT	CTTGACGAAT
1051	GCCGGACGCG	CGACGTTTCA	CGTTGCCATG	ACTTCGGTCG	GGGTCAATTT
1101	CCTGATTGGA	GAGCAATATT	TGAGCATCCT	GCTTTCGGGA	GAAACGTTCA
1151	AACCCGTTTA	CGACAACTC	GGCCTGCATT	CGTGCAACCT	GTCGCGGACT
1201	CTGGAAGATG	CGGGGACGGT	GATTAACCCG	CTCGTGCCGT	GGAGCGTGTG
1251	CGGCGTATTT	ATCAGCCACG	CCCTTGCGCT	ACCCGTTTGG	GAATATCTGC
1301	CTTATGCCTT	TTTCTGCTAT	TTGAGTTTGG	CTTTAACCCT	GTTATTCGGC
1351	TGGACGGGGC	TGACTTTGAG	CAAAAAATAA		

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

1	MFAFKSLDDM	PRGEALAVVV	ALIAAMGYTI	ISLEWLPHMS	IIAAIVVLIL
51	YGLARGLKYN	DMQAGMIGAL	NOGMGAVYLF	FFIGLMVSAL	MMSGAIPTLM
101	YYGFLGISPT	YFYFSAFALC	SVIGVSISS	LTACATVGVA	FMGMAAFQA
151	DMAMTAGAIV	SGVFFGDKMS	PLSDTTGISA	SIVGIDLFEB	IKNMMYTTIP
201	AWLISAALML	WLLPSVAAQD	LNSVESFRSQ	LEATGLVHGY	SLIPFALLVV
251	LALMRVNAV	AMLETVIAAV	AVTYLHSTPD	LRQLGAWFYG	GYKLEGEAFK
301	DIAKLISRG	LESNFFTQTI	VILGMSLGGL	LFALGVIPSL	LEAVRTFLTN

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
451 WTGLTSLKK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq
1 ATGTTGCTT TCAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51 CGTCTGCTG GCTCTGATTG CCGCGATGGG CTATACCATC ATTTTCATTGG
101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGCGCGGTG AATCAGGGTA TGGGCGCGAT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGACT TATTTTATT TTCTCTCCTT
351 CGCGCTGTGT TCCGTCAATG CCGTGTCCAT CGGCAGCAGC CTGACCACCT
401 GCGCCACTGT CGGCGTTGCC TTTATGGGGA TGGCGCGCGC GTTTCAGGCC
451 GATATGGCGA TGACGGCGGG CGCGATTGTT TCGGGCGCAT TTTTGGCGA
501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCGGCG TCCATCGTCG
551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTCGC
651 CCGCGCAGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTG CGTTTGGCGT GTTGGTCATT
751 TTGGCATTGA TCGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT
801 GGTGTCCGTT GCTGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGCGA AGCGTTTAAA
901 GATGTTGTCA AACTGATTTC GCGCGCGCGT TTGGAAGTA TGTTTTCAC
951 GCAAAACATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTGCGC
1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT
1051 GCGCGACGCG CGACGTTTCA CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTGCGGT GAAACGTTCA
1151 AACCCGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT GATTAACCCG CTCGTACCGT GAGACGTATG
1251 CGGCGTGTTC ATCAGCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCCT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep
1 MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
51 YGLARGLKYN DMQQGMIGAL NQMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGSLIPT YFYFSSFALC SVIGVSIGSS LTTTCATVGA FMGMAAFQA
151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFEH IKNMYYTIP
201 AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DVVKLISRGG LESMFFTQTI VILGMSLGLL LFAFGVIPS LLEAIRTELTN
351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLRSRT
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
451 WTGLTSLKK*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAFKSLDDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
m709.pep	DMQQGMIGALNQMGAIYLF FFIGLMVSALMMSGAIPTLMYYGFGSLISPTYFYFSSFALC					
g709	DMQAGMIGALNQMGAVYLF FFIGLMVSALMMSGAIPTLMYYGFGSLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	SVIGVSIGSSLTTCATVGVAFMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVAFMGMAAFQADMAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SIVGIDLFEHIKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFEHIKNMYYTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

1144

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLFVTVMVAVTYLHSTPDRLQLGAWFYGGYKLEGEAFK					
g709	SLIPFALLVVLALMRVNAVVMVAMLFVIAAVAVTYLHSTPDRLQLGAWFYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESMTFTQITIVILGMSLGGLLFALGVIPSLLEAIRFTLTNAGRATFSVAM					
g709	DIAKLISRGGLESMTFTQITIVILGMSLGGLLFALGVIPSLLEAVRTLTNAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTRTLEDAGTVINPLVPWSVCGVF					
g709	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSCNLSRTLEDAGTVINPLVPWSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKX					
g709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1  ATGTTTCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTNGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTNNTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGGACT TATTTTATT TTTCCGCCTT
351 CCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCACCT
401 GCGCCACTGT CCGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC
451 NANATGGNGN NGNNGNNGN CNNGATTGTN NNGGNCGCAT TTTTNGGCGN
501 CAAAATGTCN CCGCTTCCG ATACGNCGGG CATNTCCGCG TCCATGTGCG
551 GTATCGACCT GTTGAACAC ATCAAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACTGCTAT TCGCTGATTC CGTTTGGCGT GTTGGTCGTT
751 TTGGCATTGA TGCGCGTCAA TGCCGTGGTC GCTATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTNTANA
901 GACATTGCCA AACTCATTTT TCGCGGCGGT TTGAAAGTA TGTTTTTCAC
951 GCAGACCATC GTGATTCTTG GGATGAGCCT TGGCGGGCTG CTGTTTGCAC
1001 TGGGCGCGAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTGAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTGNGGT GAAACGTTCA
1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTT ATCANCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1  MFAFXSLDM PRGEALAVVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMOQGMIGAL NOGMGAIYLF FFIGLMVSAL MMSGAIPTIM
101 YYGFLISPT YFYFSAFALC SVIGVSIGSS LTTCATVGVA XMGXXXAFXA
151 XMXXXXXIV XXAXGXKMS PLSDTXGXA SIVGIDLFEH IKNMMYTTIP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLVV
251 LALMRVNAV VAMLFVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMTFTQI VILGMSLGG LFGALGAIPL LDAVRSFLT N
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST

```


1145

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTSLKK*

a709/m709 91.1% identity in 459 aa overlap

	10	20	30	40	50	60
a709. pep	MFAFXSLDMPRGEALAVVVALIAAMGYTIIXLEWLPHMSIIAAIVVLILYGLARGLKYN					
m709	MFAFXSLDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a709. pep	DMQOGMIGALNQGMGAIYILFFFIGLMVSALMMSGAIPTIMYYGFLISPTYFYFSAFALC					
m709	DMQOGMIGALNQGMGAIYILFFFIGLMVSALMMSGAIPTIMYYGFLISPTYFYFSSFALC					
	70	80	90	100	110	120
	130	140	150	160	170	180
a709. pep	SVIGVSGSSLTTCATVGVAIXMXXXXXAFAXMXXXXXIVXXGXKMSPLSDTXGXA					
m709	SVIGVSGSSLTTCATVGVAIFMGAFAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
	190	200	210	220	230	240
a709. pep	SIVGIDLFEHIKNMYYTTPAWLISXXLMXLPLPSVAAQDLNSVESFRSQLEATGLVHCY					
m709	SIVGIDLFEHIKNMYYTTPAWLISAAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240
	250	260	270	280	290	300
a709. pep	SLIPFALLVVLALMRVNAVVALFTVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAXX					
m709	SLIPFALLVILALMRINAVVALFTVMVAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a709. pep	DIAKLISRGGLSMFFTQTIVILGMSLGGLLFALGAIPSLDAVRSFLTNAGRXTFSVAM					
m709	DVVKLISRGGLSMFFTQTIVILGMSLGGLLFALGVIPSLLEAIRTFLTNAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
a709. pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF					
m709	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
a709. pep	IXHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKKX					
m709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKKX					
	430	440	450	460		

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq

1	ATGGAAACCC	ACGAAAAAAT	CCGCCTGATG	CGCGAATTGA	ATAAATGGTC
51	CCAGGAGGAT	ATGGCGGAAA	AGCTGGCGAT	GTCGGCAGGC	GGGTATGCCA
101	AAATCGAACG	GGGCGAAACG	CAGTTAAATA	TCCCGCGTTT	GGAGCAGTTG
151	GCTCAGATT	TCAAATCGA	TATGTGGGAC	TTGCTCAAAT	CGGGCGGTGG
201	TGGGATGGTG	TTTCAGATTA	ATGAAGGTGA	TAGTGGTGGC	GATATTGCGT
251	TGTATGCGTC	GGGTGATGTT	TCGATGAAAA	TAGAATTTTT	AAAAATGGAG

m710.pcp

a710.seq

a710.pwp

	10	20	30	40	50	60
a710.pep	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
m710	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a710.pep	LLKSGGGMVLQINDVDTNSGEFAIYTAQDASGKAGFVKMELKHCKEMLEHKDKKEIELLR					
m710	LLKSGGGMVFQINEGDSG-GDIALYASGDVSMKIEFLKMELKHCKEMLEQKDKKEIELLR					
	70	80	90	100	110	

```

a710.pep      KLTETVX
               |||||
m710          KLTETVX
               120

```

g711.seq not found

g711.pap not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

m711.seq

```

1 ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAGGC
51 AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
1 01 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
1 51 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
2 01 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
2 51 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
3 01 CCAGCCACCG GCGAGGTATT CGGTTCGCCG CGGAGGTTGG AGACGATTTA
3 51 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
4 01 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
4 51 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
5 01 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
5 51 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
6 01 ATTGTGGGCA AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAATCTA
6 51 CAACAAAAAA GGCATACTT ATCTGACCTT TGCTATAAAA GCACCGGATG
7 01 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
7 51 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
8 01 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACGAGC TTTAAACAGC
8 51 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
9 01 CCCGATAAAG AGCAGAAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
9 51 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
10 01 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
10 51 GACAGCCGTG AGGGGCAGAA TTTGATGAC TCCTACTATG CTTTTTGGCC
11 01 GGATATGCTG CAAAACCCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
11 51 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
12 01 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
12 51 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

m711.pap

```

1 MFAPDLGFAL SLPPKAIEV LESKKVTAES YRNLTAIEIA KVTIARMTD
51 LDMLNDIKTS MVESAKSQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
1 01 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWYDAVGD
1 51 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
2 01 IVGQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFQYNAGRM
2 51 NYRPDLKDYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRDLIDGK
3 01 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
3 51 DSREGQNFDD SYIAFLPDM LQNPHEVIRDN RELIFTARYK GSALWAVLKY
4 01 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

a711.seq

```

1 ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAGGC
51 AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
1 01 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
1 51 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
2 01 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
2 51 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
3 01 CCAGCCACCG GCGAGGTATT CGGTTCGCCG CGGAGGTTGG AGACGATTTA
3 51 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
4 01 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
4 51 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
5 01 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
5 51 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
6 01 ATTGTGGGCA AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAATCTA
6 51 CAACAAAAAA GGCATACTT ATCTGACCTT TGCTATAAAA GCACCGGATG
7 01 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
7 51 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
8 01 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACGAGC TTTAAACAGC
8 51 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG

```

1148

```

901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTTCATGAC TCCTACTATG CTTTTTGGCC
1101 GGATATGCTG CAAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

a711.pep

```

1 MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVTIARMTD
51 LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSlyTTD RGFdynAGRM
251 NYRPDLKDYD RALAHQFAKA EMGGADFkTS FKQLEKEfYE VKQRLDIDGK
301 PDKEQIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

a711/m711 99.8% identity in 431 aa overlap

a711.pep	10	20	30	40	50	60
m711	10	20	30	40	50	60
a711.pep	70	80	90	100	110	120
m711	70	80	90	100	110	120
a711.pep	130	140	150	160	170	180
m711	130	140	150	160	170	180
a711.pep	190	200	210	220	230	240
m711	190	200	210	220	230	240
a711.pep	250	260	270	280	290	300
m711	250	260	270	280	290	300
a711.pep	310	320	330	340	350	360
m711	310	320	330	340	350	360
a711.pep	370	380	390	400	410	420
m711	370	380	390	400	410	420

1149

a711. pep

AKFMAKKKVLKX

m711

|||||

430

1150

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

n712.seq

```

1 ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
51 CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTTCGCCGC
101 AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201 TTTGTTCCGA CAAGGCTCGC TGGCGCATTG GATGGTGCGC CAAGCATTTG
251 CCAACAACCC TTATTTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301 GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTTCCGGCA CGGCCACCGC
351 GCCGGGCGTG GTGGAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451 ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
501 TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551 CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
601 GCGCGTGCCA AAAATGCGGA CATTGCCACG GCCTTGTCCTA AAGTGGCGGG
651 CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751 GGCTGTATCG GCGTATTGGG TATGAGTGGC GCCTTGAGCA CGGCCACCAC
801 CGCTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851 GTCGCGTAGA GCCAACCGGC ATCATCGCCG CAGGTTATGC GGCGGTGTTG
901 GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
951 GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA TACTCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTAAAGAGC GAGATTTTGG ACGTGTGAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GCGCGGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCGCCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GCGCATTTGA
1401 TTTGATTTTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>:

n712.pep

```

1 MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPQKVL MVAPMLTAGI
51 QPALEPVQLF SDAEAADLFG QGSLAHLMVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNAIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301 AFEEDPAKPL NTLEIKGLAV TPDQWPLFA ECNNALYNGL TPLTVVNNRV
351 QIMRAVSTYT KSANNTDDPA LLDITTIRTL DYVRRSVKER IALRFPKDKL
401 SDRLLPKVKS EILDVLKLD QAEIENAEA NKGKLVVVAR QNDPNRVNAI
451 IPADVNLGH VFAGRIDLIL *

```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pap not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```

m713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCCTTTG GGCAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CCGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGCGAGCG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTACT ACATAACCG
851 TGGGCGGCCA TAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCCGCATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAAAGGC GGCAAAAAC AAGCAGAAAC GCGGTGTTT GAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```

m713.pap
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLGSESCV VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTLVDAAKKL AAPWPQIKAV VLKAENNPAL KIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLLVVGAD YSSPPVATLC WSRTDSRCNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLLWVYKD PTMTLHRPKT
251 VVVSADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVLWQPLR
301 VHVIDDEHGI DAVFFLMGRR FMLSRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGRK KGVSHKGKKG GKKQAETAVF E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```

a713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CTGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGCGAGCG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTACT ACATAACCG
851 TGGGCGGCCA TAAACCCGC GACGGCGTAT TGTGGCAACC TGGCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGCATGGA TGGCACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG

```

1152

1101 CAAAAAAGGC GGCAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

a713.pep

```
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTLVDAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLLVVGVD YSSPPVATLC WSRTDSRRNI
201 ERMDIEWDTD NRFSEVTFLL QSHGRSGDSA KHDWKVYKD PTMTLHREPKT
251 VVVSADNLA ALQKQAKQL ADWRLEGFTL TITVGGHKTR DGVWLWQPGQR
301 VHVIDDEHGI DAVFFLMGRR FLSRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGRK KGVSHKGGKG GKQAEAVF E*
```

a713/m713 98.4% identity in 381 aa overlap

	10	20	30	40	50	60
a713.pep	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLSGESCE					
m713	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLSGESCE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a713.pep	VVIDGQIVMTGIIGSQRHGKSKGGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAKKL					
m713	VVIDGQIVMTGIIGSQRHGKSKGSRRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAKKL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a713.pep	AAPWPQIKAVVLKVENNPALDKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLLVVGVD					
m713	AAPWPQIKAVVLKAENNPALDKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLLVVGAD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a713.pep	YSSPPVATLCWSRTDSRRNIERMDIEWDTNRFSEVTFLLAQSHGRSGDSAKHDLKVYKD					
m713	YSSPPVATLCWSRTDSRCNIERMDIEWDTNRFSEVTFLLAQSHGRSGDSAKHDLKVYKD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a713.pep	PTMTLHREKTVVVSADNLAALQKQAKQLADWRLEGFTLTITVGGHKTRDGVWLWQPGQR					
m713	PTMTLHREKTVVVSADNLAALQKQAKQLADWRLEGFTLTITVGGHKTRDGVWLWQPGRL					
	250	260	270	280	290	300
	310	320	330	340	350	360
a713.pep	VHVIDDEHGIDAVFFLMGRRFMLSMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
m713	VHVIDDEHGIDAVFFLMGRRFMLSMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
	310	320	330	340	350	360
	370	380				
a713.pep	KGVSHKGGKGGKQAEAVFEX					
m713	KGVSHKGGKGGKQAEAVFEX					
	370	380				

1153

g714.seq not found yet

g714.pap not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```

m714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGCCTG TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201 CCGTACGGGC AAAAACC GCCGACCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGCTA A

```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```

m714.pep
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVA DA VDP
51  RSAGQMLADW ERLGLDGTG KNRQHRVLAV MAKLN ETGGL SIPYFVRLAE
101 AAGYQIQIDE POPFRAGVNR AGDRLAPQEI MWVWHVNV RG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```

a714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGTCTG TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201 CCGTACGGGC AAAAACC GCCGACCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGATA A

```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```

a714.pep
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVA DA VDP
51  SSAGQMLADW ERLGLDGTG KNRQRRVLAV MAKLN ETGGL SIPYFVRLAE
101 AAGYQIQIDE POPFRAGVNR AGDRLAPQEI MWVWHVNV RG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVA DA VDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVA DA VDPSPSAGQMLADW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLN ETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLN ETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a714.pep	AGDRLAPQEI MWVWHVNV RG GNNRITRFAGISAAGDRLTDYSDAVIESL FNRLKPAHTA					

1154

m714 AGDRLAPQEIMVWHVNVVRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
 130 140 150 160 170 180

a714.pep IRFTYRX

|||||||

m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
 201 GGGTCGCTCG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGGLIP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
 201 GGGTCGCTCG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWLGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGGLIP*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq
 1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
 51 GGCCGCCGGC GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCAAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
 201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
 251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
 301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAKHKT KASKAKARSA

101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

m716.seq
 1 ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCGCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
 201 CAAATGCGGT GCGACCGTAA AAAAAACCA CAAACACACC AAAGCATCTA
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
 301 TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

m716.pep
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
 101 SK*

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50	
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----					
g716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGCASKSAEGSCGASKSAEG					
	10	20	30	40	50	60
	60	70	80	90	100	
m716.pep	-----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
g716	SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

a716.seq
 1 ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCGCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
 201 CAAATGCGGT GCGACCGTAA AAAAAACCA CAAACACACC AAAGCATCTA
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
 301 TCTAAATAA

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

a716.pep
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
 101 SK*

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

g717.seq
 1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC

```

51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCTCTG  CCGCCGCTGC
251  TGTTTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATTC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  GCGGAACACC  TCCGTCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCTT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CGCGCGCCGT  TTTGCGCCGC  CGTCTGCAC  CGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTCCT  GAAAAAATAT  GCGGGCTGG  AACAGCTCGG  CGTTTATTCG
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGTGC  AATCGAAGAA  AACGCCACGC
851  CCGCCGCTT  CTCGGCAACG  GCAGAATCCG  CCGCCGCTT  GCTTGCTTCC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCTCCC  TCCTGCTGCC
951  GGAAAACTAC  CCGCCGCTCC  GGTTTACCGT  CGTATCGTGT  ATGCTGCCG
1001  cgcTGTTTTA  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGCACG  CGCGGCGCGG
1151  CGGTTGCTTG  TGCCGCTCA  TTCTGGTTGT  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCG  TTTATATGCA
1251  CACATTGTTT  TGCTGCTGCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCCctgttt  gccggcgat  GGGCGGCATA  TCTGGCAGGC
1351  TGCACTCTGC  GCCACCGGAA  AAATTGAC  AACTGTTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

g717.pep

```

1  MDTKEILGYA  AGSIGSAVLA  VIILPLLSWY  FPADDIGRIV  LMQTAAGLTV
51  SVLCGLDQAA  YVREYYAAD  KDTLEKTLFL  PLLFSAIA  ALLSRPSLP
101  SEILFSLDDA  AAGIGLVLE  LSFLPIRFL  LVLMEGRAL  AFSSAQLVPK
151  LAILLPLPT  VGLLHFPANT  SVLTAVYALA  NLAAAFLLF  QNRCRLKAVR
201  RAFFSFAVLH  RGLRYGIPLA  LSSLAYWGLA  SADRLFLKXY  AGLEQLGVYS
251  MGISFPGAAL  LLOSIFSTVW  TPYIFRAIEE  NATPARLSAT  AESAAALLAS
301  ALCLTGIFSP  LASLLLPENY  AAVRETUVSC  MLPPLFYTLT  EISGIGLNVV
351  RKTRPIALAT  LGALANLLL  LGLAVPSGGT  RGAAVACAAS  FWLFFVFKTE
401  SSCRLLWQPLK  RLPLYMHTLF  CLASSAAYTC  FGTPANYPLF  AGVWAAYLAG
451  CILRHRKNLH  KLFHYLKKQG  FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

m717.seq

```

1  ATGGACACAA  AAGAAATCCT  CGGCTACGCG  GCAGGCTCGA  TCGGCAGCGC
51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCCCGCCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  GCTGACGGTG
151  TCGGTGTTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACCT  TGTTCAAAAC  CCTGTTCTCTG  CCGCCGCTGC
251  TGTGTCGCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCACT  CGACGATGCC  GCCGCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  AGCGAACACC  GCCGTCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCTT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CACGCACCGT  TTTGCGCCGC  CGTCTGCAC  CGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTCCT  GAAAAAATAT  GCGGCGCTGG  AACAGCTCGG  CGTTTATTCG
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGTTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGCGC  AATCGAAGAA  AACGCCCCGC
851  CCGCCGCTT  CTCGGCAACG  GCAGAATCCG  CCGCCGCTT  GCTTGCTTCC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCTCTCC  TCCTGCTGCC
951  GGAAAACTAC  CCGCGCGTCC  GGTTCATCGT  CGTATCGTGT  ATGCTGCCG
1001  CGCTGTTTTC  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCCGATCGC  GCTCGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTCCCGTC  CGGCGGCGCG  CGCGGCGCGG
1151  CGGTTGCTTG  TGCCGCTCA  TTCTGGCTGT  TTTTGCCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCG  TTTATCTGCA
1251  CACATTGTTT  TGCTGACCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  TCCCCTGTTT  GCGGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCACTCTGC  GCCACCGGAA  AGATTGAC  AACTGTTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

m717.pep
 1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
 51 SVLCGLGDDA YVREYYATAD KDTLFTLFL PPLLSAAAIA ALLSRPSLP
 101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLMEGRAL AFSSAQLVPE
 151 LAILLPLLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
 201 HAPFSPAVLH RGLRYGPIA LSSIAWGLA SADRLFLKY AGLEQLGVYS
 251 MGISFGGAAL LFQSFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLS
 301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
 351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
 401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAAYLAG
 451 CILRHRKDLH KLFHYLKKQG FPL*

m717/g717 96.4% identity in 473 aa overlap

	10	20	30	40	50	60
m717.pep	MDTKEILGYAAGSIGSAVLA VIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCGLGDDA					
g717	MDTKEILGYAAGSIGSAVLA VIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCGLGDDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m717.pep	YVREYYATADKDTLFTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE					
g717	YVREYYAADKDTLFTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m717.pep	LSFLPIRFLLLVLRMEGRALAFSSAQLVPEKLAILLPLTVGLLHFPANTAVLTAVYALA					
g717	LSFLPIRFLLLVLRMEGRALAFSSAQLVPEKLAILLPLTVGLLHFPANTSVLTAVYALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m717.pep	NLAAAFLLFQNRCRLKAVRHAPFSPAVLHRLRYGPIALSSIAWGLASADRLFLKY					
g717	NLAAAFLLFQNRCRLKAVRHAPFSPAVLHRLRYGPIALSSIAWGLASADRLFLKY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m717.pep	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLS					
g717	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m717.pep	ALCLTGIFSPLASLLPENYAAVRFIVVSCMLPPLFCTLA EISGIGLNVVRKTRPIALAT					
g717	ALCLTGIFSPLASLLPENYAAVRFIVVSCMLPPLFCTLA EISGIGLNVVRKTRPIALAT					
	310	320	330	340	350	360
	370	380	390	400	410	420
m717.pep	LGALANLLLGLAVPSGGARGA AVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
g717	LGALANLLLGLAVPSGGARGA AVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
	370	380	390	400	410	420
	430	440	450	460	470	
m717.pep	CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLHLYLKKQGFPLX					
g717	CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLHLYLKKQGFPLX					
	430	440	450	460	470	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

a717.seq
 1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
 51 GGTTTATGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
 101 ACGCATCGG ACGCATCGTG CTGATGCAGA CGGCGCGGG GCTGACGGTG
 151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
 201 CGCCGCGGAC AAAGACACTT TGTTCAAAAC CCTGTTCTG CCGCCGCTGC

1158

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251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTTGCTT CGACGATGCC GCCGCCGGCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTCG
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGCCAAG
451 CTCGCCATCC TGCTGCTGCT GCGCTGACG GTCGGGCTGC TGCACTTTCC
501 GGCGAACACC GCCGTCCTGA CCGCCGTTTA CCGCTGGCA AACCTTGCCG
551 CCGCGCCCTT TTTGCTGTTT CAAAACCGAT GCCGCTGAA GGCCGTCGGG
601 CGCGCACCGT TTTATCCGC CGTCCTGCAT CGCGGCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTTGTTTCT GAAAAAATAT GCCGCTTAG AACAGCTCGG CGTTTATTCG
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTCCGCGC AATCGAAGCA AACGCCCGC
851 CCGCCCGCCT CTCGGCAACG GCAGAATCCG CCGCCGCCCT GCTTGCCCTC
901 GCCCTCTGCC TGACCGGCAT TTTCTGCCC CTCGCTCCC TCCTGCTGCC
951 GGAAACTAC GCCGCCGCTC GGTATATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTG CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCGTCTGCTG CTGGGGCTTG CCGTACCGTC CGGCGGCGCG CGCGGCGCGG
1151 CGGTGCTGCTG TGCCGCTCA TTTGCGCTGT TTTTGTGTTT CAAGACCGAA
1201 AGCTCTGCC GCCTGTGGCA GCCGCTCAA CGCCTGCCG TTTATATGCA
1251 CACATTGTTT GCCTGGCCTT CCTCGGCGGC CTACACCTGC TTCGGCACTC
1301 CGGCAAACTA CCCCCTGTTT GCGGCGGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCACTCTGC GCCACCGGAA AGATTGTCAC AAACGTGTTT ATTATTTGAA
1401 AAAACAAGGT TTCCCATAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

a717.pep

```

1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51 SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PPLLSAAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLEF LSFLPIRFL LVLMEGRAL AFSSAQLVSK
151 LAIIIIIIPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPFSSAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301 ALCTGIFSP IASLLPENY AAVRFIVVSC MLPPLFCTLV EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFVFKTE
401 SSCLRWQPLK RLPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLAG
451 CILHRKDLH KLFHYLKKQG FPL*

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a717/m717 97.9% identity in 473 aa overlap

```

a717.pep      10      20      30      40      50      60
MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
|||||
m717          10      20      30      40      50      60
MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA

a717.pep      70      80      90      100     110     120
YVREYYAAADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLEF
|||||:|||||
m717          70      80      90      100     110     120
YVREYYATADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLEF

a717.pep     130     140     150     160     170     180
LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAIIIIIIPLTVGLLHFPANTAVLTAVYALA
|||||
m717         130     140     150     160     170     180
LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAIIIIIIPLTVGLLHFPANTAVLTAVYALA

a717.pep     190     200     210     220     230     240
NLAAAFLLFQNRCLKAVRRAPFSSAVLHRLRYGIPIALSSIAWGLASADRLFLKKY
|||||:|||||
m717         190     200     210     220     230     240
NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY

a717.pep     250     260     270     280     290     300
AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEANAPPARLSATAESAAALLAS

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|||||
m717      AGLEQLGVYSMGISFSGGAALLFQSIFFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
           250       260       270       280       290       300

           310       320       330       340       350       360
a717.pep  ALCLTGIFSPLASLLL PENYA AAVRFIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
           |||||
m717      ALCLTGIFSPLASLLL PENYA AAVRFIVVSCMLPPLFCTLAISGIGLNVVRKTRPIALAT
           310       320       330       340       350       360

           370       380       390       400       410       420
a717.pep  LGALAANLLLGLAVPSGGARGA AVACA ASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF
           |||||
m717      LGALAANLLLGLAVPSGGARGA AVACA ASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF
           370       380       390       400       410       420

           430       440       450       460       470
a717.pep  CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKL FHYLKKQGFPLX
           ||:|||||
m717      CLTSSAAYTCFGTPANYPLFAGVWAAYLAGCILRHRKDLHKL FHYLKKQGFPLX
           430       440       450       460       470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCCG AGCGTTGTGG CCGCTGGGCT GGGTCGTTCA TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTGTG
251 AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGAGAT GGCCGACTGG
451 TCGGAAAAAT CGGCGGCGCG GCTGATTTTG GGGCAAACGC TGACCAGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCGCGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCTTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTGTA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCGAAAC TGGTGGATGT CGGCGTACAA
751 ATCCCGAAA GCTGGGTGCG CGACAACTG GTCATTCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGTTGAGCC
951 CGATTTCAAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1   SDGLYVPRNF IHRPQSWFKW DKDNGLLLRT RENPEGEALW PLGWVVHTQK
51  SRSVQQARNG LFRILSWLYM FKHYAVHDFE EFLELYGMPY RIGKYGAGAT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLOMADW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRDLIV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKFEFDTRE PKDIAVFADA IPKLVDVGVO
251 IPESWVRDKL VIPDVQEGEA VLVVRQVDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

a718.seq

```

1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACGCCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGGTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGGAAATC GGTCAACACG CCGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CCGACGGA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTGA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

a718.pep

```

1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHFLFADI EERDS DIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEKLSD QAYEMMDSLP TLEDLIMDL DAVGHGFSAL EWEVVFSDGL
151 YLPRNFHHRP QSWFKWDKDN GLLRLTREN EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLLRAVAEI GHNAAGIMPE GMEIELHNA NGMTSAGNPF LQMDWCEKS
301 AARLILQOTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGFFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQGEAVLVR QVPDNPVNR ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAA NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

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a718/m718 98.4% identity in 380 aa overlap

	120	130	140	150	160	170
a718.pep	DSLPTLEDLIMDLMDAVGHGFSALEVEWVSDGLYLPRNFHHRPQSWFKWDKDNGLLLRT					
m718	SDGLYVPRNFHHRPQSWFKWDKDNGLLLRT					
				10	20	30
	180	190	200	210	220	230
a718.pep	RENPEGEALWPLGWVVHTQKRSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
m718	RENPEGEALWPLGWVVHTQKRSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
	40	50	60	70	80	90
	240	250	260	270	280	290
a718.pep	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFQMDADW					
m718	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQMDADW					

1161

	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQ					
m718	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQ					
	160	170	180	190	200	210
a718.pep	360	370	380	390	400	410
	INYPHADPNRVPKFEFDTREPKDIAVFADAI PKLVDVGVIQIPESWVRDKLVIPDVQEGEA					
m718	INYPHADPNRVPKFEFDTREPKDIAVFADAI PKLVDVGVIQIPESWVRDKLVIPDVQEGEA					
	220	230	240	250	260	270
a718.pep	420	430	440	450	460	470
	VLVRQVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	VLVRQVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
	280	290	300	310	320	330
a718.pep	480	490	500	510	520	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	340	350	360	370	380	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTATTA CGCGCCAAAC GATGCGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGGCGACATC CGCGCCAAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAA ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCCGCCC GCCGCGAAAT
301 CGGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGGTACCCG CGAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCTTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCCTG TTCGAGCGGT GCGGGAATC GGTCAACACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCAAG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACG AACGCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTG GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACCT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep

```

1  MEPIMAKNN KTKIQPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHLEFADI EERDSIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEEKLS QAYEMMDSLP TLEDLINDLM DAVGHGFSAL EWEVFSDDL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNRP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRLRAVAEI GHNAAGIMPE GMEIELHNA NGTTATSNPF LQADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

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351 IGPFLQINYP HADPNRVKPF EFDTPREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq

```

1 ATGGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTGCAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAACGCGCG GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCCGGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGGCCTT
451 TACCT'ACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAATATGGG
501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGCGCG GCACCGGGCT TTTCCGACG CTTTCTCTGG TGTATATGTT
651 CAAACACTAC CCGGTCCACG ATTTTGGCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCTGCG TTCGAGCGGT GGCAGAAATC GGTCAACAAC GCGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGCG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCCGCT
1101 GCCGAAATTT GAATTTGACA CGCGCAGGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAG
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGACG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCTTGTG TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep

```

1 MEPIMAKKNN KTKIQKPEAA LOTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHELFAADI EERDSIDIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEEKLSD QAYEMMDSLP TLEDLIMDLN DAVGHGFSAL EVEVWFSDDL
151 YLPRNFIHRP QSWFKWDKDN GLLLTRENTP EGEALWPLGW VVHTQKRSRV
201 QOARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMDWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVKPF EFDTPREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

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a718/m718-1 99.0% identity in 526 aa overlap

	10	20	30	40	50	60
a718.pep	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
m718-1	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
	10	20	30	40	50	60
a718.pep	RAQHELFAADIEERDSIDIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP					
m718-1	RAQHELFAADIEERDSIDIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP					
	70	80	90	100	110	120
a718.pep	RAQHELFAADIEERDSIDIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP					
m718-1	RAQHELFAADIEERDSIDIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP					
	70	80	90	100	110	120
a718.pep	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRENTP					
m718-1	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRENTP					
	130	140	150	160	170	180
a718.pep	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRENTP					
m718-1	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRENTP					
	130	140	150	160	170	180

	190	200	210	220	230	240
a718.pep	EGEALWPLGWVVHTQKSRVQQARNGLFRTLWLYMFKHYAVHDFAEFLELYGMPIRIGK					
m718-1	EGEALWPLGWVVHTQKSRVQQARNGLFRTLWLYMFKHYAVHDFAEFLELYGMPIRIGK					
	190	200	210	220	230	240
	250	260	270	280	290	300
a718.pep	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQADWCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQADWCEKS					
	250	260	270	280	290	300
	310	320	330	340	350	360
a718.pep	AARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
	370	380	390	400	410	420
a718.pep	HADPNRVPKFEFDTREPKDIAVFADAI PKLVDVGVOIPESWVRDKLVIPDVQEGEAVLVR					
m718-1	HADPNRVPKFEFDTREPKDIAVFADAI PKLVDVGVOIPESWVRDKLVIPDVQEGEAVLVR					
	370	380	390	400	410	420
	430	440	450	460	470	480
a718.pep	QVPDPNPVRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAL					
m718-1	QVPDPNPVRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAL					
	430	440	450	460	470	480
	490	500	510	520		
a718.pep	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

```

1  ATGGCAAACG GGAACATGAA ACTGTCGTTG GTGTTAACCG CCCGAGATGA
51  CGGAGCGAGA CGGCTACTGG CTGATACTCA ACGACAATTA GATCGTACCG
101 CGAATCGCGG GCGCAACTT  GAACGGCAAA GCCATACTTA TCGGTTGACC
151 GGCATCCGCT CAGAAAAACA GATTCAACGC GAAATCATGC TGACACAGGC
201 TCGCTTTAAC CGTTTGCGGC GCAGCGGCAA GGCATCACAA AATGATTTGG
251 CACGGGCGGC GGTGCTACG  CGTAACCGAA TTCGCGAGCT GAACGCGGAA
301 CTGAAACAGG GCACGGGATT TGGCGACAAG ATGGGAAAAA TCGGAAGATT
351 CGGTGCAGCT GCGGTGGCTG GTGGCGCGGC AGCGTATACG GTGCTTAAGC
401 CTGCTATGGA CAACAGAAAG CAGCTTGATG AGAACATCAA CCGCGTGTCC
451 AGACAGGCAT TTATTGAGGA TAACAGTAAA TCGGCAGCGT GGATTGCAAC
501 TGAAGGTGCG CAACAGATCA AGGATTTGGC ACTTGAACCT GTCGAGAAAA
551 ATGGCGGGAC CCACGATAAG GCTTTGGATT TAATCAGCGG CATGATGACC
601 ACCGGTCTGA ATTTTGCCCA AACCAAGAAT GAAGCGCAGG CGGCATATGC
651 TTTTGCACCT GCCTCAGAAG GCAGTGGCGA GGATACGGCA AAACCTGATTA
701 AAACCTTGAA AGATGGCGGC ATGAGCGGTA AAGACCTGCA ACTCGGGCTT
751 GAGCACGTCT TGCAATCGGG TTTAGACGGC ACTTTCGAGG TCGGGGATAT
801 GGTTCGGGAG CTGCCGAGCC TGCTCTCTGC CGCGCAACAG GCAGGGATGA
851 ATGTGTGTCG CGGTTTGAC  TACCTGCTCT CACTCTTACA ATCTGCGGCG
901 AATAAATCGG GCAGTCTGCT CGAAGCGGCG ACTAATGTGC AAAATCTTTT
951 GAGTAAAACT CTGTCGCTTG ACACGATAGG TCGTCTGAAG AAGATGGCAA
1001 ATCGAATGA  CCCGAAGAAA GGTGTCGATT GGATAGGCTC GGTGTGCGAA
1051 GGCAAGCAAA ACGGCGAAAA CGCAGTGCAG GTGTTGTCCT GTCTTGCCGA
1101 TGCCATGCTA GTAAAGGATA AGCAATACCA AGATTATAAG AAACGCGCGG
1151 CTGCAGGCGA TAAGACGGCG GCGGAGCAGG CAAATATGCT TAAGGCGCGC
1201 CTTTGGCGC  AACTGCTGCC TGATTGTCAG GCAAAACAAG GTTTGCTGGC
1251 TGCAACGGAT ATGACGCAAA TCCGTGAATA TATGGCTTCG TTGGCTGGCG

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1164

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1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCGGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGCAGG CGGCGTGGCA GCAGGTGCCA CAGCGGCAGG CGGTAAGTTG
1651 CTGTCATGGG GAAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAAG GGTTCGCTG GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAA CAACGGTATC CGATTGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTGGCT GCTCCGTGAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTTTCAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GCGCGAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAAGT
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CGGTATCAAG TGGCCATGTT
2151 CCGCCGTGGA GCGGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

m719.pep

```

1 MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL ERQSHTYALT
51 GIRSEKQIQR EIMLTQAAFN RLARSGKASQ NDLARAATVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPPAMDNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAYAFAL ASEGSGEDTA KLIKTLKDG MSGKDLQLGL
251 EHVLSGLDGF TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLLQSAA
301 NKSGPSAEAA TNVQNLLSKT LSPDTIGRLK KMANPNDPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLDNKG IAKNNEARML
451 SAAQQEQQE SLAMLRSLT GTLVDMETSF KKLAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNPNALVKR AGLLGMLLYS ESLGDGTLPK GLRGTKTTPE
601 MINRLKNNGI RFEPAPKREQ ARGGVPOYLA APSAQPTDKM LSPLFSTQTA
651 AYQAAIQQOT AAYQAALAQD TAAVTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVS RYQVAMFGRG AGQ*

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a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

m720.seq

```

1 ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCGG
51 CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTGTGTCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGCAGG TGCAGATTAA TGCGGTGTTT TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGGCGTGC
251 TGGTGACCCC TGTTGGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTTT GAAAACGCCT
401 TTTTGGTCTG GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTTGTTGA TGCGGTGTTG GCGGTGGATG CGGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTG GAGTGCGGCA TCGGTTACGT
551 TTGGCGCGGT GCGCCGTTTG TTTGATTGGA ACAAAATTGC CTTTCCCGAT
601 CGGGGCGGAT ACGTGCAGC GCGCTTAA AACCAGCTCG CCAAGCTGTT
651 TCGCGATATA TCGGTATGAG TAGATACTGG CATACGCCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGTT GGTCCGCGC ACAGCGGTTT
751 GACGGGGCTG CGGCTGTTGC CGACCGGCC GCGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCAG ACGGCCTGCA AAACCGCCTG AACCAGTTAA

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1165

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851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CGGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTGCGGTGGC AACGGCATT AATCGAGGCGC ATGGCGGAAGA
951 GATGACCGCG CCCGATTGTA TTGAGGTTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGGCGG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
1151 TCATCAACCA AAAGCCGCGC CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTAC GCGGATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
51 GRQVQINAVF WGKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AAEAEIEFVF ENAFLEVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPQRQF
251 DGAAAVADRA AAIPDNLLTG RFSDDLQNLRL NRLTAKQVOP VAQAVRLLST
301 SSLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGLTANAVY TEAYQTAESE RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPHIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
1 GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCGGT
51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GCGGAAGAGA TGACCGCGCC CGATTGTATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
201 ACGGGCGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGCA
301 GGCCGTCTGA ATGCGTTGGT TGCGGCGGTC ATCAACCAAA AGCCGCGGCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGCG GCTCAATCCC
451 CATATCCACC ACCCGCGGTT TATCAAGCGC GGCACCTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
1 GLQNLRLNLT AKQVQPVAQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51 EVNRAMRRRM QAEIAALRAV QTAAESGGL TANAVYTEAY QTAESELRRAA
101 GRNLALVA AV INQKPLIVR QAPIDGTIHQ IAHEFYGDIA RAAELVRLNP
151 HHHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

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250      260      270      280      290      300
m720.pep  SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNLRLNRLTAKQVQPVAQAVRLLSTSSLL
a720      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          10      20      30

310      320      330      340      350      360
m720.pep  SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
a720      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          40      50      60      70      80      90

370      380      390      400      410      420
m720.pep  QTAESELRRAAGRLNALVAAVINQKPLIVRQAPIDGTIHQIAHEFYGDIAARAAELVRLNP
a720      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
          100     110     120     130     140     150

430      440
m720.pep  HHHHPAFIKRGTLVNSYAKX

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a720
|||||
HIHHPAFIKRGTLVNSYAKX
160 170

g721.seq not found

g721.pap not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACGTCT GCCATATGGC GAATTTTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCCG CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCGC AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCCGCGTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA
851 AAGGCGTATT GAAACAGCCG GCGCGCTTGG CATTTTGTAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTCCG TGCACCTGCA GGCTCGCAAA CGGGCGGCAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG
1001 CAAAATGTCT GGGCATGTCC GCGAAGAAT TTGTAAAAAT CAAAGAAAGC
1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>:

m721.pap
1 MSKNAQKILL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAYLLEE
51 NGHDVALLAN SSRNQLVVDY EHQTLYKEKN GQPAPAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEQN PMKELLQOLF DLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTXYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAKGVLRQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACGTCT GCCATATGGC GAATTTTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCCG CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCGC AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCCGCGTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAG
851 AAGGCGTATT GAAACAGCCG GCGCGCTTGG CATTTTGTAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTCCG TGCACCTGCA GGCTCGCAAA CGGGCGGTAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG
1001 CAAAATGTCT GGGCATGTCC GCGAAGAAT TTGTAAAAAT CAAAGAAAGC

1167

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

a721.pep

```

1  MSKNAQKTL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
51  NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQOLF GLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTXYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

```

a721/m721 99.2% identity in 353 aa overlap

	10	20	30	40	50	60
a721.pep	MSKNAQKTLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
m721	MSKNAQKTLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a721.pep	SSRNQLVVDYEHXTLYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
m721	SSRNQLVVDYEHQTLYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a721.pep	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQOLF					
m721	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQOLF					
	130	140	150	160	170	180
	190	200	210	220	230	240
a721.pep	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a721.pep	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAGVLKQPGGLAFLTGFI					
m721	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAGVLKQPGGLAFLTGFI					
	250	260	270	280	290	300
	310	320	330	340	350	
a721.pep	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAAKMLGMSGEEFVKIKESEGGKX					
m721	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAAKMLGMSGEEFVKIKESEGGKX					
	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

m722.seq

```

1  GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51  TACCAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCTT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TCGCGGCTT GAGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGACCTGC AAGTGCATAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG

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1168

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401 AGCCGGGCGC GGCCGCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCGCGCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAACGTGCGC CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTCGACA CCCTGATCCC CGCGCACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

m722.pep

```

1 VFETPTFEQI RERILRDTKS LWPDADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAIV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

a722.seq

```

1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCCG ATGCCGATAT CAGCCCGGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCCGAT
151 CAAAGCTGGA TTGTGCGGCA GATTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCCTCA TCGCGGGCTT GCGCCGCGGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGCGCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGCGC GGCCGCCAAT GTGCGGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCGCGCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAACGTGCGC CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTCGACA CCCTGATCCC CGCGCACGGC
901 CTGACTGTGT CGCAAATCGA GGCGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

a722.pep

```

1 VFETPTFEQI RERILRDTKS LWPDADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAIV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

m723.seq

```
1 ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51 AGTGATCACG CCCGAACACC TTATTTTAC CGTTTACAA CACAATACCG
101 TCTTCGCCCC CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTGTAGC
201 GGTTCGGGAT TTCGTCGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTCG GCAGTGGCGT
351 CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CGGTGCGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTAACCGTTC GCGTATGCCA TTAATCGACC GCCTTGCCTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTGCGGCCA GCCGCCGTC AACAGCAGGC CGCCGCGCCA AAATCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTTT CCAAGGCTGT GGTCAGCATT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTCGGCG GTTTCTGGTT
851 TGTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

m723.pep

```
1 MRPKPRFRRS VIACISVIT PEHLIFTVYK HNTVFARGHF FAIIHAQLH
51 FAFGHSTQQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFSGVHQR GLCDLAVNQP LVVAVGELQD FOLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RVCCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGA AVSA VSGLLLVFAM MTPCFRRRRI
301 RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

m724.map

```
ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
1 -----+-----+-----+-----+-----+-----+ 60
TACTCAAACCTCATTTAACCGCTTTTTTGGCCGTGTTGACGATTTTATAGCCGCTTTGG
a M S L S K L A K K T A Q T A K N I G E T -
CTGCGCGCGGCCTTTCGGGGAAAAATCACGCTGGTGGTGTGCTCCGAGCCGATACAGCGC
61 -----+-----+-----+-----+-----+ 120
GACGCGCGCCGGAAGCCCTTTTGTAGTGCACACCACAGCAGGCTCGGCTATGTCGCG
a L R A A F R G K I T L V V S S E P I Q R -
GTGCAGTTGAGCGGCTTGGCCGACGAAACCCTGCAAGACCTGAACATTTGCAGGAATAC
121 -----+-----+-----+-----+-----+ 180
CACGTCAAACCTCGCGAACCAGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
a V Q L S G L A D E T L Q D L E H L Q E Y -
GGCTTTGCCAGCCATCCGCCCCGACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181 -----+-----+-----+-----+-----+ 240
CCGAAACGGTCCGTAGGCGGGCTGCCGTCGCTTCGCCATCACTATGGCGACCCGCCGTTA
a G F A S H P P D G S E A V V I P L G G N -
```

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241  -----+-----+-----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACACTAACACACGTCGGTCGTGCCGTGCGTAGTGTGGAATTC
a      T S H G V I V C S Q H G S Y R I K N L K -

      CCCGGCGAGACGGCGATTTTAAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301  -----+-----+-----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATTAGTACTCCACGTTTTTAGCTAATTCGTTCCGTTT
a      P G E T A I F N H E G A K I V I K Q G K -

      ATCATTGAGGCCGATTGCGACGTGTACCGGGTTAACTGCAACAATACGAGGTTAATGCG
361  -----+-----+-----+-----+-----+-----+-----+ 420
      TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a      I I E A D C D V Y R V N C K Q Y E V N A -

      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAGTGCAAGTGTGACGGCGCAA
421  -----+-----+-----+-----+-----+-----+-----+ 480
      CCGTGCCCTACGGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACCTGCCGCGTT
a      A T D A K F N A P L V E T S A V L T A Q -

      GGCCAAATCAACGGCAACGGCGGCATGGCCGTCGAGGGCGGCGACGGAGCCACCTTTAGC
481  -----+-----+-----+-----+-----+-----+-----+ 540
      CCGGTTTAGTTGCCGTTGCCGCCGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAATCG
a      G Q I N G N G G M A V E G G D G A T F S -

      GGCGATGTTAACCAACGGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
541  -----+-----+-----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGCCCGCCGTCGAAATTGTGGCTGCCGCTGCACCACCGGCCGTTA
a      G D V N Q T G G S F N T D G D V V A G N -

      ATATCGTTGCCCGAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGGCGGAA
601  -----+-----+-----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCGTGGGCGTATGGCTGTGCTAGCCGCGTTTTGGAATGGCCGCGCTT
a      I S L R Q H P H T D S I G G K T L P A E -

      CCGGCATAG
661  ----- 669
      GGCCGTATC
a      P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglII EcoRI HindIII KpnI NdeI NheI PstI SacI
Sall SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

m724.pep

```

1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSIYRIKNLK
101 PGETAIFNHE GAKIVIKQK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

a724.seq

```

1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAAATCACG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGGCAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAA TCCTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGTACCGG GTTAACTGCA
401 AACAATACGA GGTAAATGCG GCCACGGATG CCAAATTTAA CGCTCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```

1171

```

501 CGGCATGGCC GTCGAGGGCG GCGACGGAGC CACCTTTAGC GGCGATGTTA
551 ACCAAACGGG CGGCAGCTTT AACACCGACG GCGACGTGGT GGCCGGCAAT
601 ATATCGTTGC GCCAGCACCC GCATACCGAC AGCATCGGCG GCAAAACCTT
651 ACCGGCGGAA CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

```

a724.pep
1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQGK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

a724/m724 100.0% identity in 222 aa overlap

	10	20	30	40	50	60
a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a724.pep	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQGK					
m724	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQGK					
	70	80	90	100	110	120
	130	140	150	160	170	180
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
	190	200	210	220		
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

```

m725.seq
1  ATGGTGCGCA CGGTTAAAAG CTACAACGGC GAGGCCGACG ATTTGGCGGG
51  GCAAATCCAT ACGCTGCCTG CGGTTTGGGT AACGTATGGC GGCAGCAAAG
101 TTGAGCCTGC CAGCACCAGC GCGTATGCG GACGTTATCA GGATACCGCC
151 GAATTTGTGG TGATGGTGGC GGCCCGCAAT CTGCGCAACG AGCAGGCGCA
201 GCGGCAAGGC GGCATCGACA GCCCGGAAAT CCGCAGCAAC GATTTAATCC
251 GCGCTGTTTC CCGCTGCTT GACGGCCAGC GGCTCGGTTT TGCCGATAGC
301 CGCGGCTTGG TGCCCAAAGC GGTGCGCGCG ATTGCCAATC ATGTGCTGGT
351 GCAAACGCC GCAGTAAGCA TATATGCGGT TGAGTATGCC ATCCGCTTTA
401 ACACCTGCGG GTTGGAAAT GACCGCTACC CCGAACGCAC CGACAATCCC
451 GACGACCCCA ACCATATCTT TACCAAGTAT CAGGGTACAT TGAGCGAGCC
501 GTGGCCTGAT TTCGAGGGGT TGGACGGCAA AATTACGAC CCGCAATCCG
551 CCGATGAAAT ACCTGTAAAC CTAACCCTTA AGGATAAGCA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

```

m725.pep
1  MVRTVKSING EADDLAQIHL TPAVWVTYG GSKVEPASTG GVCGRYQDTA
51  EFVVMVAARN LRNEQAQRQG GIDSREIGSN DLIRAVRRLD DGQRLGFADS
101 RGLVPKAVRA IANHVLVQNA AVSIYAVEYA IRFNTCGLEN DRYPERTDNP
151 DDPNHIFTKY QGTLSEPWPD FEGLDGKIYD PQSADEIPVN LTLKDKQ*

```

a725.seq not found yet

a725.pep not found yet

g726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

m726.seq

```

1   ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
51  CCCGAAGGC  GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC  GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC  CGCCGCGCCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
201 ATGGAAATC   AGCAAAGCCG CCGCCGCCGC CCGTTTCGCC AAACAAAAAA
251 CCGCTTGGC   ATTCCGCCTC GCGGAAAAGG CGGACGAACT CAAAAACAGC
301 CTCTTGGCGG  GCTATCCCCA AGTGGAAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC  CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCGGATGC
401 TGGCGCAAAT  CGCCGCGCA  AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTATCG  AAAAATCCGC CCGCTGGCT  GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGT  CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CCGATTGGA   CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

m726.pep

```

1   MTIYFKNGFY DDTLGGIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTTPRPSPDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
101 LLAGYPQVEI  DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVLE
151 KVIEKSARLA  VAAGAIIGKR QLEDKLNTI  ETAPGLDALE KEIEEWTINI
201 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

a726.seq

```

1   ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCGGCAT
51  CCCGAAGGC  GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC  GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC  CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
201 ATGGGAAATC  GCGGAAGCCG CTGCCGCCGC CCGTTTCGCC GAACAAAAAA
251 CCGCCACGGC  ATTCCGCCTC GCGGCAAAGG CGGACGAACT CAAAAACAGC
301 CTCTTGGCGG  GCTATCCCCA AGTGGAAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC  CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCGGATGC
401 TGGCGCAAAT  CGCCGCGCA  AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTGTCT  AAAAATCCGC CCGCTGGCC  GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGG  CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CAGGATTGGA  CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

a726.pep

```

1   MTIYFKNGFY DDTLGSIPGE AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTTPRPSEY  HEWDGKKWEI GEAAAAARFA EQKTATAFRL AKADELKNS
101 LLAGYPQVEI  DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVLE
151 KVVEKSARLA  VAAGAIIGKR QLEDKLNTI  ETAPGLDALE KEIEEWTINI
201 G*

```

a726/m726 95.5% identity in 201 aa overlap

	10	20	30	40	50	60
a726.pep	MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPRPSEY					
m726	MTIYFKNGFYDDTLGGIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPRPSPDY					
	10	20	30	40	50	60

1174

```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQYKSAFAKQQAVIDKMERDKAQALLLSAQN
              10      20      30      40      50      60

              70      80      90      100     110     119
a727.pep   YARELEQARAEAKKYEYVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m727      YARELELARAFAAKKYEYVKAHAVGMALAKKQAEVSRLKTE--RDLCKIPFPDSDRNPTGTF
              70      80      90      100     110

              120     130     140
a727.pep   IDGFGHGLQLYKRALGYGNX

m727      RLFSPQIPNFTQIPPX
              120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

```

g728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGTTTGTG TGGCAACCGG
551 ACGGTTCCGG ATTTGATGCG GCGGGGCGCG GGAATAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCGG GGGGATGAAG GCGAACAGTC TTGTGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTT
901 ATTGCAACAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGCGCGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAAGATT TGGAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

```

g728.pep
1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT EVPENPNFAV
51  AKLARLFERNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PFAFVNAEYL
151 YRNDRPFVSN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGCMQ AOVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVGIDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

```

m728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACCG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCTT TGCCGGAACG GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

```

1175

```

501  CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
551  ACGGTTCCGGT ATTTGATGCG GCGGGGCGCG GGAAATCCG GGAAGATGTT
601  TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651  ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
701  AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751  ATGCGGGAAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801  CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851  GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901  ATTGCACAAT CTTCGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951  TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GGCGGGCGGA
1001 TTGTCGCGCA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAAAATT TGGAAAAGA GGTGCCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCCGGC GGCAGGCGCG ACCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

```

m728.pep
1  MEKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFVSU VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRKGIGEDV
201 YEHLGCGYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
251 MRRLMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYLLKNGNLF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

```

          10      20      30      40      50      60
m728.pep  MEKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
          |||
g728      MEKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNNAFVAKLARLFRNA
          10      20      30      40      50      60

          70      80      90      100     110     120
m728.pep  DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV
          |||
g728      DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV
          70      80      90      100     110     120

          130     140     150     160     170     180
m728.pep  WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFVSU VYGGTVHGENYETTGEYRVV
          |||
g728      WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFVSU VYGGTAHGENYETTGEYRVV
          130     140     150     160     170     180

          190     200     210     220     230     240
m728.pep  WQPDGSVFDAAGRGKIGEDVYEHCLGCGYQMAQVYLAKYRDVANDEQKVWDFRKNRIAS
          |||
g728      WQPDGSVFDAAGRGKIGEDVYEHCLGCGYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS
          190     200     210     220     230     240

          250     260     270     280     290     300
m728.pep  DSRNSVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSF EYLLKNGNLF
          |||
g728      DSRDYVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSF EYLLKNGNLF
          250     260     270     280     290     300

          310     320     330     340     350     360
m728.pep  IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR
          |||

```

1176

g728 IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
 310 320 330 340 350 360

m728.pep YAEAAARRSGGRRDLSHX
 |||||
 g728 YAEAAARRSGGRRGLSHX
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

a728.seq
 1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
 51 TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
 101 TTTTGAGCGA TACGGCAACT GAAATCCGA ATGCTTTTGT GCGGAACTT
 151 GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTATCG TGAAGGAATC
 201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
 251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA
 301 GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGAAGAGGT
 351 TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTTT
 401 CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
 451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
 501 TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
 551 TATTTGATGC GTCGGGGCGC GGGAAAATCG GGAAGATGT TTATGAGCAT
 601 TGCCTCGGGT GTTATCAGAT GGCCAGGTA TATTTGGCGA AATATCGGGA
 651 TGTGCGAAT GATGAGCAGA AGGTTGGGA CTTCCGCGAA GAGAGTAACC
 701 GGATTGCGTC GGAATCGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
 751 TTGATGCCCC GAGGGATGAA GGCAACAGT CTTGTGGTCG GCTATGATGC
 801 GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTCGACAAT GGGAAAAAAC
 851 GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
 901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
 951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCCGC
 1001 AAGAGAAACA GGGGACAGA CTGCCTGATT TTCCTTGAA CTTGGAAGAT
 1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
 1101 CGGCAGGCGC GACCTTTCTC ACTGA

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

a728.pep
 1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
 51 ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
 101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
 151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
 201 CLGCQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
 251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKQRQSFYY LKGNLFLIAQ
 301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREKQGDR LPDFPLNLED
 351 LEKEVSRYAE AAARRSGGRR DLSH*

a728 / m728 96.3% identity in 377 aa overlap

	10	20	30	40	50
a728.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA				
m728	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNFVAKLARLFRNA				
	10	20	30	40	50
	60	70	80	90	100
a728.pep	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLLALAVRLSRLKEKAKWFHVTEQEHGEEV				
m728	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLLAIALRLSRLKEKAKWFHVTEQEHGKEV				
	70	80	90	100	110
	120	130	140	150	160
a728.pep	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV				
m728	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV				
	130	140	150	160	170
					180

1177

	180	190	200	210	220	230
a728.pep	WQPDGSVFDASGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVFYQNMRELMPRGMKANSILVVGVDADGLPQKVYWSFDNGKKRQSF EY Y L K N G N L F					
m728	DSRNSVFYQNMRELMPRGMKANSILVVGVDADGLPQKVYWSFDNGKKRQSF EY Y L K N G N L F					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDEKEVSR					
m728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAARRSGGRRDL SHX					
m728	YAEAAARRSGGRRDL SHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

1	AT GAATACTA	CATTGAAAAC	TACCTTGACC	TCTGTTGCAG	CAGCCTTTGC
51	AT TGTCTGCC	TGCACCATGA	TTCCTCAATA	CGAGCAGCCC	AAAGTCGAAG
101	TT GCGGAAAC	CTTCCAAAAC	GACACATCGG	TTTCTTCCAT	CCGCGCGGTT
151	GATTTGGGTT	GGCATGACTA	TTTGGCCGAC	CCGCGCCTGC	AAAAGCTGAT
201	CGACATCGCA	CTCGAGCGCA	ATACCAAGTT	GCGTACAGCC	GTATTGAACA
251	GC GAAATCTA	CCGCAACAA	TACATGATCG	AGCGCAACAA	CCTCCTGCCC
301	AC GCTTGCCG	CCAATGCGAA	CGGCTCGCGC	CAAGGCAGCT	TGAGCGGCGg
351	ca aTGTCAGC	AGCAGCTACA	ATGTCGGACT	GGGTGcGGca	tCTTACGAAC
401	TCGATCTGTT	CgGGCGCGTG	CGCagcaacA	GcgaagcAGC	ACTGcaggGC
451	tATTTTGCCA	GCGTTGCCAA	CcgcGATGCG	GCACATTGa	ttCtGATTGC
501	CACCGTTGCC	AAAGCCTATT	TCAAcgaGcG	TTATGCCGAA	AAAGcgaTgT
551	CT TTGGCGCa	gcGTGTCTTG	AAAACGCGCG	AGGAAACCTA	CAAGCTGTCC
601	GAATTGCGGT	ACAAGGCAGG	CGTGATTTC	GCCGTGCCCC	TGCGCCAGCA
651	GGAAGCCTTG	ATTGAATCTG	CCAAAGCCGA	TTATGCCCAT	GCCGCGCGCa
701	gc CGCGAACA	GGCGCGCAAT	GCCTTGCCAA	CCTTGATTAA	ccGTCCGATA
751	CCCGAagaCC	TGCCCCCGGG	TTTGCCGTTG	GACAagcAGT	TTTTTGTTGA
801	AAAACCTGCCT	GCCGGTTTGA	GTTCCGAAGT	ATTGCTCGAC	CGTCCCAGCA
851	TC CGCGCCCG	CGAACACGCG	CTCAAACAGG	CAAACGCCAA	TATCGGTGCG
901	gc gCGCGCCg	ccTTTTTCCC	GTCCATCCGC	CTGACCGGAA	GCGTCGGTAC
951	GGGTTCTGTC	GAATTGGGCG	GGCTGTTCAA	AAGCGGCACG	GGCGTTTGGG
1001	CGTTGCTGCC	GTCTATTACC	CTGCCGATT	TTACTTGGGG	AACGAACAAG
1051	GC GAACCTTG	ATGTGGCAAA	ACTGCGCCAA	CAGGCACAAA	TTGTGCTTA
1101	TGAATCCGCC	GTCCAATCCG	CCTTTCAAGA	CGTGGCAAAC	GCATTGGCGG
1151	CGCGCGAGCA	GCTGGATAAA	GCCTATGACG	CTTTAAGCAA	ACAAAGCCGC
1201	GCCTCTAAAG	AAGCGTTGCG	CTTGGTCGGA	CTGCGTTACA	AACACGGCGT
1251	ATCCGGCGCG	CTCGATTGTC	TCGATGCGGA	ACGCATCAGC	TATTCGGCGG
1301	AAGGTGCGGC	TTTGTGCGCA	CAACTGACCC	GCGCCGAAAA	CCTTGCCGAT
1351	TTGTACAAGG	CGCTCgacGG	CGGATTGAAA	CGGGATACCC	AAACCGGCAA
1401	ATAA				

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

1	MNTTLKTTLT	SVAAAFALSA	CTMIPQYEQP	KVEVAETFQ	DTSVSSIRAV
51	DLGWHDYFAD	PRLQKLIDIA	LERNTSLRTA	VLNSEIYRKQ	YMIERNLLP
101	TLAANANGSR	QGSLSGGNVS	SSYNVGLGAA	SYELDLFGRV	RSNSEAALQG
151	YFASVANRDA	AHLILIATVA	KAYFNERYAE	KAMSLAQRVL	KTREETYKLS

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201 EL RYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINRPI
251 PE DLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 AR AAFPSIR LTGSVGTGSV ELGGLFKSGT GVWAFAPSIT LPIFTWGTNK
351 AN LDVAKLRQ QAQIVAYESA VQSAFQDVAN ALAAREQLDK AYDALSKQSR
401 AS KEALRLVG LRYKHGVSGA LDLLDAERIS YSAEGAALSA QLTRAENLAD
451 LY KALDGLK RDTQTK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2465>:

```

m729.seq
1 ATGGATACTA CATTGAAAAC CACCTTGACT TCTGTTGCAG CAGCCTTTGC
51 ATTGTCTGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGCGCCGTC
151 GATTTAGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAAGTT GCGTACCGCC GTATTGAACA
251 GC GAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCCTGCCC
301 AC GCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
351 CAATGTAAAGC AGCAGCTACA AAGTCGGACT GGGTGCGGCA TCTTACGAAC
401 TC GATCTGTT CGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTGCCA GCACCGCCAA CCGCGATGCG GCACATTGA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTACGCCGAA GAAGCGATGT
551 CT TGGCGCA ACGTGT TTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTACGTT ACAAGGCAGG CGTGATTTCC GCCGTCGCCC TACGTCAGCA
651 GGAAGCCCTG ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA
701 GCCGCGAACA GCGCGCAAT GCCTTGCAA CCTTGATTAA CCAACCGATA
751 CCCGAAGACC TGCCTGCCGG TTTGCCGCTG GACAAGCAGT TTTTGTGTA
801 AAAACTGCCG GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAACAGG CAAACGCCAA TATCGGTGCG
901 GCACGCGCCG CCTTTTCC ATCCATCCGC CTGACCGGAA CCGTCCGTAC
951 GGGTTCTGCG GAATTGGGTG GGTTGTTCAA AAGCGGCACG GGCCTTGGT
1001 CGTTCGCGCC GTCTATTACC CTGCCGATT TTACCTGGGG TACGAACAAG
1051 CGGAACCTTG ATGTAGCCAA GCTGCGCCAA CAGGTACAAA TCGTTGCCA
1101 TGAATCCGCC GTCCAATCCG CATTTCAGA CGTGGCAAAC GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG CTTGGTCGGC CTGCGTTACA AGCACGGCGT
1251 ATCCGCGCGG CTCGACTTGC TCGATCGGGA ACGCAGCAGC TATGCGGCGG
1301 AGGGTGCGGC TTTGTCGGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2466; ORF 729>:

```

m729.pep
1 MDTTLKTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
51 DLGWHDYFAD PRLQKLIDIA LERNLSLRTA VLNSEIYRQ YMIERNLLP
101 TLAANANDSR QGSLSGNV SSVKVLGAA SYELDLFGRV RSSSEALQG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRLV KTREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PEDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGTVGTGSA ELGGLFKSGT GVWSFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QVQIVAYESA VQSAFQDVAN ALAAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSGA LDLLDAERSS YAAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*

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Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 729 shows 95.7% identity over a 467 aa overlap with a predicted ORF (ORF729.a) from *N. gonorrhoeae*:

m729 / g729 95.7% identity in 467 aa overlap

```

          10      20      30      40      50      60
m729.pep  MDTTLKTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDYFAD
          1:|||||:|||||:|||||:|||||:|||||:|||||:
g729      MNTTLKTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTSVSSIRAV DLGWHDYFAD
          10      20      30      40      50      60

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	70	80	90	100	110	120
m729.pep	PRLOKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANDSRQGSLSGGNVS					
g729	PRLOKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANGSRQGSLSGGNVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m729.pep	SSYKVGLGAASYELDLFGRVRSSEAAALQGYFASTANRDAAHLSLIATVAKAYFNERYAE					
g729	SSYNVGLGAASYELDLFGRVRSNSEAAALQGYFASVANRDAAHLILIATVAKAYFNERYAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m729.pep	EAMSLAQRVLKTRREETYKLSELRYKAGVISAVALRQOEALIESAKADYAAHAARSREQARN					
g729	KAMSLAQRVLKTRREETYKLSELRYKAGVISAVALRQOEALIESAKADYAAHAARSREQARN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m729.pep	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
g729	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m729.pep	ARAAFFPSIRLTGTGTGSAELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLRQ					
g729	ARAAFFPSIRLTGSGVTGSGVELGGLFKSGTGVWAFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
m729.pep	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
g729	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
	370	380	390	400	410	420
	430	440	450	460		
m729.pep	LDLLDAERSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	LDLLDAERISYAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQGX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

1	ATGGATACTA	CATTGAAAAC	CACCTTGACT	TCTGTTGCAG	CAGCCTTCGC
51	ATTATCCGCC	TGCACCATGA	TTCCCAATA	CGAGCAGCCC	AAAGTCGAAG
101	TTGCCGAAAC	GTTCAAAAAC	GATACCGCCG	ACAGCGGCAT	CCGTGCGGTC
151	GATTTGGGTT	GGCATGACTA	TTTTGCCGAC	CCGCGCCTGC	AAAAGCTGAT
201	CGACATCGCA	CTCGAGCGCA	ATACCAGTTT	GCGTACCGCC	GTATTGAACA
251	GCGAAATCTA	CCGCAACAA	TACATGATTG	AGCGCAACAA	CCTCCTGCCC
301	ACGCTTGCCG	CCAATGCGAA	CGACTCGCGC	CAAGGCAGCT	TGAGCGGCGG
351	CAATGTAAGC	AGCAGCTACA	AAGTCGGACT	GGGTGCGGCA	TCTTACGAAC
401	TCGATCTGTT	CGGGCGTGTA	CGCAGCAGCA	GCGAGGCGGC	ACTGCAAGGC
451	TATTTGCGCA	GCACCGCCAA	CCGCGATGCG	GCACATTTGA	GCCTGATTGC
501	CACCGTTGCC	AAAGCCTATT	TCAACGAACG	TTATGCCGAA	GAAGCGATGT
551	CTTTGGCGCA	ACGTGTTTTG	AAAACGCGCG	AGGAAACCTA	CAAGCTGTCC
601	GAATTACGTT	ACAAGGCAGG	CGTGATTTC	GCCGTCGCCC	TACGTCAGCA
651	GGAAGCCCTA	ATCGAATCTG	CCAAAGCCGA	TTATGCCCAT	GCCGCGCGCA
701	GCCGCGAACA	GGCGCGCAAT	GCCTTGCGAA	CCCTGATTAA	CCAACCGATA
751	CCCGACGACC	TGCCCGCCGG	TTGCCGTTG	GACAAGCAGT	TTTTTGTTGA
801	GAAGCTGCCG	GCCGTTTGA	GTTCCGAAGT	ATTGCTCGAC	CGTCCCGATA
851	TCCGTGCTGC	CGAACACGCG	CTCAAACAGG	CAAACGCCAA	TATCGGTGCG
901	GCACGCGCCG	CCTTTTTC	ATCCATCCGC	CTGACCGGAA	GCGTCGATAC
951	GCATTCTGCC	GAATTGGGCG	GGCTGTTCAA	AAGCGGCACC	GGCGTTTGGT
1001	TGTTGCGACC	TTCCATTACC	CTGCCGATTT	TTACCTGGGG	TACGAACAAG

1180

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1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTTCAAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGATAAA GCCTATGACG CTTTAAGCAA ACAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

a729.pep

```

1 MDTTLKTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
51 DLGWHDFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANDSR QGSLSGGNVS SSYKVG LGAA SYELDLFGRV RSSSEALQG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PDDLPA GLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSGA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*

```

a729 / m729 98.1% identity in 467 aa overlap

a729.pep	MDTTLKTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDFAD
m729	MDTTLKTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDFAD
a729.pep	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS
m729	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS
a729.pep	SSYKVG LGAA SYELDLFGRV RSSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE
m729	SSYKVG LGAA SYELDLFGRV RSSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE
a729.pep	EAMSLAQRVLK TREETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN
m729	EAMSLAQRVLK TREETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN
a729.pep	ALATLINQPI PDDLPA GLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
m729	ALATLINQPI PEDLPA GLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
a729.pep	ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK ANLDVAKLRQ
m729	ARAAFFPSIR LTGTGTGS AELGGLFKSGT GVWSFAPSIT LPIFTWGTNK ANLDVAKLRQ
a729.pep	QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR ASKEALRLVGLRYKHGVSGA
m729	VQIVAYESA VQSAFQDVAN ALAAREQLDK AYDALSKQSR ASKEALRLVGLRYKHGVSGA

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          430      440      450      460
a729.pep  LDLLDAERSSSYSAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX
          |||||
m729      LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

```

g730.seq
1  GTGAAACCGC TGCGCAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
51  GCGCGTCGCA CTCATACAGC CCGCCCTCGC GCGGCACTTG GCGCAAGACC
101 CGTTTCATTAC CGATAACACC CAACGGCAGC ACTACGAACC CCGCGGCAAA
151 TACCACCTCT TCGGCGaCCC GCGCGGCAGC GTTTCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCACCA GATGGGCAAC CTGCTCATCC
251 AACAGCGCGC AATCCAAGGC AATCTTGGTT ACACCGTCCG CTTTTCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCGC CCGACAGCGC
351 AAGCGAAGAA AAAGGCAACG TTGACGACGG CTTTACCGTG TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCGCGCG ATGCCTACGA CGGCCGGAAG
451 GCGCGCAATT ACCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CAATCCGACC GACACCGCA
551 GCATCCGGCA ACGCATATTC GACAACTACA ACAACCTCGG CAGCAATTTT
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TGTCAACGGC GTCGCCGCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCGA TCGCAACAT
801 CGCCCCCTTA CCCGCGGAGG GCAAATTCGC CGCCATCGGC GGCTTGGGCA
851 GCGCGGCGGG CTTTGAAAAA AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAACC CCAATGCCGC CGAAACCGTC GAAGCCCTGG TCAACGTCCT
951 GCCGTTTGCC AAAGTCAAAA ACCTGACAAA GGCGGCAAAA CCGGGGAAGG
1001 CTGCGGTTAG TGGGGATTTT TCTAAATCCT ACACCTGCTC CTTCCACGGC
1051 AGCACCTTGG TCAAAACGGC AGACGGCTAC AAAGCCATTG CCCATATTCA
1101 AGCCGGAGAC CGCGTCCTTT CCAAGGACGA GGCAAGCGGA GAAACGGGAT
1151 ACAAAACCGT TACCGCCCGA TACGGCAATC CGTATCAAGA AACCGTTTAC
1201 ATTGAAGTTT CAGACGGCAT CCGCAACAGC CAAACCTGA TTTCCAACCG
1251 CATCCACCCG TTTTATTCGG ACGGCAAATG GATTAAAGCG GAAGATTTAA
1301 AAGCGGGAAG CCGGTGTTA TCCGAAAGCG GCAAAACCCA AACCGTCCGC
1351 AACATCGTTG TCAAACCAA ACCGCTCAA GCCTACAATC TGACCGTTGC
1401 CGATTGGCAT ACCTACTTCG TCAAGGGTAA TCAGGCGGAA ACGGAAGGGG
1451 TTTGGGTTCA TAATGATTGT CCGCCTAAAC CAAAACCAAC CAATCATGCC
1501 CAACAAAGAA AAGAAGAAGC TAAAAACGAT TCTCATCGAA GTGTGGGAGA
1551 TTCCAATCGT GTCGTTGCGG AAGGAAAGCA ATATTAGAT TCCGACACAG
1601 GAAACCATGT TTATGTAAAA GGAGATAAAG TGGTTATTCT AACTCCTGAT
1651 GGAAGACAGG TAACTCAATT TAAGAACTCG AAAGCCAATA CGTCAAAAG
1701 GGTAAAAAAT GGGAAATGGA CACCAAAATA A

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This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

```

g730.pep
1  VKPLRRLTNL LAACAVAAVA LIQPALAADI AQDPFITDNT QRQHYEPGGK
51  YHLFGDPRGS VSDRTGKINV IQDYTHOMGN LLIQQAIIQG NLGYTVRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDDGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIF DNYNNLGSNF
201 SDRADEANRK MFEHNAKLDR WGNMSEFVNG VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFFAIG GLGSAAGFEK NTREAVDRWI
301 QENPNAAETV EALVNVLPFA KVKNLTKAAK PGKAAVSGDF SKSYTCSFHG
351 STLVKTADGY KAIAHQAGD RVLSKDEASG ETGYKPVTA R YGNPYQETVY
401 IEVSDGIGNS QTLISNRIHP FYS DGKWIKA EDLKAGSRLL SESGKTQTVR
451 NIVVKPKPLK AYNLTVADWH TYFVKGNQAE TEGVWVHND C PPKPKPTNHA
501 QQRKEEAKND SHRSVGDSNR VVREGKQYLD SDTGNHVYVK GDKVVILTPD
551 GRQVTQFKNS KANTSKRVKN GKWTPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

```

m730.seq
1  GTGAAACCGC TGCGCAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
51  GCGCGCCGCA CTCATACAGC CCGCCCTCGC GCGGCACTTG GCGCAAGACC

```

g730 / m730 93.0% identity in 344 aa overlap

m730.pcp						
1	VKPLRRLTNL	LAACAVAAAA	LIQPALAADL	AQDPFITDNA	QRQHYEPGGK	
51	YHLFGDPRGS	VSDRTGKINV	IQDYTHOMGN	LLIQQANING	TIGYHTRFSG	
101	HGHEEHAPFD	NHAADSASEE	KGNVDEGFTV	YRLNWEGHEH	HPADAYDGPK	
151	GGNYPKPTGA	RDEYTYHVNG	TARSIKLNPT	DTRSIRQRIS	DNYSNLGSNF	
201	SDRADEANRK	MFEHNAKLDR	WGNSMEFING	VAAGALNPFI	SAGEALGIGD	
251	ILYGTRYAID	KAAMRNIAPL	PAEGKFAVIG	GLGSVAGFEK	NTREAVDRWI	
301	QENPNAAEV	EAVFNVAAAA	KVAKLAKAAK	PGKAAVSGDF	ADSYKKKLAL	
351	SDSARQLYQN	AKYREALDHI	YEDLIRRKTD	GSSKFINGRE	IDAVTNDALI	
401	QAKRTISAI	KPKNFLNQKN	RKQIKATIEA	ANQQGKRAEF	WFKYGVHSQV	
451	KSYIESKGGI	VKTGLGD*				

g730 / m730 93.0% identity in 344 aa overlap

	10	20	30	40	50	60
g730.pep	<u>VKPLRRRLTNLLAACAVAAVALIQPALA</u> ADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS					
m730	<u>VKPLRRRLTNLLAACAVAAAALIQPALA</u> ADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
g730.pep	VSDRTGKINVIQDYTHQMGNLLIQAAAIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
	130	140	150	160	170	180
g730.pep	KGNVDDGFTFYRLNWEHGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTFYRLNWEHGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g730.pep	DTRSIRQRIFDNYNNLGSNFSDDRADEANRKMFEHNAKLDRWGSMEFVNGVAAGALNPFI					
m730	DTRSIRQRI SDNYSNLGSNFSDDRADEANRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
	190	200	210	220	230	240

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	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAKAPGKAAVSGDFSYSYTCFSHGSLVKTADGY					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVATARYGNPYQETVYIEVSDGIGNSTLISNRIHP					
m730	AKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNFNLQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1  GTGAAACCGC  TCGGAAGACT  CATCAAGCTC  CTTGCCGCCT  GTGCCGTAGC
51  GCGGCGCCGA  CTCATACAGC  CCGCCCTCGC  GCGGCGACTG  GCGCAAGACC
101 CGTTCATTAC  CGATAACGCC  CAACGGCAGC  ACTACGAACC  CGGAGGCAAA
151 TACCACCTCT  TCGGCGACCC  GCGCGGCAGC  GTCTCCGACC  GCACCGGTCA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCG  GATGGGCAAC  CTGCTCATCC
251 AGCAGGCAAA  CATCAACGGC  ACAATCGGCT  ACCACACCCG  CTTTTCGGGA
301 CACGGATACG  AAGAACACGC  CCCCTTCGAC  AACCACGCGG  CCGACAGCGC
351 GAGCGAAGAA  AAAGGCAACG  TTGACGAAGG  CTTTACCGTA  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCGCGCG  ATGCCTACGA  CGGCCCGAAG
451 GCGGCGCAAT  ACCCAAACCC  TACGGGTGCA  CGCGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCAGGCA  GCATCAAAC  CAATCCGACC  GACACCGGCA
551 GCATCCGGCA  ACGCATATCC  GACAATTACA  GCAACCTCGG  CAGCAATTTT
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTTCGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TATCAACGGC  GTCGCGCGCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCAA  TGCACAACAT
801 CGCCCCCTTG  CCCGCCGAGG  GCAAATTCGC  CGTCATCGGC  GGCTTGGGCA
851 GCGTGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTTGA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GGCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTAG  CGGGGATTTT  TCTGCTGCAT  ACAATACAAG  AACAACTAGA
1051 AAAGTTACTA  CAGAAACAGA  GGGGTAAAT  AGAATCAGAC  AGAACCAGAA
1101 AAATAGTAAT  ATACATGAGA  AAAATTATGG  AAGAGATAAT  CCTAATCATA
1151 TTAATGTTTT  ATCTGGAAAT  TCTATACAAC  ATATACTGTA  TGGAGATGAA
1201 GCAGGAGGTG  GGCATCTTTT  TCCTGGCAAA  CCTGGTAAGA  CAACATTCCC
1251 CCAACATTGG  TCAGCCAGTA  AAATAACTCA  TGAAATTAGT  GATATCGTTA
1301 CATCCCCAAA  AACGCAATGG  TATGCACAGA  CTGGAACAGG  CGGCAAATAT
1351 ATTGCTAAAG  GAAGACCAGC  TAGGTGGGTA  TCATATGAAA  CGAGAGATGG
1401 AATTCTGATC  AGAACAGTTT  ATGAACCTGC  AACAGGAAAA  GTGGTAAGTG
1451 CATTCCCCGA  TAGAACCTCT  AATCCCAAAT  ATAACCCTGT  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1  VKPLRLRIKL  LAACAVAAAA  LIQPALAADL  AQDPFITDNA  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGQINV  IQDYTHRMGN  LLIQANING  TIGYHTRFSG
101 HGYEEHAPFD  NHAADSASEE  KGNVDEGFTV  YRLNWEGHEH  HPADAYDGPK
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIS  DNYSNLGSNF
201 SDRADANRK  MFEHNAKLDR  WGNMSEFING  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAVIG  GLGSAAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVNLTAKA  PGKAAVSGDF  SAAYNTRTTR
351 KVTTETEGLN  RIRQNQKNSN  IHEKNYGRDN  PNHINVLSGN  SIQHILYGE
401 AGGGHLFPGK  PGKTTFPQHW  SASKITHEIS  DIVTSPKTQW  YAQGTGGKY
451 IAKGRPARVW  SYETRDGIRI  RTVYEPATGK  VVTAFPDRTS  NPKYNPVK*

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	10	20	30	40	50	60
a730 . pep	VKPLRRLRIKLAAACAVAAAALIQPALAADLAQDPFITDNAQRQHYPGGKYHLFGDPRGS					
m730	VKPLRRLTNLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYPGGKYHLFGDPRGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a730 . pep	VSDRTGQINVIQDYTHRMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a730 . pep	KGNVDEGFVTYRLNWEGHEHHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFVTYRLNWEGHEHHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
	190	200	210	220	230	240
a730 . pep	DTRSIRQIRISDNYSNLGSNFSDDRADEANRKMEHNAKLDRWGNSMEFINGVAAGALNPFI					
m730	DTRSIRQIRISDNYSNLGSNFSDDRADEANRKMEHNAKLDRWGNSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a730 . pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFVAVIGGLGSVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFVAVIGGLGSVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a730 . pep	QENPNAAETVEALVNVLFPFAKVKNLTAKAPGKAASVGDFSAAYNTRTTTKVTTETEGLN					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAPGKAASVGDFADSY-----KKKLALSARSAR					
	310	320	330	340	350	
	370	380	390	400	410	420
a730 . pep	RIRQNQKNSNIHEKNYGRDNPNNHINVLSGNSIQHILYGEAGGGHLFPKGPGKTTFPQHW					
m730	QLYQNAKYREALDIHYEDLIRRKTGSSSKFINGREIDAFTNDALIQAKRTISAIDKPKNF					
	360	370	380	390	400	410

```
g731.seq
1   gatttttcgag  cgttttcatG  CGAGAACGGT  TTGTCTGTGC  GCGTCCGCAA
51  TTTGGACGGC  GGCAAAATCG  CGTTGCGGCT  GGACGGCAGG  CGTGCCGTCC
101 TCTCTTCCGA  CGTTGCCGCA  TCCGGCGAAC  GCTATACCGC  CGAACACGGT
151 TTGTTCCGAA  ACGGAACCGA  GTGGCACCAG  AAAGCGGCGC  AAGCCTTTT
201 CGGCTTTACC  GATGCCTACG  GCAATTCGGT  CGAAACTTCC  TGCCGCGCCC
251 GTTAA
```

g731.pap
1 DFRFSCENG LSVVRNLDG GKIALRLDGR RAVLSSDVAA SGERYTAEHG
51 LFGNGTEWHO KGGEAFFGFT DAYGNSVETS CRAR*

```
m731.seq
1  ATGAATATCA  GGTTTTTCGC  GCTGACCGTA  CCGGTTTTGT  CTTTGGCGGC
51  CTGTGCCGTG  CCGGAGGCGT  ATGATGACGG  CGGAGCGGGG  CATATGCCGC
101 CCGTTCAAAA  CCAAGCCGGC  ACGGACGATT  TTCGGGCGTT  TTCCTGCGAG
151 AACGGTTTGT  CTGTGCGCGT  CCGCATATTG  GACGAGCGCA  AAGTCGCGTT
201 GCGCGCTGGC  GGCAGGCGTG  CGCTCCTCTC  TTACGACGTT  GCCGCATCCG
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251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
 301 CACCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

m731.pep
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSCE
 51 NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

g731/m731 95.2% identity in 84 aa overlap

g731.pep				10	20	30
				DFRAFSCENGLSVRVRNLDGGKIALRLDGR		
m731	L	S	L	A	A	C
	20	30	40	50	60	70
g731.pep		40	50	60	70	80
		RAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX				
m731		RAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX				
	80	90	100	110	120	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

a731.seq
 1 ATGAATATCA GGTTCCTCGC GCTGACCGTA CCGGTTTGT CTTGGCGGC
 51 CTGTGCCGTG CCGGAGCGCT ATGATGACGG CGGACGAGGG CATATGCCGC
 101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCCTGCGAG
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTTG GACGGCGGCA GAATCGCGTT
 201 GCGTTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGG AACCGAGTGG
 301 CATCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

a731.pep
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSCE
 51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

a731/m731 94.4% identity in 126 aa overlap

a731.pep		10	20	30	40	50	60
		MNIRFFALTVPVL	SLAACAVPEAYDDGGRGHMPPVQNQAGTAD	DFRAFSCENGLSVHVRRL			
m731		MNIRFFALTVPVL	SLAACAVPEAYDDGGRGHMPPVQNQAGTDD	DFRAFSCENGLSVRVRHL			
		10	20	30	40	50	60
a731.pep		70	80	90	100	110	120
		DGGRIALRLDGRRAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE					
m731		DSGKVALRLDGRRAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE					
		70	80	90	100	110	120
a731.pep	TSCRARX						
m731	TSCRARX						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

g732.seq
 1 ATGTCGAAAC CTGTTTTTAA GAAATCGCA CTTTATACTT TGGGTGCAAT
 51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGTTTTGCC GCCGagaagg
 101 ACGGgcgGGA TAACGAagtc CTGCCGGTGC AATCCATCCG TACGATGGCG

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151 GAGGTTTACG GTCAGATTAA GGCAAACTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGAGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACCTTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTCGGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GACTGAAAG
851 CCGTTCCCGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCTCTCCG AGTTGAAAAC GATTCCGATG ACgtaATTGG TcaaTTCCGG
951 TTCggcttCC GCGTCGGAGA TTGtcgCCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTcAGGC ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GGGCGACCTG
1201 GTCGGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAC
1251 CCTtgcCGTA CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

g732.pep

```

1 MSKPVFVKIA LYTLGAISGV AVSLAVQGFA AEKDRDNEV LPVQSIRTMA
51 EVYGOIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IQQEDGFVKV VSPIEDTAE RAEVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVNLTIRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDPGGGL
251 LTGAVGVSAF FLPSEAVVVS TKGRDGDGDM VLKAVPEDYV YMGGDPLAG
301 IPAELKTIPT TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFKGVSQVT
351 LIPLNNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSSETLAV PLEKDDADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKDK K*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

m732.seq

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1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGGCGTG GCCGTCAGTC TGCGCGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACCTTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GACTGAAAG
851 CCATTCTCGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCTCTCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA

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1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GGCGGATTTG
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACACCAGTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732.pep

```

1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EVYGOIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIDETPAE RAGVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLGA
301 IPAELKTIPT TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAK FVSNKDKKDK KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

m732.pep	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
g732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
	10	20	30	40	50	60
m732.pep	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
m732.pep	130	140	150	160	170	180
	VSPIDETPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
g732	VSPIDETPAERAEVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
m732.pep	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
m732.pep	250	260	270	280	290	300
	LDLRDPGGLLTGAVGVSA AFLPSEAVVSTKGRDGKDRMV LKAIPEDYVYGMGGDSLGA					
g732	LDLRDPGGLLTGAVGVSA AFLPSEAVVSTKGRDGKDMVLKAVPEDYVYGMGGDPLAG					
	250	260	270	280	290	300
m732.pep	310	320	330	340	350	360
	IPAELKTIPTTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
g732	IPAELKTIPTTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
	:					
g732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERTFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	:					
g732	PLEKDADKPAAKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
	490					
m732.pep	PVSNDKKDKDKKX					
g732	PVSNDKKDKKX					
	490					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

```

a732.seq
1  ATGTCGAAAC CTGTTTTTAA GAAATCGCA CTTTATACTT TGGGTGCAAT
51  CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTGTCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGTGTC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCCG
251 GATTACTTTG ACGCTGTCTG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTCTG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCGGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAGAGCTT GGTAAAGGAA AATAAAGGAA
701 AACCCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CCGTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCGGG
951 TTCGGCTTCC GCGTCGGAGA TTGTCGCAGG TGCATTGCAG GATCATAAAG
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCTCT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA
1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCAGTG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTGT AAAGCCCGCA GCGGATTTTG
1201 GTCGGACACA TCGGCAATCC TTTGGGCGGC GAGGATGTGA ACAGTGAAGC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAGGAC GAGGATTGTG CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAG ACGACCAAGT GCGGAAAGCT TTGGATTAGT TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAG CCGGTTTCAA
1451 AATAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

```

a732.pep
1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EYVQGIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGLGME IGQEDGFVKV VSPIDTPAE RAGVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGYIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDPDGGI
251 LTGAUGVSAA FLPSEAVVVS TKGRDGKDRM VLKAVPEDYV YGMGGDSLAG
301 IPAELKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFKGSGVQT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDVKSPEQW QKSLGLAAKK PVSNDKKDKD KDKK*

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a732/m732 99.6% identity in 494 aa overlap

	10	20	30	40	50	60
a732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPQSIRTMAEVYGOIKANY					
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPQSIRTMAEVYGOIKANY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGLGMEIGQEDGFVKV					
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
a732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
a732.pep	IVVNLTRAIKVKSVRHHLEIPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
m732	IVVNLTRAIKVKSVRHHLEIPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
a732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGDSLAG					
m732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGDSLAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
a732.pep	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFQKGSVQTLIPLSNGSAV					
m732	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFQKGSVQTLIPLSNGSAV					
	310	320	330	340	350	360
	370	380	390	400	410	420
a732.pep	KLTTALYYTPNDRSIAQGGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
m732	KLTTALYYTPNDRSIAQGGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
a732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAALK					
m732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAALK					
	430	440	450	460	470	480
	490					
a732.pep	PVSNDKKDKKDKKX					
m732	PVSNDKKDKKDKKX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq
1 ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51 GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTTATCC CGATACCGTC TATGAAGGTT TGA AAAACGa cgACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCCG CGGGTGCGCA CGCCATTG GGA CTGCTGC

1190

251 TT'TCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG
 301 AA'AAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep

1 MMNPKTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDTTS
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEED
 101 KR.LFPESGVF MDFLMKTGKG GKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq

1 ATGATGAATC CGAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACTTCTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCCC CGGGTGCACA CGCCCATCTG GGAAGCTGTC
 251 TT'TCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AA'AAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep

1 MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDTTS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEED
 101 KR.LFPESGVF MDFLMKTGKG GKR*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

	10	20	30	40	50	60
m733.pep	MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDTSLGKQTEKMEK					
g733	MMNPKTLGRLSLCAAVLALTACAGGGHKNLYYYGGYPDTVYEGLKNDTSLGKQTEKMEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEDKRLFPESGVFMDFLMKTGKG					
g733	YFAEAANKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEDKRLFPESGVFMDFLMKTGKG					
	70	80	90	100	110	120
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq

1 ATGATGAATC CGAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACTTCTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCCC CGGGTGCACA CGCCCATCTG GGAAGCTGTC
 251 TT'TCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AA'AAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

1191

1 MMNPKTLSRL SLCAAVLALT ACGGNGOKSL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

a733/m733 100.0% identity in 123 aa overlap

	10	20	30	40	50	60
a733.pep	MMNPKTLSRLSLCAAVLALTACGGNGOKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
m733	MMNPKTLSRLSLCAAVLALTACGGNGOKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
a733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEERKLFPEESGVFMDFLMKTGKG					
m733	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEERKLFPEESGVFMDFLMKTGKG					
	70	80	90	100	110	120
a733.pep	GKRX					
m733	GKRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

g734.seq
 1 ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGACTGCGGC
 51 GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
 101 AGGATGCAAA CGATGTTTTG CAGGTTAAAA CCACAAAAGA AGATTCCGGC
 151 AAAAGCGAAG CGTTTGCCGA GTTGAAGCC TTTTGCAAAG GTCAGGACAC
 201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
 251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTGGGCGCG
 301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
 351 TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC
 401 AATGCGGCTT GGAAACAGTG TATTGCACGT CATCTTCTTA TTACGGCGGG
 451 GCTGTTGCT CTTAATCCA ACACCTGAAA TAA

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

g734.pep
 1 MMKILAVSA LCLMTAAQA ADTYGYLAVW QNPODANDVL QVKTTKEDSA
 51 KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
 101 MRVENAVVIT SPRFTSVHGV ALNQCIKKYG AQGQCGLTV YCTSSSYGG
 151 AVRSLIQHLK *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

m734.seq (partial)
 1 TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCGG TCGTGTGCTG
 51 GAACAATACC TGTGTCGCGC TGGCATACCC GAAAGCCTTG GGCGCGCTGC
 101 GTGTCGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTAC GAGCGTTCAT
 151 CAGGTCGCAC TCAACCAGTG CATCAAAAAA TACGGCGTAC AGGGACAATG
 201 CGGCTTGGAA ACAGTGATT GCACATCTTC TTCTTATTAC GGCGGAACGT
 251 TGGCTCTTT GATTCAAAAT CTCAAATAA

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

m734.pep (partial)
 1 SGIAEDEPTG CRSVSLNNT CVALAYPKAL GALRVDNAV VITSRFTSVH
 51 QVALNQCIKK YGVQGCGLT TVYCTSSSY GGTVRSLIQN LK*

m734/g734 92.4% identity in 92 aa overlap

	10	20	30
m734.pep	SGIAEDEPTGCRSVVSLNNTCVALAYPKAL		
g734	VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKAL		

		40	50	60	70	80	90	
m734.pep		GALRVDNAVVITS	SPRFTSVH	QVALNQCIKKYGVQGQCGL	ETVYCTSSSY	YGTVRS	LIQN	
g734		GAMRVENAVVITS	SPRFTSVH	QVALNQCIKKYGAQQQCGL	ETVYCTSSSY	YGAVRS	LQH	
		100	110	120	130	140	150	
m734.pep	LKX							
g734	LKX							
	160							

```
a734.seq
1 ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGACTGCGGC
51 GGCACGGGGT GCCGATACTT ACGGCTATCT CGCGCTTTGG CAGAATCCGG
101 AGAATGCAAA CGATGTTTTC CAGGTTAAAA CCACAAAAGA AGATTGCGAG
151 AAAAGCGAAG CGTTTGGCCA GTTGGAAGCT TCTGCAAAAG GTCAGACAC
201 GCTTGCGGGC ATTGCCGAAG AGGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TTATCAGGTC GCACTCAACC AGTGCATCAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAACAGATG TATTGCACGT CTTCTTCTTA TTACGGGGGA
451 ACTGTGCGCT CTTTGTATCA AAATCTCAAA TAA
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a734.pep
  1  MMKKILAVSA LCLMTAAARA ADTYGYLAVW QNPQNANDVL QVKTTKEDST
51  KSEAFAELEA FCKGQDTLAG IAEDPTGCR SVVSLNNTCV ALAYPKALGA
101 MRVENAVVIT SPRTSVYQV ALNQCIKKYG AQGCQGLETV YCTSSSYGG
151 TVRSLIOLNK *
```

	10	20	30	40	50	60
a734.pep	MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA					
g734	MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a734.pep	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVALAYPKALGAMRVENAVVITSPRFTSVYQV					
g734	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV					
	70	80	90	100	110	120
	130	140	150	160		
a734.pep	ALNQCIKKYGAQGQCGLETVYCTSSSYYGTVRSLIQNLKX					
g734	ALNQCIKKYGAQGQCGLETVYCTSSSYYGGA VRSLIQHLKX					
	130	140	150	160		

```
m735.seq
1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTTGC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTTCG GAAGCAGCAG GCGGTCATCG AACAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAACT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAG GCTGTCGGCA
251 TGGCTTTGCG GAAAAAACAG CGGGAAGTCA GCCGCTGTA AACTGGAAAA
301 AAAAAGGAAA TCGAAATGTG CCTTACTCAA GACGCTAAAA ATGCAAGCGG
```


1193

351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNASGGCI DFGSHGLQL YNRALGYGN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGC GCGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCGAA AACGGAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DFGHHGLQL YKRALGYGN*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a735.pep	YARELEQARA EAKKYEVKAH AVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEVKAH AVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
	130	140				
a735.pep	DFGHHGLQLYKRALGYGNX					
m735	DFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCGGCAGT ATCAGCTGT TTCTGCTGAA CATTGTCG AAATCCGGCA
101 CGGCTTTGCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTGCG TGCTGATTGT TGCCGTTTCG GGGCTGTCG TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TCGCGAACT GGGTCCCGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCGCGC GTGGTTGCCC CGCGTTTTCG GCGGGCGGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTC AACGTGCGCG GCATTTCGG
501 CGCGTATTTC GTGCGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT

1194

601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

g736.pep

1 MNFIRSVGAK TLGLIQSFGS ITLFLNILA KSGTAFARPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NVMVNPVAR VVAPRFWAGV
 151 FSPMLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMONN ITIHYDVING
 201 LIKSAAFGVA VTLIAVHQQF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

m736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
 51 CTTCGCGAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGCGA
 101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
 151 GTGCTGTCCG TGCTGATTGT TGCCGTTTCG GGGCTGTCG TCGGTATGGT
 201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATCAAAA TCCGCCGATA
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGC CGCAACT GGGTCCCCTG
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGGTGCGA TGACCAGCGA
 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
 401 CCGTCAACCC CGTCGCCCGC GTGGTTGCCG CGCGTTTTTG GCGGGCGGTG
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTC AACGTCGCGG GCATTTTCGG
 501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
 551 GGCCGCGAGT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT
 601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

m736.pep

1 MNFIRSVGAK TLGLIQSLGS ITLFLNILA KSGTAFVRPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMVNPVAR VVAPRFWAGV
 151 FSPMLLASIF NVAGIFGAYL VGVTWLGLDS GIFWSQMONN ITIHYDVING
 201 LIKSAAFGVA VTLIAVHQQF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

m736/g736

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNILAKSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
m736.pep	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
g736	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
	130	140	150	160	170	180
m736.pep	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
g736	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVSS					
g736	GIFWPQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCPTSEGILRASTRVSS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

a736.seq

```

1  ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51  TCTCGGCAGT ATCACGCTGT TTCTGCTGAA TATTCTGGCG AAATCCGGTA
101 CGGCTTTCGT CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGTTGATTGT TGCCGTTTCA GGGCTGTTTG TCGGCATGGT
201 CTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCGCTGT TGC CGAACT GGGTCCGGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGAACAGCT CGAAGCGATG AACGTGATGG
401 CGGTAAACCC CGTCGCCCGA GTGGTTGCGC CGCGCTTTTG GCGGGCGGTG
451 TTTTCCATGC CGCTTTTGGC TTCGATTTTC AACGTGGCGG GTATTTTCGG
501 CGCGTATTTG GTCGGTGTA CTTGGCTGGG CTTGGACAGC GGTATTTTCT
551 GGTGCGAAAT GCAGAACAA ATCACGATAC ATTACGATGT AATCAACGCT
601 CTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCGTCC CGACCTCGA AGGCATTTTG CGGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

a736.pep

```

1  MNFIRSVGAK TLGLIQSLGS ITLFLNLA KSGTAFVRPR LSVRQVYFAG
51  VLSVLIVAVS GLFVGMVLGL QGYTQLSKEF SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NMAVNPVAR VVAPRFWAGV
151 FSMPLLASIF NVAGIFGAYL VGVTLWGLDS GIFWSQMNN ITIHYDVIN
201 LIKSAAFGVA VTIAVHQGF HCVPTSEGIL RASTRTVSS ALTILAVDFI
251 LTAWMFTD*

```

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
m736	MKTTEQLEAMNMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVSS					

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```

m736      GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS
           190      200      210      220      230      240

           250      259
a736.pep   ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

```

g737.seq
1  atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51 CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

```

g737.pep
1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51 AQAEKAALAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

```

m737.seq..
1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51 CATTTCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

```

m737.pep
1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

m737/g737

```

           10      20      30      40      50      60
m737.pep   MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR AQAEKAALAR
           |||||
g737        MNIKHLLLTAAATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR AQAEKAALAR
           10      20      30      40      50      60

           70      80      90      100     109
m737.pep   VGGKITDIDLEH DNGRPHYD VEIVKNGQEY KVVVDARTGR VISSRRDDX
           |||||
g737        VGGKITDIDLEH DGRPHYD VEIVKNGQEY KVVVDARTGR VISSRRDDX
           70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

a737.seq

```

1 ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51 CATTTCGCC CCCGCACTCG CCCACCAGCA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGCCGC
301 GTGATTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep

```

1 MNFKRLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51 AQAEEAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQY KVVVDARTGR
101 VISSRRDD*

```

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLTAAATALMGISAPALAHHDGHGDDDHGHAHQHSKQDKIISRAQAEEAALAR					
m737	MNIKHLTLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEEAALAR					
	10	20	30	40	50	60

	70	80	90	100	109
a737.pep	VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX				
m737	VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX				
	70	80	90	100	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq

```

1 ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCG CCAAACCTGCC
51 GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCG
151 GCGGCCGCGC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTATACC CGGAATGAAC
301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG
351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCAtcgtT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
451 CAGTTTGCCG GCTGGGAAAA CACCCCTCTG CTTCAAACA TCATCGTTCA
501 CAGAGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGCATA CTCGCCTCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCGT
651 TTTAGGTTTG GTCAATTGCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
751 ACGATGCTCG GCATAGCCCG AGCCGTATTC CTTACCGCGC TGTTCGAAT
801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACTTGCC GCGCCAAAGC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTGTGCC AACAAACCTT CCTGATCAAT GCCGAACAGC
1001 ACACCATACA CGACAACCTT CTCAGCACCT TGTTCAACCA TCCCACAAC
1051 ATCATCTTCC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCCG GCTGCTGAAA CGCTCCCTGA
1151 CCCCCGCATC ACTTTTCTCT GTGTGCGCGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
1401 CCCC GCCGCT GACGACAGT CCAAAACCTT CAACCGGAAA ATCAACGAAC
1451 TGCGCTATAT TTCCGCAAC AGCCCGATGC TGTCTTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAG CACTAAAATA CCGCCCTTAC TCCGCCACCT

```

```

1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAACAA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pap

```

1  MSAETTVSGA RPAAKLPYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51  AAGLIVLLEF TAGKKLFDVK IPAISLLEFA MAAFWWLOAR LMNLIYPGMN
101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLIQSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KI PAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPEW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAFO SAPIFGHGWV SFAQQTFLIN AEQHTIHDFN LSTLFTHSHN
351 IILQLLAEMG ISGTLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAEASDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTT RLVSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEAA TLKALKYRPY SATYRIALYL MRQKVAEAK
551 QWMRATQSYI PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
601 KPCK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

```

1  ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCGCGCG CCAAAGTGGC
51  GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCGCGC
151 GCAGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAAGTGT
201 TGATGTCAA ATCCCCGCCA TCAGCTTCCT TCTGTTTGA ATGGCGCGCT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTACGCG CGTGGGCGTG
351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAAACA TCATCGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCGCGCG CTAACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCTT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACGCGCG TGTTCGAAT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAATG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCAAATC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTACCCCA TTCCCAAC
1051 ATCGTCTCTC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGTGACGG GCATTGCCGG GCTGCTTAAA CGCCCTTGA
1151 CCCCCGCATC GCTTTTCTTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTTCA TCCCTTTCGG
1251 ACTGATGCTC TTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCGC CATATTGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGT CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTAA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCGGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCgTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pap

```

1  MPAETTVSGA HPAAKLPYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

```

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

m738/q738

	10	20	30	40	50	60
m738.pep	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAAAAGLIVLLFL					
g738	MSAETTVSGARPAAKLPIYILPCFLWIGIIPFTFALRLKPSPDFYHDAAAAAGLIVLLFL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m738.pep	TAGKKLFDVKIPAIISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRS					
g738	TAGKKLFDVKIPAIISFLLFAMAAFWWLQARLMNLIYPGMNDIASWVFILLAVSAWACKSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m738.pep	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
g738	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGQRN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m738.pep	NLGHYLMWVGILAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
g738	NLGHYLMWVGILASAYLNGQRKIPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
	250	260	270	280	290	300
m738.pep	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
g738	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNAILETFTGIRYETAVERVANGGFTDLPRQS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m738.pep	EWNKALAAFQSAPIFGHGWSFAQQTFLINAEQHNINYDNLLSNLFTSHSNIVLQLLAEMG					
g738	EWNKALAAFQSAPIFGHGWSFAQQTFLINAEQHTIHDNLFSTLFTSHSNIIQLLAEMG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m738.pep	ISGTLVVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
g738	ISGTLVVAATLLTGIAGLLKRSPLTPASLFLCALAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
	430	440	450	460	470	480
m738.pep	FLSPAASDGIAFKKAANLGILTASAAIFAGLLHLDWTYTRLVNAFSPATDDSAKTLNRK					
g738	FLSPAASDGIAFKKAANLGILTASAAIFAGLLHLDWTYTRLVNSFPAADDSAKTLNRK					

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKSLKYRPHSATYRIALYL					
g738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKALKYRPYSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQGVKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQGVKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPET					
	550	560	570	580	590	600
m738.pep	KPCKX					
g738	KPCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

```

a738.seq
1  ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCGCGCG CCAAAC TGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCGACT TTTACCACGA TGCCGCGGCC
151 GCAGCCGGCC TGATTGTCTT GTTGTCTCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTACTC GCCGTCAGCG CGTGGGCGTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATTGTTTA
501 CAGCGGGCAA GGCGTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCGC CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCTT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGTACTCTG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCGAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACCTGCC GCGCCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
951 CGCCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTCAACCA TCCCAACAA
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCTCT ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTCTCG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTTCGA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCCGCCACT GACGACAGTG CCAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAT CACTAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCGC CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

```

a738.pep
1  MPAETTVSGA HPAAKLPYIY LPCFLWIGIV PFTFALRLQP SPDFYHDAAA
51  AAGLIVLLEF TAGKKLFDVK IPPISFLLEA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYGQERIV TFAWSLLIG SLLQSCIVVI
151 QFAGWEDTFL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR

```


1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
 251 TILGIAAAVF LTALFQFSMN TILEFTTGIR YETAVERVAN GGFTDLPRQI
 301 EWRKALAAFO SAPIFGHWN SFAQOTFLIN AEQHNHNDNL LSNLFTSHSN
 351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
 401 SMLEYPLWYV YFLIPFGLML FLSPAASDG IAFKKAANLG ILTASAAIFA
 451 GLLHLDWYTY RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
 501 SILNFALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQKVAEAK
 551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
 601 KPCK*

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAHPAAKLPYILPCFLWIGIVPFTFALRLQPSPDFYHDAAGLIVLLFL					
m738	MPAETTVSGAHPAAKLPYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
a738.pep	70	80	90	100	110	120
m738	TAGKKLFDVKIPISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
	70	80	90	100	110	120
a738.pep	130	140	150	160	170	180
m738	VAHYGOERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVSYSGQGVIGHIGQRN					
	130	140	150	160	170	180
a738.pep	190	200	210	220	230	240
m738	NLGHYLMWGILAAAYLNGQRKIPALGVICIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
a738.pep	250	260	270	280	290	300
m738	YFRSDKSNRRITILGIAAAVFLTALFQFSMNTILEFTTGIRYETAVERVANGGFTDLPRQI					
	250	260	270	280	290	300
a738.pep	310	320	330	340	350	360
m738	EWRKALAAFO SAPIFGHWN SFAQOTFLINAEQHNHNDNL LSNLFTSHSNIVLQLLAEMG					
	310	320	330	340	350	360
a738.pep	370	380	390	400	410	420
m738	ISGTLLVAATLLTGIAGLLKRLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
a738.pep	430	440	450	460	470	480
m738	FLSPAASDGI AFKKAANLGILTASAAIFAGLLHLDWYTYRMVNAFSPATDDSAKTLNRK					
	430	440	450	460	470	480
a738.pep	490	500	510	520	530	540
m738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKSILKYRPHSATYRIALYL					
	490	500	510	520	530	540

1202

	550	560	570	580	590	600
a738 . pep	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
m738	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
	550	560	570	580	590	600

a738 . pep	KPCKX
m738	KPCKX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739 . seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTc AAACCGGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGGCCAA ACCCATATA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739 . pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVG QDAAQPEHHH AASSEPAQPD GTEESGSGLP
101 SPAAPKKNRV KPRPSDARA ADSLTGTGTQ AENTLKETPV LPTNAPHEP
151 RKETPEKQQA PKETPKEKET PKENHTKPD TPKNTPAKPHK EILDNLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739 . seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CGCCAAAGA
501 AAACCATACC AAACCGGACA CCCCAGAAA CACGCCGCC AAACCCATA
551 AAGAAATTCT CGACAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739 . pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQADTAQT DRQPDAGTQ AENTLKETPV LPTNVRPEP
151 RKETPEKQQA PKETPKENHT KPDTPKNTTP KPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

1203

	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAEPOHTDSPRET					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTEPOHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT					
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSLPSPAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD					
g739	ADSLTGTGTAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPHKEILDKLF					
g739	PKNTPAKPHKEILDNLF					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

a739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACGCG CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTC AAC CCGAACGGCG ACAAACCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCACAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACA
551 CGCCGCCTAA ACCCCATAAA GAAATTCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

a739.pep

```

1  MAKKPNKPFRLTPKLLIRAVLLICITAIGA LAIGIVSTFNPNGDKTLQTE
51  POHTDSPRET EFWLPNGVVGQDAAQPEHHH ASSSAPAQPD GTDESGSGLP
101 SPAAPKKNRV KQPADTAQT DRQPDDAGAQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPD PKNTPPKPHK EILDNLF*

```

a739/m739 93.9% identity in 197 aa overlap

	10	20	30	40	50	60
a739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAIGA LAIGIVSTFNPNGDKTLQTEPOHTDSPRET					
m739	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAEPOHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
a739.pep	EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT					
m739	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a739.pep	DRQPDDAGAQ AENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
m739	DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD					
	130	140	150	160	170	

1204

```

                190
a739.pep      PKNTPPKPHKEILDNLEX
                |||||
m739          PKNTPPKPHKEILDKLF
                180    190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gcCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gTTTGATT
201 GAAACgtcaa ACCATGTTTC TGTATTATCC GATTGTTTG CTGGTTGTGT
251 ATTTGTTCCA CTATTCGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFETIKHH LKQGFDLKRQ TMLFFIPIVL LVVYLFHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCCTT
51 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTAAa
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIL LIVYLFHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

                10      20      30      40      50      60
m740.pep      MSRNLLVRWLAVCLIPLATLAVFAANPPEDKLOHLINGIILACEATFLFKFVLFDTIKHH
                |||||
g740           MSRNLLVRWLAVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFETIKHH
                10      20      30      40      50      60

                70      80      90
m740.pep      LKQEFDLKRQTMLLFIPILLIVYLFHYFGAFX
                |||
g740           LKQGFDLKRQTMFLFIPIVLLVVYLFHYFGAFX
                70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT
51 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIL LIVYLFHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

                10      20      30      40      50      60

```

1205

```

a740.pep  MSRNLLVRWLVVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
|||||
m740      MSRNLLVRWLVVCLIPLATLAVFAANPPEDKLOHLINGIILACEATFLFKFVLFDTIKHH
              10      20      30      40      50      60

              70      80      90
a740.pep  LKQEFDLKRQTMLLFIPILLIVLYLFHYFGAFX
|||||
m740      LKQEFDLKRQTMLLFIPILLIVLYLFHYFGAFX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1  GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTC
51  TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTG GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAAACG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCAG CGATTGCGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGCGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAAACCTG ACCTATACCA TAGATTTCGC CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCCTCCGCC GAACCTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACCTACCG CCTCGCCCTT
751 TCGGCGGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1  VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPQNGTTL SAQGAETFK AGGKDNSLNT GKLNKDISR
101 FDFVQKIEVD GQTITLASGE FQIYQDHSA VVALRIEKIN NPKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAQ
201 GHGKIEHLKT PEQNVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGEKV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1  GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCGGAC ATCGGTGCGG
101 GGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAACGAGA AACTGAAGCT
201 GGCGGCACAA GGTGCGGAAA AAACCTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGCGAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTCCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GGCGACATAG CGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGAAA CGGCAAAATC
601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAACCGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1  VNRTAFCCLS LTTALILTAC SSGGGVVAAD IGAGLADALT APLDHKDKGL
51  QSLTLDSVR KNEKLKLAQ GAERTYGNQD SLNTGKLKND KVSREFDFIRQ
101 IEVDGQLITL ESGEFQYKQ SHSALTAFQT EQIQDSEHSG KMAKRFRI

```

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLYTID FAAKQNGNKI
201 EHLKSPELNV DLAADAIKPD GKRHAVISGS VLYNQAEKGS YSLGIFGGKA
251 QEVAGSAEVK TVNGIRHIGL AAKQ*

[illegible]

```
a741.seq
1      GTGAACCGGAA CTGCCTTCTG CTGCCTTTCT TTGACCGCCG CCCTGATTCT
51     GACCGCGTGC AGCAGCGGAG GCGCGGGTGT CGCCCGCCGAC ATCGGCGCGG
101    TGCTTGGCCA TGCACTAACC GCACCGCTCG AC0AAGTACGA CAAAAGTTTG
151    CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201    GCGGCGACAA GGTGCGGAAA AAAC TTATGG AACGCGCGAC AGCCTCAATA
251    CGGGCAAAAT GAAGAACGAC AAGGTCAGCG GCTTCGACTT TATCCGTCAA
301    ATCGAAGTGG ACGGGCAGCT CATTACCTTC GAGAGCGGAG AGTTCCAAGT
351    GTACAAACAA AGCCATTCCG CCTTAACCGC CCTTCAGACC GAGCAAGTAC
401    AAGATTCGGA GCATT CAGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451    GCGATATATAG CGGGTGAACA TACATCTTTT GAC AAGCTTC CCGAAGGCGG
501    CAGGGCGACA TATCGCGGGA CGGCATTCCG TTCAGACGAT GCGCAATGGA
551    AACTGAGTCA CACCATAGAT TTCGCGCCA AGCAGGGACA CGGCAAAATC
601    GAACATTGGA AATCGCCAGA ACTCAATGTT GACCTGGCCG CCTCCGATAT
651    CAAGCCGGAT AAAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701    ACCAAGCCGA GAAAGGCAGT TACTCTCTAG GCATCTTTGG CGGGCAAGCC
751    CAGGAAGTTG CCGGCAGCGC AGAAGTGGAA ACCGCAAACG GCATACGCCA
801    TATCGGTCTT GCGCGCAAGC AGTAA
```

```
a741.pep
1  VNRTAFCCLS  LTAALILTAC  SSGGGGVAAD  IGAVLADALT  APLDHKDKSL
51  QSLTLDQSVR  KNEKLKLAQ  GAEKTYGNGD  SLNTGKLKND  KVSREFDFIRQ
101 IEVDGQLITL  ESGEFQVYKQ  SHSALTALQT  EQQVDSEHSQ  KMVAKRQRFRI
151 GDIAGEHTSF  DKLPEGGRAT  YRGTAFGSDD  ASGKLTYYTD  FAAKQGHGKI
201 EHLKSPELNV  DLAASDIKPD  KKRHAVISGS  VLYNQAEEKS  YSLGIFGGQA
251 QEVAGSAEVE  TANGIRHIGL  AAKO*
```

a741/m741 95.6% identity in 274 aa overlap

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCLSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
m741	VNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKCLKLAAQGAEKTYGNGDSLNTGKLNKDKVSRFDFFIRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKCLKLAAQGAEKTYGNGDSLNTGKLNKDKVSRFDFFIRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMKVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDD					
m741	SHSALTAFQTEQIQDSEHSGKMKVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLYTIDFAAQQGHGKIEHLKSPELNVDLAASDIKPKDKRHAIVISGSVLYNQAEKGS					
m741	AGGKLYTIDFAAQQGNKIEHLKSPELNVDLAAADIKPDGKRHAIVISGSVLYNQAEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAQKX					
m741	YSLGIFGGKAQEVAGSAEVTNNGIRHIGLAQKX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

m742.seq

1	ATGGTTTACG	GCATTGCCGA	AGCCGATGCG	GGCGACAGCA	GTGTGCTTAC
51	TTTGGGCGGC	ATGTATCAGA	AGAGTAGGGA	GTTCTCTGAT	TTTTCGGGCA
101	TTATTTTGCC	CTGTGAAAT	CAGAAAACG	CCCCGTTTCA	TTCAACGCCT
151	GCCTGCAACC	GGCCTTTGCA	ACTGCCGCGC	AACACTTATT	TGGGGGAGGA
201	TTGGTCGCGG	TTAAGTGCCG	ACAAATACAA	CCTTTTCTCA	GGATTCAAAC
251	ATGTGTTTGA	CAACGGTTGG	CAGCTCAATG	CCGAAGTGTC	TTATACCAAG
301	AATGAATCCG	ATGCGAAGGT	GGGGCAGTTT	TTTCTGAAAA	ACGAATATGC
351	GGCGGGTTTG	TCGGGTGAGG	ATGCGGTAGG	CTTTTTGACT	GAAAAAACC
401	AAGTCATCCC	GTTTCGAGCCG	AAAGATAAGG	CATTGGAGAA	ACTGAAAGCA
451	TATCGTGATG	AAACCGCCAA	GGAATACCGG	GAGCGCAAAG	ACGATTTTGT
501	TAAAAACCGT	TTTGATAATA	CTGCTTTCGA	ACAGTATCGC	AGCCGCGGTG
551	CCGCAGAACG	CAAAGCCGGT	TTTGACAAGT	GTATGAGTGA	CCCTTTCGCG
601	CTGGACTTTA	TCTGTCAAGG	TTCTTGGGGG	GATCCGGGCG	TTGATGCCGA
651	CAAGGCGGAA	TTTGTCGATA	AAGCCCTTGC	GAAGGAGGGC	ATCTTTAATA
701	ATGCGGCACA	ACGTTTTCCA	AACAGCCTGT	ATGACTCTTC	CTTTAATCGG
751	AAGGCTACCG	CCAACCGACG	ATACAGTTAT	ATGCCGTTGC	GGCATACCAA
801	AGACGACCGC	CAATGGGGAA	TTAACTTGA	CCTGACCGGC	ACATATGGGC
851	TGTTCCGGCG	GGAGCATGAT	TTCTTTGTGC	GCTATGCCTA	CGGTGATGAA
901	AAGATACGTT	CGGAATATCT	AGAAATCTAC	GAACGCCGCT	ACAGAGTACG
951	TCCGAATACG	GGGGCAACGC	ACGGCGTGTA	TGCGGGAAGT	TGTCAGGAGG
1001	AGCCGGACGG	CGATTTGTCT	TCTCCTTTGG	TCAGGGGGCA	TAAAGAACCC
1051	GATTGGCAGG	CGTACGATGA	AAAAGGCAAC	CGTACCGTTT	ATGCCGAAGA
1101	ATGCAGGAAC	GCCAAGAAAA	TAAAAACCGA	GCCCAAGCTC	GATGCCGAAG
1151	GCAAGCAGGT	GTATTACTAT	GACGAATACA	GCGGCAGCCG	GACACCGGTA
1201	TATGTCGATG	TATATGAGCT	GGACGAAAAA	GGCAACAAGA	TTCAGGAGAC
1251	CAATCCCAGC	GGCAGCCCTG	CCTTTACCGG	TTTTTCCGGT	ACGGTGCCGG
1301	TTTGGAAGAC	CGTCAAAGTG	GCAGACGACC	ATGTTCTCTG	GCTGTATAAC
1351	TACGCCAAAT	ACCTCAACAC	CAACAAAACC	CATTGCTGTA	CTGCCAGCAC
1401	GCGTTTCAAC	GTAACCGGCC	GACTGCACCT	TTTGGGCGGG	CTGCACTACA

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1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTT GCATTGTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTCCGCTA TGTTCCTGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATCCA GTGCAGACCC GTACAACTTC AGCAATTTC
2051 CACCCGTGCA CATATTCCTG TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGCGCG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAAACA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

m742.pep

```

1  MVGIAEADA GDSSVLTGG MYQKSREVPD FSGIILPCEN OKTAPFS STP
51  ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNGW QLNAEVS YTK
101 NESDAKVGQF FLKNEYAAGL SGEDAVGFLT EKNEVIPFEP KDKALEK LKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDKCMSD PFA
201 LDFICQGSWG DPGVDADKAE FVDKALAKEG IFNNAQRFP NSLYDSS FNR
251 KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FVVGAYGDE
301 KIRSEYLEIY ERRYRVRPNT GATHGVYAGS CQEEP GDLS SPLVRGHKEP
351 DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKTVKV ADDHVPALYN
451 YAKYLNNTKT HSLTASTREN VTGRLHLLG LHYTRYETSQ TKDMPVR YGQ
501 PASDFQTASS IRADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGKVVV RGAEFELSGE LNEWDKV FAG
651 YTYNKSRYKN AAEVNAERLA KNSSADPFYN SNFTPVHIFR FGTSFHI PNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFY GEPRTVSMKLD WQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

a742.seq

```

1  ATGGTTTACG GCATTGCCGA AGCCGATGCG GGCACAGCA GTGTGCTTAC
51  TTTGGCGGCG ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTTCGGGCA
101 TTATTTTGTC CTGTGAAAT CAGAAACTG CCCCCTTCTAG TTCAACGCCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTGAGTGCTG ACAATAACAA CCTTTCTCA GGTTCATAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCGAGTT TTTCTGAAA ACGAACATGC
351 GCGGGGTTTG TCAGATGAGG ATGCGGTAGG CTTTTTGACC GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGACG AAACCGCCAA GGAATACCGT GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTCGA GCAGTACCGC AGCCGCCGTC
551 CCGCAGAACG CAAAGCCGCT TTTGACGAGT GTATGAGTGC CCCTTTTGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGTG TTGATGCCGA
651 CAAGTCGGAA TTTGTCGATA AAGCCCTTGC GAAGGAAGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTGTC GGCATACCAA
801 AGACGACGCG CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTTCCGGCG GGAGCATGAT TTCTTTGTCG GCTATGCCTA CGGCGATGAA
901 AAGATACGTT CCGAATATCT GGAAATCTAC GAACGCCGCC ACAGAGTACG
951 TCCGAATACA GGGCAACGCG ACGGCGTGTA TCGGGGAAGT TGTGAGGGGG
1001 AGCCGGACGG TGATTTGTCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAT GCCAAGAAAA TAAAAACCGA GCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACGCCAGTA

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1209

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1201 TATGTCGATG TATATGAACT GGATGAAAAA GGCAATAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCGTG CCTTTACCGG TTTTTCGGGT ACGGTGCCGG
1301 TTTGGAAAAC CGTCAAAGTG GCCGACGACC ATGTTCTCTG GCTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTGCTGTA CTGCCGGCAC
1401 GCGTTTCAAC GTAACCGGCC GACTGCATCT TTTGGGCGGG CTGCACTACA
1451 CGCGCTATGA AACCTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAAGGCGG ATCAGGACCA
1551 TTATACGGCC AAGATGCAAG GTCATAAAT GACGCCCTAT GCAGGCATTA
1601 CCTATGATTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCCGG ACAAACATAT AGGTAGGCTG GAAAGCGCGG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTT GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTTGCTTA TGTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTCAAAAAC GCCGCGAAG TCAACGCCGA
2001 ACGCCTCGCC AAAACACAG GCGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCGTGCA CATATCCGT TCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGCGCG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCT AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCTATGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2542; ORF 742.a>:

```

a742.pep
1  M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L S C E N O K T A P F S S T P
51  A C N R P L Q L P R N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K
101 N E S D A K V G Q F F L K N E H A A G L S D E D A V G F L T E K N E V I P F E P K D K A L E K L K A
151 Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R S R R A A E R K A G F D E C M S A P F A
201 L D F I C Q G S W G D P G V D A D K S E F V D K A L A K E G I F N N A A Q R F P N S L Y D S S F N R
251 K A T A N R R Y S Y M P L R H T K D D R O W G I K L D L T G T Y G L F G R E H D F F V G Y A Y G D E
301 K I R S E Y L E I Y E R R H R V R P N T G A T H G V Y A G S C Q G E P D G D L S S P L V R G H K E P
351 D W Q A Y D E K G N R T V Y A E E C R N A K K I K T E P K L D A E G K Q V Y Y Y D E Y S G S R T P V
401 Y V D V Y E L D E K G N K I Q E T N P D G T P A F T G F S G T V P V W K T V K V A D D H V P A L Y N
451 Y A K Y L N T N K T H S L T A G T R F N V T G R L H L L G G L H Y T R Y E T S Q T K D M P V R Y G Q
501 P A S D F Q T A S S I K A D Q D H Y T A K M Q G H K L T P Y A G I T Y D L T P Q Q S I Y G S Y T K I
551 F K Q O D N V D V S A K T V L P P L V G T N Y E V G W K G A F L Q G R L N A S F A L F Y L E Q K N R
601 T V V D F G Y V P G A G G K Q G S F Q T V A K P I G K V V S R G A E F E L S G E L N E D W K V F A G
651 Y T Y N K S R Y K N A A E V N A E R L A K N T G A D P Y N F S N F T P V H I F R F G T S F H I P N T
701 G L T V G G G V S A Q S G T S S L Y N I R O G G Y G L I D G F V R Y E L G K H A K L S L I G T N L N
751 G R T Y F E N N Y N R T R G A N N F Y G E P R T V S M K L D W Q F *

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a742/m742 98.5% identity in 783 aa overlap

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a742.pep      10      20      30      40      50      60
M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L S C E N O K T A P F S S T P A C N R P L Q L P R
|||||
m742          10      20      30      40      50      60
M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L P C E N O K T A P F S S T P A C N R P L Q L P R

a742.pep      70      80      90      100     110     120
N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K N E S D A K V G Q F F L K N E H A A G L
|||||
m742          70      80      90      100     110     120
N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K N E S D A K V G Q F F L K N E Y A A G L

a742.pep     130     140     150     160     170     180
S D E D A V G F L T E K N E V I P F E P K D K A L E K L K A Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R
| |||||
m742         130     140     150     160     170     180
S G E D A V G F L T E K N E V I P F E P K D K A L E K L K A Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R

a742.pep     190     200     210     220     230     240
S R R A A E R K A G F D E C M S A P F A L D F I C Q G S W G D P G V D A D K S E F V D K A L A K E G I F N N A A Q R F P

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m742	SRRAAERKAGFDKCMSDPFALDFICQGSWGDPGVADKAEFVDKALAKEGIFNNAQQRFP	190	200	210	220	230	240
a742.pep	NSLYDSSFNRKATANRRYSYMLRHTKDDRWGQIKLDTGTGTYGLFGREHDFVGYAYGDE	250	260	270	280	290	300
m742	NSLYDSSFNRKATANRRYSYMLRHTKDDRWGQIKLDTGTGTYGLFGREHDFVGYAYGDE	250	260	270	280	290	300
a742.pep	KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGE PDGDLSSPLVRGHKEPDWQAYDEKGN	310	320	330	340	350	360
m742	KIRSEYLEIYERRRVRPNTGATHGVYAGSCQE EPDGDLLSSPLVRGHKEPDWQAYDEKGN	310	320	330	340	350	360
a742.pep	RTVYAECECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNPD	370	380	390	400	410	420
m742	RTVYAECECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNPD	370	380	390	400	410	420
a742.pep	GTPAFTGFSGTVPVWKTVKVADDHVPALYNYAKYLNTNKTSLTAGTRFNVGTGRLHLLGG	430	440	450	460	470	480
m742	GTPAFTGFSGTVPVWKTVKVADDHVPALYNYAKYLNTNKTSLTAGTRFNVGTGRLHLLGG	430	440	450	460	470	480
a742.pep	LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLT PYAGITYDLTPQ	490	500	510	520	530	540
m742	LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLT PYAGITYDLTPQ	490	500	510	520	530	540
a742.pep	QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLQGRNLNASFALFYLEQKNR	550	560	570	580	590	600
m742	QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLQGRNLNASFALFYLEQKNR	550	560	570	580	590	600
a742.pep	TVVDFGYVPGAGGKQGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKN	610	620	630	640	650	660
m742	TVVDFGYVPGAGGKQGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKN	610	620	630	640	650	660
a742.pep	AAEVNAERLAKNTGADPYNFSNFTPVHIFREGTSFHIPNTGLTVGGGVSAQSGTSSLYNI	670	680	690	700	710	720
m742	AAEVNAERLAKNSSADPYNFSNFTPVHIFREGTSFHIPNTGLTVGGGVSAQSGTSSLYNI	670	680	690	700	710	720
a742.pep	RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPTVSMKLD	730	740	750	760	770	780
m742	RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPTVSMKLD	730	740	750	760	770	780
a742.pep	WQFX						
m742	WQFX						

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a742/ p25184
sp|P25184|PUPA_PSEPU    FERRIC-PSEUDOBACTIN    358    RECEPTOR    PRECURSOR
>qi|94923|pir||S15169

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1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi|45723 (X56605)
 pseudobactin uptake protein [*Pseudomonas putida*]Length = 819
 Score = 152 bits (381), Expect = 6e-36
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADHDV-PALYNYAKYLNTNKTHTSLTAGTRFNVLTGRLLHLLGGLHYTRYETSQTKDM 494
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y

Sbjct: 511 QTPKPGDDEIIPGI-----QYNISNRQSGYFVASRFNLTDLLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQFASDFQTASSIKADQDHYTAKMQGHKLTPTYAGITYDLTPQQSIYGSYTKIFKQQ 554
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q

Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPK 609

Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLOQRLNASFALFYLEQKNRTVVDFGYVPGAGGK 614
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG

Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGEFLEGRNLNANIALYMKRDNLAESTNEVVPDSSGGL 668

Query: 615 QGSFQTVAKPIGKVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674
 S + + ++G + ELSGE+ W VF GY++ ++

Sbjct: 669 IAS-----RAVDGAETKGVDELSEGLVPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IROGGYGL 727
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +

Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGWEKLTGGGVNWNKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
 RY + + +L N+ + Y Y G+ YG PR ++ L + F

Sbjct: 768 TSLMARYRINESLAATLNVNINFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq

```

1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC
201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC
351 GCGGTTTGTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TGACCGTCAA TGTTCAGGCG CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGCGG GGTTCATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT
551 TGATCCGTAA GTGA

```

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep

```

1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
51 GKTEKTRSYT IDRMSTATGM RIAGKDT PQS VSVITRSLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
151 SPSTD LAVYD HIEVV RGATG LTQSNSEPGG TVNLIRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq

```

1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTCTG
151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC
201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC

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1212

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351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTTGCAGGC CGTTCCGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGGC GGTATTATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```

a743.pep
  1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
 51 GKTEKTRSYT IDRSTATGM RIAGKDPQS VSVITRSLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

```

a743.pep      10      20      30      40      50      60
MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT
|||||
m743          10      20      30      40      50      60
MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT

a743.pep      70      80      90     100     110     120
IDRSTATGMRIAGKDPQSVSVITRSLDDKAVHTLEEA MKNTTGVNVVRD SGLQTRFL
|||||
m743          70      80      90     100     110     120
IDRSTATGMRIAGKDPQSVSVITRSLDDKAVHTLEEA MKNTTGVNVVRD SGLQTRFL

a743.pep      130     140     150     160     170     180
SRGFYIDQIGEDGITVNVAGRSYGTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG
|||||
m743          130     140     150     160     170     180
SRGFYIDQIGEDGMTVNVAGRSYGTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG

a743.pep      TVNLIRKR
|||||
m743          TVNLIRKX

```

g744.seq not found yet
g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

```

m744.seq
  1 ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
 51 CAGAAGAAGA GAAATAAAG ATTTATTTAA CCGAATATTT GTAAAAGGAG
101 AATATTGGA TGAATTATGT GAACCAAATA TTTCGTTTTT AATCGGAGAA
151 AAGGGAAC TG AAGACAGC ATATGCTGTT TATTTAACTA ATAACCTCTA
201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACTGTTTC AGATTTTACA
301 AGTATTGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCAATATT TAATAAATTT AAAGCCTTAG
401 ATGAGGCTAT AATGAATAT TATTATGGCG CTTTGTATCC GGAAATTGTA
451 CAAGCAATTA CTTTAATAGA AAATTCARAA GAAGCTGCGG AAATGATTTT
501 TGGAAATTT GTTAACTAG GTGAAGAGGA ATCCCAACAA ATAACTTTAA
551 CAGAAAGTAA ATTCCAAGCA AATTAGGTT TTATTGAAAG AAAATTTAAA
601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTTTATTGA
651 TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701 GTGTAAAAGG TCTTGCTAAC GCCATATGGA TGTAAATAA TGATATCTTC
751 CCTTCCATTA AAGATAGTAA GGAAGGATG AGAGTTGTGT TATTGATTAG
801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAT ACCAACTTC
851 AAGATAATTC AGTATTTTGA GACTGGAGGA CGGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTGATCAT CTTTGAGAA CCCAGCAAGA
951 AAAACAAGAT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTCCAT
1001 GGAATGCTCC TAATTTACAT GATGAGTATA AAAATTTAAC TTCATTATT
1051 AGCTTCCTAA GAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTACTT
1201 GGTGAAATCA AAGATCATCT TTTGTTTTAT TATAGTCAAA GTGATTATCA
1251 AAATTTCTCG AAATTTTGTG AATTTTAA CCGGAAAGAT AGATTAAAT

```

1213

```

1301 ATAGTGATTT TTAAAGCA TTTGAACGTT TGAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTT GACTTGAATG TTATTGCTTA TTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTA AAGATAGAAA TTATGCAAT
1501 ATTTCTCTA AAATAAAAC TGAAGCTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAGCC CTGATGTTG GTACTCCATT TAAGAACAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

```

m744.pep
  1 MKPLKLEFG FVDAANYRRR ENKDLFNRIF VKGEYLDEL C EPNISFLIGE
 51 KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLK ARHLTVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIENKF KALDEAINEY YGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEESQ ITFTESKFOA NLGFIERKFK
201 DALSQLKLD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVLLIRPDI FDSLGLQON TKLQDNSVEL DWRTDYKSYR
301 SSKIFGVFDH LLRTQQEKQD SLEKNSWDY YFPWNPALH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKSKEDY VVAEDFDNTS FQREYSIYLL
401 GEIKDHLIFY YSQSDYQNFL KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVIIPKEMS TANEFLOFLF DLNVIAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTPEFKNK Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

```

m745.seq
  1 ATGTTTTGGC AACTGACCGT TGTTTCAGTA ACCGCCGTCA TTGCACTGGC
 51 GACAATATTC ATCAATAAGA AAACCTCAA GCAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTTGCGCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGGC ACGAGTTTGA TGCCTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTTG TTTAAACGGC TGCATTGCAC
351 CAACTTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTGGTT
451 GCATTATGGA AAGCAAACCC CCTAAGGCA TCTGATTTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

```

m745.pep
  1 MFWQLTVVSV TAVIALGTIF INKKTSKOKA TLDVILNDYQ DAQFVEADNH
 51 ISPYIRGTAV DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPV MKIREEERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

```

g746.seq
  1 ATGTCCGAAA ACAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
 51 ACGGCGCAAC CGCGCGCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGTT CCGATCCTGC CGACAGCAAT
151 CCCGCACCGC AGGCCGCGCA AACCAGCGCA ACGGAAGCC AAACGGCAAA
201 CACGGCACAA ACCCTGCCT TGAATCCGC CGCCGAAAAC GGGGAAACCG
251 CCGCCGACAA ACCGCAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAAACGTA GCGCGCGCGC TGGTGCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGGTTTGAA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCGAAGCA GGCAAAACAA
451 CGCGTGCCG AAAAAGTGTC GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCGAAAC TGCTGCCGAA AAAACCAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAGAC AGCCGAAAA GACCGTTCCG ACGGCAAAA ACACGAAACG

```

751	GC GCAAAAAA	CCGACAAAGC	GGACAAACC	AAAACCGCGC	AGAAGGAAAA
801	AT CCGGCAAG	CGGGGCAAAA	AAGCGGCCAT	TCAGGCAGGT	TATGCCGAAA
851	AA GAACGCGC	CTTGAGCCTC	CACGCGCAAA	TGAAGGCGGC	GGGTATCGAT
901	TC GACCATCA	CCGAAATCAT	GACCGACAAC	GGCAAAAGTT	ACCGCGTCAA
951	AT CAAGCAAC	TATAAAAACG	CAGGGGATGC	CGAACGCGAT	TGGAACAAC
1001	TG CGCGTGCA	CGGCATCGCC	GGCCAGGTAA	CGAATGAATA	G

```
g746.pap
1 MS ENKQNEVL TGYEQLKRRN RRLVTASSL VAASCILLAA ALSSDPADSN
51 PA PQAGETGA TESQTANTAQ TPALKSAEN GETAADKPDQ LAGEDKPSAA
101 DSEISEPENV GAPLVLINDR LEDSNIGLE ESEKLQQAET AKTEPKQAKQ
151 RAAEKVSATA DSTDTVAEVD PKRTAEKPKQ KAERTAEAKP KAKETKTAEK
201 VADKPKTAAE KTKPDTAESK SAVKEAKKD KAEGKKTAEK DRSDGKKHET
251 AQKTDKADKT KTADEKESGK AGKKAIIQAG YAEKERALS QRMKKAAGID
301 ST ITEIMTDN GKVYRVKSSN YKNARDAERD LNKLRVHGIA GQVTNE*
```

```

m746.seq
1      ATGTCGCGAAA  ACAACACAAA  CGAAGTCCTG  AGCGGTTACG  AACAACTCAA
51     ACCGCGCGAAC  CGCGCGCGCC  TCGTAACGGC  AAGTTGCGCTG  GTTGCCGCGT
101    CCTGTCATCCT  GCTGGCAGCC  GCCCTCAGTT  CCGGCCCTGC  CGAACAGACT
151    GCCGGCGGAAA  CAAGCGGGCT  AGAAAAACAA  GCGGCAGGTG  CGGCAACAAC
201    CCGTCGCTTG  AATATCCGCG  CCGACAACCC  GCAGGACTTG  CGAGGCGGAG
251    ACAAGCCTTC  TGCCGCGGAC  AGCGAAATCA  GCGAGCCTGA  AAACGTAGGC
301    GCGCCGCTGG  TGCTGATTAA  CGAGCGCCTC  GAAGACAGCA  ACATCAAAAG
351    TTTTGGGAACA  TCCGGAAGAC  TGCAACAGCC  AGAAACCGCC  AAAACCCGAC
401    CGAAGCAGCG  AAAACACACG  GCTGCGCGAA  AAGTCCGCGC  AACTGCCGAC
451    AGTACGGATA  CGGTAGCGGT  TGAAAAACCG  AAACGCACGT  CCGAAACAAA
501    ACCGCAAAAA  GCGGAACGCA  CTGCCAAGC  CAAGCCCAAG  GCCAAGAAAA
551    CCAAAACCGC  CGAAAAGTT  GCCGACAAAC  CGAAAACCTG  CGCCGAAAAA
601    ACCAAACCGG  ATACCGCAAA  ATCCGACAGC  GCGGTAATAAG  AAGCGAAAAA
651    AGCGACAGAC  GCTGAAAGCA  AAAAAACAGC  CGAAAAGACG  CGTTCGGACG
701    GCAAAAAACA  CGAACCGGCA  CAAAAACCG  ACAAAACGGG  CAAGACCTAA
751    ACCGCGCGAG  AGGAAAAATC  CGGTAAAAAA  GCCGCATTTC  AGGCAGGTTA
801    TGCCGAAAAA  GAACGCGCCT  TAAGCCTCCA  GCGCAAAATG  AAGGCGCGCG
851    GTATCGATTG  GACCATACC  GAAATTATGA  CCGACAAACG  CAAAGTTTAC
901    CGCGTCAAT  CAAGCAATA  TAAAAACGCA  AGGGATGCGC  AATCGGATTG
951    GAAACAAATT  CGCGTACAG  GTATCGCGG  TCAGGTAACG  AATGAATAG

```

m746.pep

1	MSENKQNEVL	SGYEQLKRRN	RRRLVTASCL	VAASCILLAA	ALSSGPAECT
51	AGETSGVENK	AAGAAQTPAL	KSADKPDQL	AGEDKPSAAD	SEISFPENVG
101	APLVLINERL	EDSNIKGLEA	SEKIQAQETA	KTAPKQAKOR	AAEKVPATAD
151	STDITVAEKP	KRTAEKTPQK	AERTAKAPFK	AKETKTAEVK	ADPKPTAAEK
201	TKPDTAKSDS	AVKEAKKADK	AESKKTAEKD	RSDGKKHETA	QKTDKADKTK
251	TAEKEKSGKK	AAIQAGYAEK	ERALSQRKM	KAAGIDSTIT	EIMTDNGKVV
301	RVKSSNYLKA	RAEDRLNLK	RVHGIAQVQT	NE*	

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

	10	20	30	40	50
m746.pep	MSENKQNEVL	SGYEQLKRRNRRLVTASCLVAASCILLAAALSSGPAEQT----	AGETSG		
g746	MSENKQNEVL	TGYEQLKRRNRRLVTASSLVAASCILLAAALSSDPADSNPAQAGETGA			
	10	20	30	40	50
	60	70	80	90	100
m746.pep	VENKAAGAAQT	PALKSAA-----DKPQDLAGEDKPSAADSEISEPENVGAPLVLINER			
	: :: ::				
g746	TESQTANTAQT	PALKSAAENGETAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDR			
	70	80	90	100	110
					120

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```

      110      120      130      140      150      160      169
m746.pep  LEDSNIKGLEASEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g746      LEDSNIKGLEASEKLQQAETAKTEPKQAKQRAAEKVSATADSTDVAVEKPKRTAEPKPKQ
          130      140      150      160      170      180

      170      180      190      200      210      220      229
m746.pep  KAERTAKAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g746      KAERTAEAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAEGKKTAEK
          190      200      210      220      230      240

      230      240      250      260      270      280
m746.pep  DRSDGKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALS LQRMKAAGID
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g746      DRSDGKKHETAQKTDKADKTKTAEKEKSGKAGKAAIQAGYAEKERALS LQRMKAAGID
          250      260      270      280      290      300

      290      300      310      320      330
m746.pep  STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g746      STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          310      320      330      340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```

a746.seq
1   ATGTCCGAAA  ACAAACAAA  CGAAGTCCTG  AGCGGTTACG  AACAACTCAA
51  ACGGCGCAAC  CGCCGCGGCC  TCGTAACGGC  AAGTTGCTGT  GTTGCCCGCT
101 CCTGCATCCT  GCTGGCAGCC  GCCCTCAGTT  CCGGCCCTGC  CGAACAGACT
151 GCCGGCGAAA  CAAGCGGCGT  AGAAAACAAA  GCGGCAGGTG  CGGCACAAAC
201 CCCTGCCTTG  AAATCCGCCG  CCGACAAACC  GCAGGACTTG  GCAGGCGAAG
251 ACAAGCCTTC  TGCCGCGGAC  AGCGAAATCA  GCGAGCCTGA  AAACGTAGGC
301 GCGCCGCTGG  TGCTGATTAA  CGACCGCCTC  GAAGACAGCA  ACATCAAAGG
351 TT'TGGAAGCA  TCCGAGAAAC  TGCAACAGGC  AGAAACCGCC  AAAACCGCAC
401 CGAAGCAGGC  AAAACAACGC  GCTGCCGAAA  AAGTGCCGGC  AACTGCCGAC
451 AGTACGGATA  CGGTAGCGGT  TGAAAACCG  AAACGCACTG  CCGAAACAAA
501 ACCGCAAAAA  GCGGAACGCA  CTGCCAAGC  CAAGCCCAAA  GCCAAAGAAA
551 CCAAAACCGC  CGAAAAAGTT  GCCGACAAAC  CGAAACTGCG  CGCCGAAAAA
601 ACCAAACCGG  ATACGGCAAA  ATCCGACAGC  GCGGTAAGAG  AAGCGAAAAA
651 AGCCGACAAG  GCTGAAAGCA  AAAAAACAGC  CGAAAAAGAC  CGTTCGGACG
701 GCAAAAAACA  CGAAACGGCA  CAAAAACCG  ACAAGCGGA  CAAGACCAAA
751 ACCGCGGAGA  AGGAAAAATC  CGGTAAAAAA  GCCGCCATTG  AGGCAGGTTA
801 TGCCGAAAAA  GAACGCGCCT  TAAGCCTCCA  GCGCAAAATG  AAGGCGGCGG
851 GTATCGATTG  GACCATCACC  GAAATTATGA  CCGACAACGG  CAAAGTTTAC
901 CGCGTCAAT  CAAGCAACTA  TAAAAACGCA  AGGGATGCCG  AACGCGATTG
951 GAACAAATTG  CGGTACACG  GTATCGCGG  TCAGGTAACG  AATGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```

a746.pep
1   MSENKQNEVL  SGYEQLKRRN  RRLVTASCL  VAASCILLAA  ALSSGPAEQT
51  AGETSGVENK  AAGAAQTPAL  KSAADKPQDL  AGEDKPSAAD  SEISEPENVG
101 APLVLINDRL  EDSNIKGLEA  SEKLQQAETA  KTAAPKQAKQ  AAEKVPATAD
151 STDVAVEKP  KRTAETKPKQ  AERTAKAKPK  AKETKTAEKV  ADKPKTAAEK
201 TKPDTAKSDS  AVKEAKKADK  AESKKTAEKD  RSDGKKHETA  QRTDKADKTK
251 TAEKEKSGKK  AAIQAGYAEK  ERALS LQRM  KAAGIDSTIT  EIMTDNGKVV
301 RVKSSNYKNA  RDAERDLNKL  RVHGIAGQVT  NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746; 99.7% identity in 332 aa overlap

```

      10      20      30      40      50      60
a746.pep  MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m746      MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
          10      20      30      40      50      60

```

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	70	80	90	100	110	120
a746.pep	AAGAAQTALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA					
m746	AAGAAQTALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
a746.pep	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKAERTAKAKPK					
m746	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKAERTAKAKPK					
	130	140	150	160	170	180
	190	200	210	220	230	240
a746.pep	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
m746	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
	190	200	210	220	230	240
	250	260	270	280	290	300
a746.pep	QKTDKADKTKTAEKEKSGKAAIQAGYAEKERALSQRKMKAAAGIDSTITEIMTDNGKVY					
m746	QKTDKADKTKTAEKEKSGKAAIQAGYAEKERALSQRKMKAAAGIDSTITEIMTDNGKVY					
	250	260	270	280	290	300
	310	320	330			
a746.pep	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
m746	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
	310	320	330			

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

```

m747.seq
1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTTCCCGCGA TGTCAGCAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGGACG GTGACAAAAC CAAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2558; ORF 747>:

```

m747.pep
1   LTPWADAYAD LRKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPPYR HKTIIKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

```

a747.seq
1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTTCCCGCGA TGTCAGCAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAACC
201 CCGTGAGATT GTTTTGGACG GCGACAAAAC CAAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2560; ORF 747.a>:

```

a747.pep
1   LTPWADAYAD LRKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPPYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

1217

Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

	10	20	30	40	50	60
a747.pep	LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKWSVGIGLNVGKQLTDSVGLFDPYYR					
m747	LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKWSVGIGLNVGKQLTDSVGLFDPYYR					
	10	20	30	40	50	60
	70	80	90	100		
a747.pep	HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX					
m747	HKTIIKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX					
	70	80	90	100		

a747/m80195

gi|150271 (M80195) outer membrane protein [*Neisseria meningitidis*] Length = 272

Score = 59.3 bits (141), Expect = 6e-09

Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKWSVGIGLNVGKQLTDSVGLFDPYYR 60

+ PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+

Sbjct: 174 INPWSSEVKFDLNSRYKLNTGVTLNKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95

+T + E + GD + ++ EYG RV F

Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

g748.seq

1	ATGAGTCAAA	ACCAACCCGC	ACAACCGACC	AAACGCAATC	TGTTCAAAAC
51	CGCCCTTGCC	GTCGGCGCAA	TGCGGCGCAAT	CGGAGGTTAT	TTCGGCGGCA
101	AAAAACAGGG	CGAAACCGCC	GAACGCACCG	CCGAAAGCCA	ACACTCGCCC
151	CAAGCCATAC	CCTGCTACGG	CGAACATCAG	GCAGGTATCG	TTACGCCGCG
201	GCAGGCGTTT	TCCATTATGT	GCGCCTTCGA	CGTAACCGCG	CAAAGTGCCA
251	AGCAGCTGGA	AAACCTGTTC	CGCACACTGA	CCGCCCGCAT	CGAGTTTCTC
301	ACCCAAGGCG	GAGAATACCA	AGACGGCGAC	GACAACTCC	CGTCAGCCGG
351	CAGCGGCATT	TTGGGTAAAG	CCTTCAACCC	CGACGGATTG	ACCGTTACCG
401	TGCGGGTGGG	CAGCAGCCTG	TTTGACGGCC	GGTTCGGACT	CAAAGACAAA
451	AAAACGGTTC	ATTTCAGGA	AATGCGCGAC	TTCCCAACG	ATAAGCTGCA
501	AAAAGAGCTG	TGCGACGGCG	ATTTGACCT	GCAATCTCG	GCCTTCACCC
551	CCGAAACCTG	CCAAACCGCC	CTGCGCGACA	TCATCAACA	CACCGCCCAA
601	ACCGCCGTCA	TCCGCTGGAG	TATCGACGGG	TGGCAGCCTA	AATCCGAACC
651	CGGCGCGATG	GCGGCGCGCA	ACCTGTTGGG	CTTCCGAGAC	GGCACGGGCA
701	ACCCAAGGT	TTCCGATCCC	AAAACCGCCG	ACGAGGTTTT	ATGGACGGGC
751	GTGGCCGCCA	ACAGCCTCGA	CGAACCGGAG	TGGGCGAAAA	ACGGCAGCTA
801	TCAGGCAGTC	CGCCTTATCC	GCCGCTTTGT	CGAGTTTTGG	GACAGGACGC
851	CGCTTCAAGA	GCAAACCGAC	ATTTTCGGGC	GGCGAAAAATA	CAGCGGGGCG
901	CCGATGGACG	GCAAAAAAGA	AGCCGACCAA	CCGATTTCG	CCAAAGACCC
951	CGAGGGTGAT	ATCAGCCCA	AAGACAGCCA	TATGCGCCTG	GCGAATCCGC
1001	GCGATCCCGA	ATTCTCTAAA	AAACACTGCC	TCTTCGCGCG	CGCCTACAGC
1051	TATTCTCGCG	GACCCGCTC	AAGCGGACAG	CTTGATGTCG	GGCTGGTGTT
1101	CGTCTGTAT	CAGGCAATC	TTGCCGACGG	TTTCATCTTC	GTGCAAAACC
1151	TCCTCAACGG	CGAACCCTG	GAAGAATACA	TCAGCCCCCT	CGGCGGCGGC
1201	TATTTCTTCG	TCTTGCCCGG	CGTGGGAAAA	GGCGGATTCT	TGGGACAAGG
1251	GCTGCCGGGC	GTATAA			

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

1	MSQNQPAQPT	KRNLFKTALA	VGAIGAIGGY	FGGKKQGETA	ERTAESQHSP
51	QAYPCYGEHQ	AGIVTPROAF	SIMCAFDVTA	QSAKOLENLF	RTLTAIEFL
101	TQGEYQDGD	DKLPSAGSGI	LGKAFNPDGL	TVTVGVGSSL	FDGRFGLKDK
151	KTVHLQEMRD	FPNDKLQKSW	CDGDLSLQIC	AFTPETCQTA	LRDIIKHTAQ
201	TAVIRWSIDG	WQPKSEPGAM	AARNLLGFRD	GTGNPKVSDP	KTADEVLTWG
251	VAANSLEDEP	WAKNGSYQAV	RLIRRFVEFW	DRPLQEQTD	IFGRRKYSGA
301	PMDGKKKADQ	PDFAKDPEGD	ITPKDSHMRL	ANPRDPEFLK	KHCLFRRAYS
351	YSRGPASSGQ	LDVGLVFVCY	QANLADGFIF	VQNLLNGEPL	EYISPFGGG

748.899

1	ATGAGCAAAA	AACAACCCGC	ACAACCGACC	AGGCGCACTC	TTTTTAAAC
51	CGCGATCGCA	GCCGGAGCAG	TCGGCGCAAT	CGGAGGTTAT	CTCGCGCGGA
101	AAAACACAGG	GCGAACCCGC	GAACCGCACG	CCGAAGGCCA	ACACTCGCCC
151	C AAGCCTATC	CCTGCTACGG	CGAACATCAG	CGAGGCATCG	TTACGCGCGA
201	GCAGGCGTTT	TCGATTATGT	GGCCTTTCGA	CGTAACCCGG	CRAAGTGCCA
251	AGCAGCTGGA	AAACCTGTTC	CGCACCGTGA	CCGCGCCGAT	CGAGTTTCTC
301	ACCCAAGGCG	CGGAAATACCA	AGACGGCGAC	GACAAACTTC	CGCCAGCCGG
351	CAGCGCGATT	TTGGGCAAGG	CCTTCAACCC	CGACGGGCTG	ACCGTTACCG
401	TGGGGGTGGG	CAGCAGCTGC	TTTGACGGCC	GTTCTGGGACT	CRAAGACAAA
451	AAACCGATTC	ATTTCGAGGA	ATATGCGGCAC	GGTCCCAACG	ATAAGCTGCA
501	AAAAGCTTGG	TGCGACGGCG	ATTTGAGCCT	GCAAACTCTG	GCCTTCACCC
551	CCGAAACCTG	CCAAGCCGCC	CTGCGCGACA	TGCTCAAAAC	CACCTCTCAA
601	ACCGCGGTTA	TCCGTTGGAG	TATCGACGGG	TGGCAGCCCA	ATTCCGAACC
651	CGGCGCGATG	GCGGCGCGCA	ACCTGTTGGG	CTTCAGGGAC	GGCACGGGCA
701	ACCCAAAGT	TTCCGATCCG	AAAACCTGCC	ACGAGGTTTT	GTGGACGGGG
751	GTGGCCGCCA	ACAGCTCCGA	CGAACCGGAG	TGGCGAAAAA	ACGGCAGCTA
801	TCAGGCAGTC	CGCCTTATCC	GCCACTTTGT	CGAGTTTTTG	GACAGGACGC
851	CGCTTCAAGA	GCAAAACCGC	ATTTTCGGGC	GGCGCAAAAT	CAGCGGTGCG
901	CCGATGGAGC	GCAAAAAGA	AGCCGACCAA	CCGGATTTTT	CCAAAGACCC
951	CGAGGTTGAT	ATCACGCCCA	AAGACAGCCA	TATACGCGTG	CGGAATCCGC
1001	GCGATCCCGA	ATTCTCTCAA	AAACACCGCC	TCTTTCGCGC	CGCCTACAGT
1051	TATTCGCGCG	GACTCGCCTC	AAGCGGACAG	CTTGATGTCC	GGCTTGTGTG
1101	CGTCTGCTAT	CAGGCAAAAC	TTGCGCAGGG	ATTATCTTTC	GTGCAAAACC
1151	TCCTCAACGG	CGAACCCTGT	GAAGAATACA	TCAGCCCTTT	CGGCGCGGGC
1201	TATTTCTTTC	TCTTGCCCGG	CGTGGAAAAA	GGCGGCTTTT	TGGGGCAAGG
1251	GCTGCTGGGC	GTATAA			

m748.pap

per	1	MSKKQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGGKKQGETA	ERTAESQHSP
51		QAYPYGEHQ	AGIVTPQQA	SIMCAFNDTA	QSAKQENLNF	RTLTAIRIEFL
101		TQGGEYQGD	DKLPPAGSGI	LKGAFNPDGL	TVTYGVGSSL	FDGFRGLKDL
151		KPIHLOEMRD	FSNDKLQKSW	CDGDLSLQIC	AFTPETCQAA	LRDIIKHTVQ
201		TAIVRWSIDJ	WQPKSEPGAM	AARNLGLFRD	G7GNNPKVSD	KTADIEVLMTG
251		VAANSLDDEE	WAKNGSYQAV	RLIRHFVEFW	DRTPLEQDET	IFGRRKYSGA
301		PMDGKKEADQ	PDFAKDFEGD	ITPKDISHIRL	ANPRDPEFLK	KHRLFRRRAYS
351		YSRGLASSGE	<u>LDVGLVFVYC</u>	<u>QANLADGFIF</u>	<u>VQNLLNGEPL</u>	EEYISPFGGG
401		YFVFLPVGEK	<u>GGVGLQGGLL</u>	<u>V*</u>		

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

m748/q748 95.0% identity in 421 aa overlap

	10	20	30	40	50	60
m748.pep	MSKKQPAQPT	RRTLFKTAIAAGAVGA	IGGGYLGKKQ	QGETAERTAESQHS	PQAYPCYGEHQ	
g748	MSQNQPAQPT	KRNLFKLTALAVGA	IGAIGGYFGGKKQ	QGETAERTAESQHS	PQAYPCYGEHQ	
	10	20	30	40	50	60
	70	80	90	100	110	120
m748.pep	AGIVTPQA	AFSIMCAFDVTAQSAKQ	LENLFR	TLTARIEFLTQ	GGEYQDGGDKLP	PAGSGI
g748	AGIVTPQA	AFSIMCAFDVTAQSAKQ	LENLFR	TLTARIEFLTQ	GGEYQDGGDKLP	SAGSGI
	70	80	90	100	110	120
	130	140	150	160	170	180
m748.pep	LGKAFNP	DGLTVTVGVGSSL	FDGRFGLKDKKPIH	LQEMRDFSNDK	LQKSWCDGDL	SLQIC
g748	LGKAFNP	DGLTVTVGVGSSL	FDGRFGLKDKKTVHL	LQEMRDFPNDK	LQKSWCDGDL	SLQIC
	130	140	150	160	170	180
	190	200	210	220	230	240
m748.pep	AFTPETCQAAL	RDIHKHTVQTAVIR	WSIDGWQPKSE	PGAMAARNLLG	FRDGTGNPKV	SDP

```

a748.seq
1  ATGAGCAAAA ACCAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51  CCGCATCGCA GCTGGAGCAG TCGCGGCAAT CGGAGGTTAT CTCCGGCGCA
101  AAAAAAGCGG CGAAACCGCC CGAAGACACG CCGAAAGCCA ACACCTGCCC
151  CAAGCCTATC CTTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
201  GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCT
251  AGCAGCTTGA AAACCTGTTC CGCAGCTGA CCGCCCGCAT CGAGTTTCTC
301  ACCCAAGCGC GCGAATACCA AGACGGCGAC GACAAACTTC CGCCAGCCGG
351  CAGCGGCATT TTGGGCAAGC CTTTCAACCC CGACGGGGTG ACCGTTACCG
401  TGGGGTGGG CAGCAGCTGT CTTACGGGCC GGTTCCGGAT CAAAGACAAA
451  AAACCGATTG ATTTGCAGGA AATGCGCGAC TTCTCAAACG ATTAGCTTGA
501  AAAAAAGCTG TCCGACGGCG ATTTGAGCCT GCAAATCTGT GCCTTCACCC
551  CCGAAACCTG CCAAGCCGCC CTCGCGGACA TCATCAAACA CACCGTCCAA
601  ACCGCGTTA TCCGCTGGAG TATGCACGGG TGGCAGCCTA AATCCGAACC
651  CGGCGCGATG GCGCGCGCCA ACCTGTTGGG CTTCGCGGAC GGCACGGGCA
701  ATCCCAAAGT TTCCGACCCC AAACTGCGCG ACGAGGTTTT GTGGACGGGG
751  GTGGCGCCCA ACAGCCTFCA CGAACC GGAG TGGGCGAAAA ACGGCAGCTA
801  TCAGGCAGTC CGCCTTATCC GCCACTTTGT TGAGTTTTGG CACAGGACGC
851  CGCTTCAAGA GCAAAACGAC ATTTTCGGGC GGCAGAAATA CAGCGGGCCG
901  CGGATGGAGC GCAAAAAGA AGCCGACCAA CCGGATTTTG CCAAAGACCC
951  CGAGGGGAAT ACCACGCCCC AAGACAGCCA TATACGCTG CGGAATCCGC
1001  GCGATCCGCA GTTCCTTAAA AAACACCGCC TCTTCGCGCG CGCCTACAGC
1051  TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTGC GGCTGGTGGT
1101  CGTCTGCTAT CAGGCAAAAC TTCCGACAGG ATTCATCTTC GTGCAAAAAC
1151  TCCTCAACGC CGAAGCCGCT GAAGAATACA TCAGCCCTTT CGGCGGCGGC
1201  TATTTCTTCG TCTTGGCCGG CGTGAAAAAA GCGCGCTTTT TGGGGCAAGG
1251  GCTGCTGGGC GTATAA

```

```

a748.pap
1  MSKNQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKRGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPQQA F SIMCAFDVTA QSAQKGLNLF RLTJARIEFL
101 TQGGEQYQDG DKLPPAGSGI LGKAFNPDLG TVTVGVGSSL F DFGREGLDKD
151 KPIHLQEMRD FSNDKLQKSW CDGDLSLQIC AFTPETCQAA LRDIKHTVQ
201 TAVIRWSIDG WQKSPEGAM AARNLGLGFRD GTGNPKVSDP KTADEVLTWG
251 VAANSLDEPE WAKNGSYQAV RLIRHVFEEF DRTPLOEQDT IFGRRKYSGA
301 PMDGKKEADG PDFAKDPGPN TTPKDSHIRL ANPRDPEFLK KHRLFRFRAYS
351 YSRGLASSGQ LDGVLVFCY QANLADGFIF VQNLNGEPL EEEYISPGGG
401 YEFVLPVEKE GGFLGOGLLG V*

```

Computer analysis of this amino acid sequence gave the following results:

#748/#748 99.0% identity in 421 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

```
g749.seq
1  ATGAGAAAAAT TCAATTGTGAC CGCATTGTCC GTGATGCTTG CCTTGGGTTT
51  AAGCCGCGTGC CAGCGCGCCG AGCGCGAGAA AGCCGCGCCG GCCGCGTCCG
101 GTGAGACCCA ATCCGCCAAC GAAGCGGTT CGGTGCGTAT CGCGCTCAAC
151 GACAAATGCT GCGAACCGAT GAATCTGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAAACAAAC CGCGCCGCAA CTCTGAATGG GAAATCTCTGA
251 AGGCGGTGAT GTGGTGTGAC GAACCGGAAA ATATCGCCCC GGGGCTTTCC
301 GACAAATATG CCGTAACcct GCTGCCGGGC GAATACGAA TGCAGTGGCG
351 CCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAGCCGAC AGCGGCTTTA
401 AAGACACCGC CAACCAAGCG GATTGGAAAG AACTGCCCCA ACCGCTGCCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG CGGCGAAAC
501 CAAACCTTTT ACCGAAGCCG TCRAAGCAGG CGACATTGAA AAGCGGAAAT
551 CCTGTTTG CGGCAACGCG GTCCATTACG AACGCATGAA ACCGATTGCC
601 GAGCTTTTCA CGCAACTCGA CCGCTCATC GATCGTGTG AAGACGACTT
651 CAAAGACGTT GCGAAAGATG CCGGTTTAC CGGCTTCCAC CGTATCGAAC
701 AAGCCCTTGT AGTGGAATAA GACGTATCCG GCGTGAAGA AACCCGCGGC
751 AAAGCTGATG CCGATGTGCA AGCCCTGCAA AAAGAAATCG ACGCATGGG
```

```

801 GttccctCCG GGCAAAGTGG TCGGCGGCGC GTCCGAAGTGG ATTGAAGAAG
851 CGGCGGGCAG TAAATCAGC GCGGAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TCGGACGGA TCTAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATTGAGG CCAAAAACAA AGCCTTGTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGCACCAAA
1051 GACGGTTTGG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

```

g749.pep
1 MRKFNLTLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIAVN
51 DNACEPMNLT VPSGQVVENI KNSGRKLEW EILKGVVVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLQPLA
151 DYKAYVQGEV KELAATKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRILGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

```

m749.seq
1 ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAGTAT CGCCGTCAC
151 GACAATGCCT GCGAACCGAT GGAACGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAAACGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
501 CAAAACTTTT ACCGAAGCCG TCAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCGCG GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTTCAC CGTATCGAAT
701 ACGCCTTTG GGTGGA AAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAACGTATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAA TCGTCGATTT
951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTGG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

```

m749.pep
1 MRKFNLTLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
51 DNACEPMELT VPSGQVVENI KNSGRKLEW EILKGVVVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRILGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

```

          10      20      30      40      50      60
m749.pep MRKFNLTLALSVMALGLTACQPPEAEKAAPASGEAQTANEGGSVSIIVNDNACEPMELT
          |||||
g749      MRKFNLTLALSVMALGLTACQPPEAEKAAPASGETQSANEGGSVGIIVNDNACEPMNLT
          10      20      30      40      50      60

```

1222

	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNSGRKLEWEILKGMVMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
g749	VPSGQVVFNIKNSGRKLEWEILKGMVMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVADSGFKDTANEADLEKLPQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRVHYERIEPIAELEFSELDPFVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
g749	KAKSLFAATRVHYERIEPIAELEFSELDPFVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
g749	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLS					
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

a749.seq

1	ATGAGAAAAT	TCAATTTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCCGCTGC	CAGCCGCCGG	AGGCGGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAC	GAGGGCGGTT	CGGTCAGTAT	CGCCGTC AAC
151	GACAATGCCT	GCGAACCGAT	GGAAGTGACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AAGGCGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATCGCCCC	CGGACTTTCC
301	GATAAAATGA	CCGTCAACCT	GTTGCCGGGC	GAATACGAAA	TGACTTGC GG
351	TCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAA	AACTGTCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTATGTTCA	AGGCGAAGTC	AAAGAGCTGG	TGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCA TC	GATGCGCGTG	AAGACGACTT
651	CAAAAGACGGC	GCGAAAGATG	CCGGATTAC	CGGCTTCCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCCG	GCGTGAAGGA	AATGCGAGCG
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC
801	GTTTCCTCCG	GGCAAGGTGG	TCGGCGGCGC	GTCCGAAC TG	ATTGAAGAAG
851	TGGCGGGCAG	TAAATCAGC	GGCGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGACT	TCCAAGCCAA	TGTGGACGGA	TCGAAAAAAA	TCGTCGATTT
951	GTTCCTGTCG	TTGATCGAGA	CCAAAAACAA	AGCCTTGT TG	GAAAAAACCG
1001	ATACCAACTT	CAACAGGTC	AACGAAATTC	TGGCGAAATA	CCGGACTAAA
1051	GACGGTTTTG	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAGCGTT
1101	ACAGGCCTCT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTT	GAAATAA			

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

a749.pep

1	MRKFNL TALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSI AVN
51	DNACEPMELT	VPSGQVVFNI	KNSGRKLEW	EILKGMVVD	ERENIAPGLS
101	DKMTVTLLPG	EYEMTCGLLT	NPRGKLVVTD	SGFKDTANEA	DLEKLSQPLA
151	DYKAYVQGEV	KELVAKTKTF	TEAVKAGDIE	KAKSLFADTR	VHYERIEPIA
201	ELFSELDPVI	DAREDDFKDG	AKDAGFTGFH	RIEYALWVEK	DVSGVKEIAA
251	KLMTDVEALQ	KEIDALAFPP	GKVVGGASEL	IEEVAGSKIS	GEEDRYSHTD

301 LSDFQANVDG SKRIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
a749.pep	MRKFNLTSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT					
m749	MRKFNLTSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT					
	10	20	30	40	50	60
a749.pep	VPSGQVVFNIKNNSGRLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
m749	VPSGQVVFNIKNNSGRLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
a749.pep	VPSGQVVFNIKNNSGRLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
m749	VPSGQVVFNIKNNSGRLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
a749.pep	NPRGKLVVTDGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTTFTEAVKAGDIE					
m749	NPRGKLVVTDGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTTFTEAVKAGDIE					
	130	140	150	160	170	180
a749.pep	NPRGKLVVTDGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTTFTEAVKAGDIE					
m749	NPRGKLVVTDGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTTFTEAVKAGDIE					
	130	140	150	160	170	180
a749.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
m749	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	190	200	210	220	230	240
a749.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
m749	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	190	200	210	220	230	240
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
a749.pep	LSDFQANVDGSKRIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
m749	LSDFQANVDGSKRIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
	310	320	330	340	350	360
a749.pep	LSDFQANVDGSKRIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
m749	LSDFQANVDGSKRIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
	310	320	330	340	350	360
a749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
m749	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380	389			
a749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
m749	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq

1	GTGAAACCGC	GTTTTATTG	GGCAGcctGC	GCCGTCCTGC	CGGCCGCCTG
51	TTCGCCCGAA	CCTGCCGCCG	AAAAAACTGT	ATcgcCGCA	TCCCAAGCCG
101	CATCCACACC	TGTCGCCACG	CTGACCGTGC	CGACCGCGCG	GGCGGATGCC
151	GTTGTGCCGA	AGAATCCCGA	ACgcgtcgcc	gtgtAcgaCt	ggCGGCGTt
201	ggaTACGCTG	ACCGAGCCGG	GCGTGAATGT	GGGCGCAACC	ACCGCGCCGG
251	TGCGCGTGGA	CTATTTGCAG	CCTGCATTG	ACAAGCGCGC	AACGGTGGGG
301	ACGCTGTTTG	AGCCCGATTG	CGAATCCCTG	CACCGCCACA	ATCCGCAGTT
351	TGTCATTACC	GGCGGGCCGG	GTGCGGAAGC	GTATGAACAG	TTGGCGAAAA
401	ACGCGACCAC	CATAGATTG	ACGGTGGACA	ACGGCAATAT	CCGCACCAGC
451	GGCGAGAAGC	AGATGGAGAC	CCTGTCGCGG	ATTTTCGGTA	AGGAAGCGCG
501	CGTGGCGGAA	TTGAATGCGC	AGATTGACGC	GCTGTTCCGC	CAAAAGCGCG
551	AAGCCGCCAA	AGGCAAAGGA	CGCGGGCTGG	TGCTGTCGGT	TACAGGCAAC
601	AAGGTGTCCG	CCTTCGGCAC	GCAATCGCGG	TTGGCAAGTT	GGATACACGG
651	CGACATCGCG	CTGCCGCCCG	TGGACGAATC	TTACGCAAC	GAAGGGCAGC
701	GGCAGCCCGT	TTCCTTCGAA	TACATCAAAG	AGAAAAACCC	CGGCTGGATT
751	TTCATCATCG	ACCGCACCGC	CGCCATCGGG	CAGGAAGGGC	CGGCTGCCGT

801 GGAAGTGTG GATAACGCGC TGGTATGCGG CACGAACGCT TGAAGCGCA
851 AGCAATCAT CGTCATGCCT GCCGCGAAT ACATTGTCGC GGGCGGCGCG
901 CGGCAGTTGA TACAGGCGGC GGAACAGTTG AAGCGGCGCT TTGAAAAGGC
951 AGAACCCGTT GCGGCGCAGT AG

This corresponds to the amino acid sequence <SEQ ID 2574; ORF 750.ng>:

g750.pap

1	VKP	RFYWAAC	AVLPAACSPF	PAAEKTVSAA	SQAASTFPVAT	LTVPTARGDA
51	VVP	KNPERVA	VDWAALDTL	TEPGVNVGAT	TAPVRVDYLO	PAFDKAATVG
101	TLF	EPDCESL	HRHNQQFVIT	GPGAEAYEQ	LAKNATTIDL	TVDNGNIRTS
151	GKE	QEMTKTL	HFGKEARVAE	LNCQADIALFA	QKREAAGKDG	RGVLVSVTGN
201	KVS	AFGTQSR	LASWINGDIT	LPVVDSELRN	EGHGGQVSFE	YIKEKNPGWI
251	FI I	DRTAAIG	QEGPAAVEVL	DNALVCGTNA	WKRKQIIIMP	AAQYIVAGGA
301	RQL	IQAAEQAL	KAAFEKAEPV	AAQ		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2575>:

```
m750.seq
1      GTGAAACCCGC GTTTTTATTG GGCAGCCTGC GCCGTCTCGC TGACCGCCGTG
51     TTCGCCCGAA CCTGCGCCGC AAAAAACTGT ATCCGCCGCA TCCGCATCTG
101    CCGCCACGCT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
151    AATCCCGAAC GCGTCGCCCT GTACGACTGG GCGGCGTTGG ATACGCTGAC
201    CGAATTGGGC GTGAATTGTG GCGCAACCAC CGCGCCGTGG CGCGTGGATT
251    ATTTCGACCC TGCATTTGAC AGCGCGCGAA CCGTGGGGAC CGTGTTGAG
301    CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351    CGGCGCGGGC GCGGAAGCGT ATGAACAGTT AGCGAAAAAC GCGACACCCA
401    TAGATCTGAC GGTGGACAA CCGCAATATCC GCACGACGGG CGAAAGACGA
451    ATGGAGACCT TTGCGCGGAT TTTCGGCAAG GAAGCGCGCG CGGCGGAATT
501    GAAAGCGCAG ATTGACGCGC TGTTCGCCCA AACCGCGGAA GCCGCGCAAG
551    CGAAGGACGC CGGGCTGGTG CTGTCGGTTA CGGGCAACAA GGTCTCCGCC
601    TTCGCACAGC AGTGCAGGTT GCGCACTTGG ATACCGCGCG ACATCGCGCT
651    ACCGCCTGTA GACGAATCTT TACGCAACGA GGGGACGGC CAGCTGTGTT
701    CCTTCGAATA CATCAAGAG AAAAACCCCG ATTGGAATTT CATCATCGAC
751    CTAACCGCTG CATCGCGGCA GGAAGGCGGG GCGGCTGTGC AGGATTGGGA
801    TAGCGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAAATCATCG
851    TCATGCTGCG CCGCAACTAC ATTGTGCGCG GCGGCGCGCG GCAGTTGATT
901    CAGCGCGCGG AGCACTTGAA GCGCGCGTTT AAAAAGGCAG AACCCGTTGC
951    GGC GGGGAAA AAGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2576; ORF 750>:

```
m750.pap
1      VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
51     NPERVAVDYW AALDTLTTELG VNVGATTAPV RVDYLQPAFD KAATVGTLFE
101    PDYEAHLRYGK PQLVITGGPG AEAYEQALAKN ATTIDTLVDN GNIRTSGBKQ
151    METLARIFRGK PAAEAELKAG I DALFAQLTRE AAKGKGRGLV LSVTGNKQVA
201    FGTQSRSLASW IHGDIGLPPV DESLRNEGHG QFVSFEYIKE KNPDWIFIID
251    RTAAEQGQEGP AAVEVLDNAL VRGTNAWKRR QIIVMPAANY IVAGGARQLI
301    RQAEPVKAAPF KKAEPVAACK K*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

m750/g750 **93.8% identity in 322 aa overlap**

	10	20	30	40	50	
m750.pep	VKPRFYWAACAVLLTACSP	EPAAEKTVSAASASA----	ATLTVPTARGDAVV	PKNP	ERVA	
		:				
g750	VKPRFYWAACAVLPAACS	EPAAEKTVSAASQAAST	PPVATLTVPTARGDAVV	PKNP	ERVA	
	10	20	30	40	50	60
	60	70	80	90	100	110
m750.pep	VYDWAALDTLT	ELGVNGATTAP	VRVDYLQPAF	DKAATVGT	LFEPDYEAL	HRYPQLVIT
g750	VYDWAALDTLT	EPGVNGATTAP	VRVDYLQPAF	DKAATVGT	LFEPDCESL	HRHNPQFVIT
	70	80	90	100	110	120
	120	130	140	150	160	170
m750.pep	GGPGAEAYEQLAK	NATTIDLTVD	NGNI	RTSGEKQ	METLARI	FGKEARA
	ELKAQIDALFA					


```

g750      GGPGAEAYEQ LAKNATTIDLTVDNGNIRTSGEKQMETLSRIFGKEARVAELNAQIDALFA
           130      140      150      160      170      180

           180      190      200      210      220      230
m750.pep  QTREAAK GKGRGLVLSVTGNKVS AFGTQSRLASWIHGDI GLPPVDES LRNEGHGQPVSF
           |||||
g750      QKREAAK GKGRGLVLSVTGNKVS AFGTQSRLASWIHGDI GLPPVDES LRNEGHGQPVSF
           190      200      210      220      230      240

           240      250      260      270      280      290
m750.pep  YIKEKNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWKRKQIIVMPAANYIVAGGA
           |||||
g750      YIKEKNPGWIFIIDRTAAIGQEGPAAVEVL DNALVCGTNAWKRKQIIVMPAANYIVAGGA
           250      260      270      280      290      300

           300      310      320
m750.pep  RQLIQAAEQ LKA AFKAEPVAAGKKX
           |||||
g750      RQLIQAAEQ LKA AFKAEPVAQX
           310      320

```

```
a750.seq
1      GTGAACCCGC GTTTTATTG GGCAGCCTGC GCCGTCTGCG TGACCCGCCTG
51     TTCGCCCGAG CCTGCCGCGG AAAAACAATT ATCCGCCCGCA TCCGCATCTG
101    CGCGCACTAC GACCGTCGCG GCGATCCG TGGTCCGGAAG TCGGCCGAAG
151    AATCCCGAAC GCGTCGCCGT GTACGACTGG GCGGCGTTGG ATACGCTGAC
201    CGAATTGGGT GTGAATGTGG GCGCAACCAC CGCGCCGGTG CGCGTGGATT
251    ATTTGCAGCG TGCATTTGAG AAGCGCGCAA CGGTGGGGAG CGTGTTCGAG
301    CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351    CGGGCCGGGG GCGGAAGCGT ATGAACAGTT GCGCAAAAAC GCGACCACCA
401    TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCGACGG CGAAAAGCAG
451    ATGGAGACCT TGGCGCGGAT TTTCGGCAAG CAGAGCGCGG CGGCGGAATT
501    GAAGGCGCAG ATTGACGGCG TGTTCCGCCA AACCGCGCAA GCCGCCAAG
551    GCAAAAGGAC GCGGCTGGTG CTGTCGGTTA CGGGCAACAA GGTGTCGCCC
601    TTCGCACGCG AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCTT
651    ACCGCCTGTA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
701    CCTTCGAATA CATCAAGAG AAAAACCCCG ATTGGATTTT CATCATCGAC
751    CGTACCGCCG CCATCGGGCA GGAAGGCGCG GCGGCTGTGC AAGTATTGGA
801    TAACGCGCTG GTACCGGCGCA CGAAGCGCTT GAAGCGCAAG CAATCATTCG
851    TCATCGCTCG CGCGACGATC ATTGTGCGGG GCGGCTCGCG GCAGTTGATT
901    CAGCGGCGGG AGCAGTTGAA GGAGGCGTTT GAAAAGGCAG AACCCGTTGC
951    GGCGGGGAAA GAGTAG
```

```
a750.pap
1 VKPFRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
101 NPFRVYAVHD AALDTLTGLG VNVGATTAPV RVDYLQPAFD KAATVGLTLE
51 PDYEALHYRN POLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
151 METLARIFGK EARAELKAQ IDALFAQTRE AAKGKGRGLV LSVTGNKVSQ
201 FGTQSRSLAS IHGDIGLPPV DESLRNEGHG QPVSFYIKE KNPDWIFIID
251 RTAAIGQEGP AAVEVLNDAL VRGTNAWKRK QIIVMPAANY IVAGGSRQLI
301 QAAEQLEKAF EKAEFVAAGK E*
```

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

	10	20	30	40	50	60
a750.pep	VKPRFYWAACAVLLTACSEPEPAEKTQVSAASASAATLTVP	TARGDAVVPKNPERVAVDW				
m750	VKPRFYWAACAVLLTACSEPEPAEKTQVSAASASAATLTVP	TARGDAVVPKNPERVAVDW				
	10	20	30	40	50	60
	70	80	90	100	110	120
a750.pep	AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVITGGPG					
m750	AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVITGGPG					

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	70	80	90	100	110	120
a750.pep	130	140	150	160	170	180
	AEAYEQLAKNATTIDLTVDNGNI RTSGEKQMETLARI FGKEARAAELKAQIDALFAQTRE					
m750	130	140	150	160	170	180
	AEAYEQLAKNATTIDLTVDNGNI RTSGEKQMETLARI FGKEARAAELKAQIDALFAQTRE					
a750.pep	190	200	210	220	230	240
	AAKGKGRGLVSVTGNKVS AFGTQSRLASWIHGDIGLPPVDES LRNEGHGQPVSFEYIKE					
m750	190	200	210	220	230	240
	AAKGKGRGLVSVTGNKVS AFGTQSRLASWIHGDIGLPPVDES LRNEGHGQPVSFEYIKE					
a750.pep	250	260	270	280	290	300
	KNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWK RKQIIVMPAANYIVAGGS RQLI					
m750	250	260	270	280	290	300
	KNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWK RKQIIVMPAANYIVAGGARQLI					
a750.pep	310	320				
	QA AEQLKEAF EKAEPVAAGKEX					
m750	310	320				
	QA AEQLKAA FKAEPVAAGKKX					

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

m751.seq..

```

1  ATGGCTTGGA GTATGTTTGC CACAACCCAA GCCGATAGAG CGGTAAGGTC
51  TGCAACTGCA CCTAAAGAAA TGTGGTTCCA TAAGAAGATA ATAGATGAAA
101 AAACAGGTAA AGTATCCTTT GATACCAGAC AAATTTGGTC ATTGAATGAT
151 TTAAGCAAGG AAGAACTGGC AAGCATTCAA GACACAAATG GCAAAGTTAT
201 TACTGTGTCT AATCCTGGTA TTTTCAATAA TCGAGAAGAT TCATTAAGCA
251 ACGCAGCAAA ACAAAATCGT AATAGTACAA ACGGTAGTGG TGTATTGCA
301 GTCATGAATC CTCCAACAGG GAAATATAAA TCTGATTCTA ATAACAAAAT
351 AAAAGATTTT TTATGGCTCG GTTCAAGTCT TGTTTCTGAA CTGATGTATG
401 TCGGTTACGA CCAATTAAT AATAAAGTGT TCCAAGGCTA TTTACCCAAA
451 ACCAATTCAG AAAAACTGAA TCAAGATATT TATCGAGAGG TTCAAAAAAT
501 GGGTAACGGC TGGTCGGTTG ATACCAGTAA TCACAGTCGT GGGGGAATTA
551 CAGCAAGCGT TTCCTTAAAA GATTGGGTAA ACAATCAAAA ACAAAATGGC
601 ATTGCCCCAA TCAGAAAAGC ACGTTTCTAT GGTACAGCCA CAAATGTGCA
651 GAATGATTAC GCCGATGTTT TACAGAAAAA CGGCTATACC TATACGGGTG
701 CAGACGGCAA AACTTATAAC AGCGGATCCT ACTCAATCGT GCATGATAAA
751 GATTTTGTGG GGAACAAATG GATACCTTTC TTGCTAGGAA CCAATGACAC
801 CACACAAGGT ACATGTAAGG GGTGTGTGCTA TTCGCATAGC AGTTATTTTG
851 CCGAGGTGCC AAAAGCAGGT ACAAAAGAAT TTGATGACTA TGTA AAAATA
901 TGGGGTGAAG TTGAATATGA CGCTCAAGGT AAGCCAATTA ACAAACTCAA
951 ACCCATACTG GTAGAACCAA ACAAAACAAA AGATAATGAA AAATATGAAA
1001 AAGAAGCTTT CTA

```

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>:

m751.pep..

```

1  MAWSMFATTQ ADRAVRSATA PKEMWPHKKI IDEKTGKVSF DTRQIWSLND
51  LSKEELASIQ DTNGKVITVS NPGIFNNRED SLSNAAKQNR NSTNGSGVIA
101 VMNPPTGKYK SDSNNKIKDF LWLGSSLVSE LMYVGYDQLN NKVFQGYLPK
151 TNSEKLNQDI YREVFQKMGNG WSVDTSNHSR GGITASVSLK DWVNNQKQNG
201 IAPIRKARFY GTATNVQNDY ADVLQKNGYT YTGADGKTYN SGSYSIVHDK
251 DFGVGNKWIPI LLGTNDITQG TCKGLCYSHS SYFAEVPKAG TKEFDDYVKI
301 WGEVEYDAQG KPINKSKPIL VEPNKT KDNE KYEKEAF*

```

a751.seq not found yet

a751.pep not found yet

1227

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

m752.seq..

```

1   ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTG ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTCTG CATTCCCGAC TCTTTCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTCG ACCGCATTGC
651 TACCAGTAAC GCTATTGAAA ACAAGGCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAATCC GTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTGTG ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTATCTTA TTACCAATGC GATATTATCA AGCGGCGCGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAACACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTG GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGTCCTCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

m752.pep

```

1   MKISRPPEFT LQOEYMOHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51  DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQWFECIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFH PVVQAILHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPQYAK SYLYAETDDL
351 DLTYFIYYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALYVAP QDILLERLEK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

m752-1.seq

```

1   ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTG ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTCTG CATTCCCGAC TCTTTCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTCG ACCGCATTGC

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```

651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTC TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTGGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCTGCCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTCACTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTG GAGCACTACA TTTCCGACAA AAAAAACAC CAACAGGAAT
1151 TCAAAAGCAGC GATTGCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDETRM KWRVAVKESRK KIQKPIDFPF
101 EHQFWFCIPD SLOARLHLID KSCGSSIGTS SLGGFGRSEQ NRELLKSLIM
151 EEAFITSAQLE GAATTRKVAR DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFH PVVQAILHF LIGYIHFPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPQYAK SYLYAETDDL
351 DLTYYFIYYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDSLKL GEYRFLVPFK
451 SGNALYVAP QDLERLEKK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTAAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTGTC GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TCGCCAGTT ATTCCTAGT ACGACAGTAC
401 GCGCCTTGTA TCATAAAGG AGCGATAAGG GTTTGAGAAT TTTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPLNII SPKLYPNEQW NESEALGAI WLWYQSPTHR QVPFIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLES D RHLRDN SDWN
101 CGDNIWLIQW FAPLGHSHQM RSAVRQLFPS TTVRALYHK G SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```
m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTTG GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTGTC TGGGCATAAA TGCCCGACAG
451 GTTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
601 CCTTGCTTGG CTGCCAATGA ATTTTATGTC ATGCAGACCA TCAAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTGTATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTCGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTCA GTACTCTATC ATGACGAATA
951 CGATGTTCGT CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATT
1051 AACCTGACTA ACCACGGTAA GAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```
m754.pep
1  MKKSILTVSG NRMKPRITY LDVWANDERI GTLEKGAMYR FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVRCND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQQYMAEIF HGRFVSVSFG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIKQAGIA VAQTSLSSEDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDL SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKITY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*
```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```
m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTAATCCGAT ATTAACCA
101 TCTTGCTAG CATGGAATT GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTT ACTCCTGTAT TTCAAACATT AAGTTTTACC
251 GCCTTGAAAG TGATTTGAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTGAA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA
```

1230

This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

m755.pep..

```

1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSVYLG
51 REGISEAHGT IAIQELTARE DWFYSCISNI KFYRLESDLN AQFIADGVYQ
101 AKQAFLLQVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*

```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

m756.seq

```

1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTGTCAG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

m756.pep

```

1 MTANFAQTLV EIQDSLVRV SVQYGGDDNL KRLTADKRKQ YELNFKISEG
51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTTLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAEQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYGA LVSDGNFTAV LSDIGD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

a756.seq

```

1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTGTCAG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

a756.pep

```

1 MTANFAQTLV EIQDSLVRV SVQYGGDDNL KRLTADKRKQ YELNFKISEG
51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTTLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAEQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYGA LVSDGNFTAV LSDIGD*

```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLVRVSVQYGGDDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLVRVSVQYGGDDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

1231

	70	80	90	100	110	120
m756.pep	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVFPYGAELVSDGNFTAV					
a756	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVFPYGAELVSDGNFTAV					
	130	140	150	160	170	180
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

m757.seq

```

1  ATGAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAAAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAGC
351 GGAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCCGAC AATGCTGCGT GATACCGCGC ACCAAATCGA AATGCGGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

m757.pep (lipoprotein)

```

1  MKILALLIAA TCALSACGSQ SEEQPASAQP OEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLEHVV PIDNAEGKNL LHDFSDGLTI LTVDTDKADK
101 ITAVRVVWNT DAMPKAEKL SKAAAALIAA TAPEDRTMLR DTGQDIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPVS VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

m758.seq

```

1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAAC TGTGGAATTT CCCGTCTGCT ACGGCGGCGA ATACGGCCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGACAGAA GGATTGAGCC
501 ATGA

```

1232

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1 MNNLTVFTRF DTLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGEYGP
 51 DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101 RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151 LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1 ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51 TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAAC TGTGGAAATT CCCGTCTGCT ACGGCGGCGA ATACGGCCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC
501 ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1 MNNLTVFTRF DTLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGEYGP
 51 DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101 RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151 LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

	10	20	30	40	50	60
m758.pep	MNNLTVFTRFDTLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGEYGPDLAEVAAFHQ					
a758	MNNLTVFTRFDTLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGEYGPDLAEVAAFHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m758.pep	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
a758	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
	70	80	90	100	110	120
	130	140	150	160		
m758.pep	GVYPFASPGGWQIIGRTELP LFRADLNPPPTLLAAGDQVRFVAERIEPX					
a758	GVYPFASPGGWQIIGRTELP LFRADLNPPPTLLAAGDQVRFVAERIEPX					
	130	140	150	160		

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1 ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51 TCTTTTGGCC GTTTCCTG CTTACTCATC CATTGTCCGC AACGATGTCG
101 ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGGCGC GTTACCCGTA
151 GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201 GGTTCTCAAC GGCATCCCCA TGCCCGACTT CCGCGTCAGC AACCGCCAAA
251 CCGCCATCGC CACCTGGT CACCCCAAT ACGTCAACAG TGTCAAACAC
301 AACGTCGGCT ACGGTTCCAT ACAATTGCGC AACGACACCC AAAATCCAGA
351 AGAACAAGCC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGGACT
401 ACGACTACCA CCTTCCCGC CTCAACAAAC TGGTTACCGA AATCTCACCT
```


451 ACCGCACTCA GCAGCGTACC CTTGCTTGGG AACGGCCAGC CAAAGGCCAA
 501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTGTACGA CTCGGCTCAG
 551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGCGTACACG AACCGCCCCG
 601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAGTAT TGGGGTTCCA
 651 AAACCACGGC TTACTCGTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA
 701 CCTACGCAAT CGCGGGAGAC AGCGGTTCCT CCCTGTTTGC CTTGACAAAG
 751 CATGAAAACC GCTGGGTGCT TCGGGGCGTA CTCAGCACCT ACGCCGGCTT
 801 CGATAATTTC TTCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT
 851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTCGGGCT GACCACCAAC
 901 GAACTCATAT GCGCGACAA CGGTAATGGC AACAGCACCC TGCAAGGGCT
 951 CAACGAACGC ATCACCTTGC CCATTGCAAA CCCTTCGCTT GCCCCACAAA
 1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GTCATCCTA
 1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA
 1101 AGGCGCAGGC GCATTGCACT TCGACAGCAA CTTACCCGTC GTCGGTAAAA
 1151 ACCACACATG GCAAGGTGCA GGCCTTATCG TAGCCGACGG CAAACGCGTC
 1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC
 1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCAGGGC GACATCAGCA
 1301 TCGGGGAAGG CACTGTCGTA CTCGCCCAA AAGCTGCTTC AGACGGCAGC
 1351 AAACAAGCAT TCAACCAAGT CGGCATCACC AGCGGCAGGG GCACGGCCGT
 1401 CCTCGCCGAC AGCCAGCAAA TCAAAACCCG AAACCTCTAT TTCGGCTTCA
 1451 GGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCTT TACCCATATC
 1501 CGCCATCGCG ACGCGGCGC GCAAATCGTC AATCACAACC CTGACCAAGC
 1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTCTG
 1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGC GGTTTACGAA
 1651 TACATCAACC CGCACCGCAA CCGTCGGACC GACTACTTCA TACTCAAACC
 1701 CGGCGGCAAC CCGCGCAAT TTTTCCGCTT AAATATGAAA AACTCAACAA
 1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCGCCGGA ACAAGTCGCC
 1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTTGGG
 1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG
 1901 AAGCAGCCAT AGAAAAAACC CGCCATATCG CAAATGCCGC CGTATACGGC
 1951 CGGCCCGAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA
 2001 ACGCACCGAC AGCAGCGTGT TGCTCAACGG CGGCATGAAC CTTAACGGGG
 2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTCAGGCAG GCCCGTACCC
 2101 CATGCTTACG ACCACCAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG
 2151 GACCGACGGC AGCTTCAAGG CTGCACGGTT CACCCTGCGA AACCATGCCC
 2201 GACTGACGGC AGGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA
 2251 TACGATCTGT CCGGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA
 2301 ATGCTACCGC TCCTACCATA GCGGCAGCAC CCACTGCACA CCCAACGCGC
 2351 TTTTAAAAGC CGAAAACATAT CGTGCACTAC CTGCAACGCA AGTACGCGGC
 2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT
 2451 GTACGGCAGC ATCCGTGCCG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG
 2501 ACAGCAACTG GACACTTTC CAGTCCAGCC ACACGGGCGC ACTGACGCTT
 2551 GACGGCGCAC AAATTACCTT GAACCCCGAT TTCGCCAATA ATACACACAA
 2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTTCGGCA
 2651 CATTCCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC
 2701 AAACCTGAAG GGGACAGCCG CGGCGCATTC CAAATCCAGC TCAAAAACAC
 2751 CCGACAAGAA CCTCAAACAA CCGAATCGCT TGCATTGTG AGCCTCAATC
 2801 CGAAACACAG CCACCAAGCC CGATTACCC TCCAAAACGG CTATGCCGAT
 2851 TTGGGTGCCT ACCGCTACAT CCTCCGCAAA AACAACAACG GATACAGCCT
 2901 GTACAACCCG CTCAAAGAGG CCGAACTTCA AATTGAAGCC ACGCGTGCGG
 2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC
 3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC
 3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT
 3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTCTGACG
 3151 CGTGCCCAAA ACCTGTGTGC CGCACAAGGA TACAGTGCCG ATATCTGCCG
 3201 TCAGGTTGCC AAAGCCGCCG ACACGAACGA CCTGACACTC TTCGAAACCG
 3251 AACTGGATAC GTATATAGAA CGTGTAGAAA TGGCCGAATC CGAACTTGAC
 3301 AAAGCACGGC AAGGCGGCGA TGGCAAGGCC GTCGAAACAG CCCGGCAGCG
 3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAATCCAC AGTTTGAAAA
 3401 CCGCGGTTGC CGGCATCCGT ATGCCGAACC TGGCCGAATC GATCAGCCGG
 3451 TCGGCCAACA CCGCGTTTC CGAACAGGCC GCCTACAATA CCGGCCGGCA
 3501 ACAGGCGGGA CGCCGATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA
 3551 ACATCTGGCT GGAAACCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA
 3601 CACCGTCCCT ACCAACAAC TACCAACTAT GCACATATCG GCATCCAAAC
 3651 CGGCATCACC GACCGTCTCA GTGTCCGTAC GATTTTAACC GATGAGCGCA
 3701 CAAACAACCG TTTTGATGAA GCGTATCCG CCCGAAACCG CAGCAACGGC

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3751 GCACATCTGT TCGTCAAAGG GGAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCGG CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CGGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCGTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCCGCCAC AAACAGGCAG GAATCAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

m759.pep

```

1 MRFTHTTFFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFTV
51 GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQYVNSVKH
101 NVGYGSIQFG NDTQNPEEQ A YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLLG NGQPKANAYL DTDRTFPYFVR LSGSQQVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
251 HENRWLAGV LSTYAGFDNF FNKYIVTQPE FIRSTIROYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQNSDRHMP SEDAGKTLIL
351 SSRFDNKTLM LADNINQAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FWQVSNPKGD RLSKLGAGTL IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGRLDL NGNNLAFTHI
501 RHADGGAQIV NHPDQAATL TLTGNPVLSP EHVEWVQWGN RPQGNAAVYE
551 YINPHRNRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAVYG
651 RPEYRYNGAL NLHYRPKRTD STLLNNGGMN LGEVLEGG NMIVSGRPVP
701 HAYDHOAKRE PVLENWTDG SFKAARFTLR NHARLTAGRN TAHLDGDTA
751 YDLSGIDLGF TQKKTPECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNDRSEL RLGAHLYGS IRAGKDTAVR MEADSNWTL SSSHTGALT
851 DGAQITLNPD FANNTNNRF NTLTVNGTLD GFGTFRELTG IVRKQNAAPL
901 KLEGDSRGAF QHVKNTGQE PQTESLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNGYSLYNP LKEAELQIEA TRAEHERNQO AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVOYLSAQLK QTDPLTGILT
1051 RAQNLCAAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESELD
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAEISR
1151 SANTAVSEQA AYNTGRQQAG RRIDRHLTDP QQQNIWLETG TQTDYHSGT
1201 HRPYQQTNY AHIGIQTGIT DRLSVGTILT DERTNNRFE GVSARNRNG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRNGN RYVLDGAEIN SPAQIQTTWH AGIRLDKTVE
1351 LGQAKLTAF SSYYHTRQN SGSALSVNDR TLLQQAAGHT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

g760.seq (partial)

```

1 AACAAACGCA ACACCCGTTA CGCCGCATTG GGCAAACGCG TGATGGAAGG
51 CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCCTGCT GGTGCCCAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCCC GGCTGACCGT CGGCGGCGGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT GCAGGGATGC ATGCAGGCGG TTATGCCACG
301 TTCGATGCGA TGGCGGCATA CCGCTTCACG CCAAGCTGA AGCTGCAAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATTCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

g760.pep (partial)

```

1 NNRNTRYAAL GKRVMGVEV EISGAITPKW QIHAGYSYLH SGIKTAANPR
51 DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1  ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAACGGCG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGCGCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCAGC CTGCCCAACC TGTTCCGCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTT GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGTTC
551 ATCGGGCGGC AGGGTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGCTCTC CGCGTCCCGC CGAGAAAAAC AACCGGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GCGCGGGGCT ATCTTTACCA GCAACGCCGC CTCGCGCCGT ACAACGGCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTAAATATGC ACAGCCACGA CGTGTTCCGC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCGGAT CGGAAAGCCG ATTCCAATTA TACGTTTGCG GGCAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCTG TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAGCGT CGCTTTAGAT
1201 GGTTCGCGG CTTTGCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCCTC TGGAAAGGTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAATTTTAC AAGCTACGCC GCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCTC CCAACTCTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA
1551 AGGCAACCAG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCGG GGTTCGTTT TACCGCATGA AGGATAAAAA CGCCGCCGCA
1651 CCGCTGGACT CAAACAACAA AAAAACCCTG TACGCCGAT TGGGCAAAACG
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTCGC GCGACGAAGG CATCTTCTCG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGGAT ACATGCAAGC
1951 GGTATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAACT
2001 GAAGCTGCAA ATCAACGCGC ACAACATCTT CAACCGCCAT TACTACGCC
2051 GCGTCGGCAG CGAGAGCACC TTTAACATTC CCGGTTCCGA GCGCAGCCTG
2101 ACGGCAAACC TGCATTACAG TTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1  MQQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKG QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQQVKDRNV DTFDQLARKT
101 PGLRVLSNDD GRSSVYARGY EYSEYNIDGL PAQMQSINGT LPNLFADFDRV
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THKQYKAED
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQRRR LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FRMHSADVFA
301 DLKHYFGNGG YGKVGMRYSR RKADSNYTFG GSKLNNTGQA DVAGLGTDIK
351 QKAFVADASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSKVALD
401 GFRALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKKI ESGDGKTLHK ASKTFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPKLKLQ INADNIFNRH YYARVGSEST FNIPGSESL
701 TANLRYSF*
```

1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760 . pep	YKGSYMDRLNTRVSFYRMKDKNAAAPLDSNNKKTRYAALGKRVMEGVETEISGAMTPKW					
				:		
g760				NNRNTRYAALGKRVMEGVETEISGAITPKW		
				10	20	30
	590	600	610	620	630	640
m760 . pep	QIHAGYSYLHSQIKTASNSRDEGIFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
g760	QIHAGYSYLHSQIKTAAANPRDDGIFLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	40	50	60	70	80	90
	650	660	670	680	690	700
m760 . pep	AGIHAGGYATFDAMAAAYRFTP K L K L Q I N A D N I F N R H Y Y A R V G S E S T F N I P G S E R S L T A N L					
g760	AGMHAGGYATFDAMAAAYRFTP K L K L Q I N A D N I F N R H Y Y A R V G G T N T F N I P G S E R S L T A N L					
	100	110	120	130	140	150
	709					
m760 . pep	RYSEFX					
g760	RYSEFX					

g761 . seq not found yet

g761 . pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

m761 . seq

1	ATGAAAATAT	CATTTCATTT	AGCTTTTATTA	CCCACGCTGA	TTATTGCTTC
51	CTTCCCTGTT	GCTGCCGCCG	ATACGCAGGA	CAATGGTGAA	CATTACACCG
101	CCACTCTGCC	CACCGTTTCC	GTGGTCGGAC	AGTCCGACAC	CAGCGTACTC
151	AAAGGCTACA	TCACTACGA	CGAAGCCGCC	GTACCCGCA	ACGGACAGCT
201	CATCAAAGAA	ACGCCGCAAA	CCATCGATAC	GCTCAATATC	CAGAAAAACA
251	AAAATTACGG	TACGAACGAT	TTGAGTTCCA	TCCTCGAAGG	CAATGCCGGC
301	ATCGACGCTG	CCTACGATAT	GCGCGGTGAA	AGCATTITTC	TGCGCGGTTT
351	TCAAGCCGAC	GCATCCGATA	TTTACC CGGA	CGCGTGCGC	GAAAGCGGAC
401	AAGTGCGCCG	CAGTACTGCC	AACATCGAGC	GCGTGGAAT	CCTGAAAGGC
451	CCGTCTTCCG	TGCTTTACGG	CCGCACCAAC	GGCGGCGGCG	TCATCAACAT
501	GGTCAGCAAA	TACGCCAACT	TCAAACAAAG	CCGCAACATC	GGAGCGGTTT
551	ACGGCTCATG	GGCAAACCGC	AGCCTGAATA	TGGACATTAA	CGAAGTGCTG
601	AACAAAACG	TCGCCATCCG	TCTCACC CGC	GAAGTCGGGC	GCGCCAATTC
651	GTTCGCGAGC	GGCATAGACA	GCAAAAATGT	CATGGTTTCG	CCCAGCATT
701	CCGTCAAAC	CGACAACGGC	TTGAAGTGGA	CGGGGCAATA	CACCTACGAC
751	AATGTGGAGC	GCACGCCCGA	CCGCAGTCCG	ACCAAGTCCG	TGTACGACCG
801	CTTCGGAATG	CCTTACCGCA	TGGGGTTCCG	CCACCGGAAC	GATTTTGTC
851	AAGACAAGCT	GCAAGTTTGG	CGTTCCGACC	TTGAATACGC	CTTCAACGAC
901	AAATGGCGTG	CCCAATGGCA	GCTCGCCAC	CGCACGGCGG	CGCAGGATTT
951	TGATCATTTT	TATGCAGGCA	GCGAAAATGG	CAACTTAATC	AAACGTAACT
1001	ACGCCTGGCA	GCAGACCGAC	AACAAAACCC	TGTCGTCCAA	CTTAACGCTC
1051	AACGGCGACT	ACACCATCGG	CCGTTTGTAA	AACCACCTGA	CCGTAGGCAT
1101	GGATTACAGC	CGCGAACACC	GCAACCCGAC	ATTGGGTTTC	AGCAGCGCCT
1151	TTTCCGCCTC	CATCAACCCC	TACGACCGCG	CAAGCTGGCC	GGCTTCGGGC
1201	AGATTGCAGC	CTATTCTGAC	CCAAAACCGC	CACAAAGCCG	ACTCCTACGG
1251	CATCTTTGTG	CAAAACATCT	TCTCCGCCAC	GCCCCGATTG	AAATTCGTCC
1301	TCGGCGGCCG	TTACGACAAA	TACACCTTTA	ATTCCGAAAA	CAAACCTACC
1351	GGCAGCAGCC	GCCAATACAG	CGGACACTCG	TTCAGCCCCA	ACATCGGCGC
1401	AGTGTGGAAC	ATCAATCCCG	TCCACACACT	TTACGCCTCG	TATAACAAAG
1451	GCTTCGCGCC	TTATGGCGGA	CGCGGCGGCT	ATTTGAGCAT	CGATACGTTG
1501	TCTTCCGCGC	TGTTCAACGC	CGACCCCGAG	TACACCCGCC	AATACGAAAC
1551	CGGCGTGAAA	AGCAGTTGGC	TGGACGACCG	CCTCAGCACT	ACGTTGTCTG
1601	CCTACCAAAT	CGAACGCTTC	AATATCCGCT	ACCGCCCCGA	TCCAAAAAAC
1651	AACCCCTATA	TTTATGCGGT	TAGCGGCAAA	CACCGTTCGC	GCGGCGTGGA

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1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACCTCA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

```

m7 61 . pep
1 MKISFHLALL PTLIIASFV AAADTODNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVYDRFGL PYRMGFAHRN DFKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQT D NKTLSNLT
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFNSENKLT
451 SSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 GSAVENADPE YTROQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGLGVMOA KVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAAANLLNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

```

a7 61 . seq
1 ATGAAAATAT CATTTTATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCTGTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCCG CCTACGATAT GCGCGCGCAA AGCATTTTCC TCGCGCGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT
451 CCGTCCTCCG TGCTTTATGG GCGTACCAAC GCGCGCGGTG TCATCAACAT
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGTTTT
551 ATGGTTCGTG GGCACACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
601 AACAAAAACG TCGCCATCCG TCTCACCAGC GAAGTCGGGC GCGCCAATTC
651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA
701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTCCGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATT
951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC
1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCTGCTCA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACCG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCGCGATTTC AAATTCGTCC
1301 TCGGCGGCCG TTACGACAAA TACACCTTA ATTCCGAAAA CAAACTCACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCG TCCACACACT TTACGCCTCG TATAACAAG
1451 GCTTCGCGCC TTATGCGGGA CGCGGCGGCT ATTGAGCAT CGATACGTTG
1501 TCTTCGCGCG TGTCAACGC CGACCCGAG TACACCGGCC AATACGAAAC
1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC
1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1238

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
  1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
 51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQT DNKTLSSNLT
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KEVLGGRYDK YTFNSENKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVFNDPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIIRYRDPKN
551 NPYYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGS LGVMA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGAARVDAM LGWNHKNVNV TFAANLENQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

	10	20	30	40	50	60
m761.pep	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
a761	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m761.pep	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
a761	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m761.pep	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVSKYANFKQSRNI					
a761	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVSKYANFKQSRNI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m761.pep	GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG					
a761	GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m761.pep	LKWTGQYTYDNVERTPDRSPKSVYDFGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND					
a761	LKWTGQYTYDNVERTPDRSPKSVYDFGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND					
	250	260	270	280	290	300
	310	320	330	340	350	360
m761.pep	KWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNIAWQQT DNKTLSSNLTNGDYTIGRFE					
a761	KWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNIAWQQT DNKTLSSNLTNGDYTIGRFE					
	310	320	330	340	350	360
	370	380	390	400	410	420

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```

m761.pep  NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
a761       NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
           370      380      390      400      410      420

           430      440      450      460      470      480
m761.pep  QNIFSATPDLKFVLGGRYDKYTFENSENKLGTSSRQYSGHSFSPNIGAVWNINPVHTLYAS
a761       QNIFSATPDLKFVLGGRYDKYTFENSENKLGTSSRQYSGHSFSPNIGAVWNINPVHTLYAS
           430      440      450      460      470      480

           490      500      510      520      530      540
m761.pep  YNKGFPYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDRLSTTLSAYQIERF
a761       YNKGFPYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDRLSTTLSAYQIERF
           490      500      510      520      530      540

           550      560      570      580      590      600
m761.pep  NIRYRPDPKNNPIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
a761       NIRYRPDPKNNPIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
           550      560      570      580      590      600

           610      620      630      640      650      660
m761.pep  RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYNSRNKEVTTLPGFARVDAM
a761       RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
           610      620      630      640      650      660

           670      680      690      700
m761.pep  LGWNHKNVNVTFAAANLLNQKYWRSDSMGPNPRGYTARVNYRFX
a761       LGWNHKNVNVTFAAANLFNQKYWRSDSMGPNPRGYTARVNYRFX
           670      680      690      700

```

g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTATTAC GATAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCTT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1  MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
51  LELLFIENFV TKSIMAIY PLYFFTIKK YYPYSRKVII LLSLALSIYF
101 SFMDFYFFSI YSDNLSYTE PLHLYIPIII NFFSLLVSNE ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTATTAC GATAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

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1240

301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
 351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT
 401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762 . pep

1 MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
 51 LELLFIFNEV TKSIYMAIIY PILYFTTIKK YYPYSRKVII LLSLALSIYF
 101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762 . pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLELLFIFNEV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLELLFIFNEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762 . pep	TKSIYMAIIYPILYFTTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFTTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762 . pep	PLHLYIPIIIINFFSLLVSNFILSFINKX					
a762	PLHLYIPIIIINFFSLLVSNFILSFINKX					
	130	140				

g763 . seq not yet found

g763 . pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763 . seq

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
 101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
 151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCGTGAAG CATGGCGGGC
 201 GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG
 251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATT CTTCACCCG
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAACCTTA TTTGACGCTG
 401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
 501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
 551 AAAAGAGAGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
 601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
 701 AAAACCAAGT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
 801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
 901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTGCGCT ATCAGAATAA
 951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
 1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
 1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
 1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT
 1201 TTGGAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
 1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC
 1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
 1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAACGG TATTGCGGA
 1401 ATAA

1241

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

m763 . pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFOASHY QDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIIVLAEK QTYENQLNDY TDLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQYQYR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

a763 . seq

```

1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTGCGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG
251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCATTGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCG CCATCGATT CTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGGCGCGG
551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACCAAGT GAACGACTAC ACCGCGCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCGTA CGCCAGGCTT
1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAGCA GCCGTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACCGCTGG AAGTAATAC GGCGCGGCAG GAAGTCGCC
1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGTTAGGG TTGGAACGG TATTGCGGA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

a763 . pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFOASHY QDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIIVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQYQYR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

m763 / a763 99.8% identity in 467 aa overlap

```

m763 . pep      10      20      30      40      50      60
MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
|||||
a763           MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
              10      20      30      40      50      60

```

1242

	70	80	90	100	110	120
m763.pep	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAFLPHVSANASYQRQPPSISSTRETQ					
a763	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAFLPHVSANASYQRQPPSISSTRETQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m763.pep	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLLKVAESYFNVLLSRDTVAA					
a763	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLLKVAESYFNVLLSRDTVAA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m763.pep	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI AVLAEKQTYENQLNDY					
a763	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI AVLAEKQTYENQLNDY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m763.pep	TGLDSKQIEAIDTANLLARYLPKLERYSLEWQRIASNNHEYRMQQLALQSSGQALRAA					
a763	TGLDSKQIEAIDTANLLARYLPKLERYSLEWQRIASNNHEYRMQQLALQSSGQALRAA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m763.pep	QNSRYPTVSAHVGYNQNLTYSSAQNNQDHYRGKGM SVGVQLNPLTYTGGE LSGKIHEAEA					
a763	QNSRYPTVSAHVGYNQNLTYSSAQNNQDHYRGKGM SVGVQLNPLTYTGGE LSGKIHEAEA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m763.pep	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLK LKSTETGQQYGIR					
a763	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLK LKSTETGQQYGIR					
	370	380	390	400	410	420
	430	440	450	460		
m763.pep	NRLEVIRARQEVAAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
a763	NRLEVIRARQEVAAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
	430	440	450	460		

1243

g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

m764.seq

```

1 ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTAAGTATG
51 GCGCAATGTT TGGGCGGTGC GCGACAGTT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAACTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTGGGGCAA AACGGTGTCT GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CCGGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCAGGAG CAGAAGCTGG TTTCGGTGGG GCGGATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCGTTTG CCGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CCGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAA
1351 ACGGGTAAAC GCGGGTGCT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

m764.pep

```

1 MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEEOAFL PAHLELTDTP
51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDGQHVKGQE TLAELEAVGT DSDVVSQSEA LQAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSAALRGHQ AELQSAKAQE QKLVSVAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEK
451 TGKRRVLDYL LSPLQTKLDE SFRER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

a764.seq (partial)

```

1 ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
51 GCGCAATGTT TGGGCGGTGC GCGACAGTT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAACTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTGGGGCAA AACGGTGTCT GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CCGGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCAGGAG CAGAAGCTGG TTTCGGTGGG GCGGATCGAG CAGCAGAAAA

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1244

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701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTT CCCTATACGC GCTACGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

```

a764.pep (partial)
  1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAF LPAHLELTDTP
 51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVKGQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLDLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

	10	20	30	40	50	60
m764.pep	MFFSALKSFLSRYITVWRNVAVRDQLEPPKRTAEQAF LPAHLELTDTPVSAAPKWAAR					
a764	MFFSALKSFLSRYITVWRNVAVRDQLEPPKRTAEQAF LPAHLELTDTPVSAAPKWAAR					
	10	20	30	40	50	60
m764.pep	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDQHVKGQE					
a764	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDQHVKGQE					
	70	80	90	100	110	120
m764.pep	TLAELEAVGTDSDDVVQSEQA LQAAQLSKLRYEAVLAALESRTVPHIDMAQARSGLSDAD					
a764	TLAELEAVGTDSDDVVQSEQA LQAAQLSKLRYEAVLAALESRTVPHIDMAQARSGLSDAD					
	130	140	150	160	170	180
m764.pep	VQSAQVLAQH QYQAWAAQDAQLQSALRGHQ AELQSAKAQE QKLVSVAIE QOKTADYRRL					
a764	VQSAQVLAQH QYQAWAAQDAQLQSALRGHQ AELQSAKAQE QKLVSVAIE QOKTADYRRL					
	190	200	210	220	230	240
m764.pep	RADNFISEHAFLEQQSKSVSNWNLDLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
a764	RADNFISEHAFLEQQSKSVSNWNLDLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
	250	260	270	280	290	300
m764.pep	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
a764	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
	310	320	330	340	350	360
m764.pep	DKMDVEVLVLNKDIGFVEQGQDAVVKIESFPYTRYGYLTGKVKSVDHDAVSHEQLGLVYT					
a764	DKMDVEVLVLNKDIGFVEQGQDAVVKIESFPYTRYGYLTGKVKSVDHDAVSHEQLGLVYT					
	370	380	390	400	410	420
m764.pep						
a764						

1245

```

a764      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          370      380      390      400      410      420
          |||||||
          430      440      450      460      470
m764 . pep AVVSLDKHTLNIDGKAVNLTAGMNVTAIEIKTGKRRVLDYLLSPLQTKLDESFRERX
          |||||||
a764      AVVSLDKHTLNIDGK
          430

```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```

m765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTGAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTCGGG TCGTTGCTGA TGTTCACGGT CATGATTCCG CCACAATGAA
201 CGCTGCGGCT GCCAAGATT ATATGAAAAC GGTGAGTTA AACAACTCTG
251 CCGGCAATGT CGATACCACA TCCAGAACAG CCCGCAGGGT GCAGGCAGTA
301 TTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCGG TGGAAAAATG GCGTTTTATA CGGGGATAGT CGACAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAACCGGCT TTATTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```

m765.pep
1  MLRCRPSVL DSDGIFLKFN FLRSKPKEYI SFLPSFKRIL CLSAVISVLG
51  ACVAADVYG HDSATMNAHA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FRRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTODEIAAI MGHENTHALH EHGKNKVGQQ ILTNTAAQIG TQIILDKKPD
201 TNPELVGLGM DILGTYGLTL PYRSLEEEA DEGGMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAIT S THPTNNARIE NLKRLLPV M PVYEQSVRNK
301 GRVNNKRRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```

a765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTGAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTCGGG TCGTTGCTGA TGTTCACGGT CAGGATTCCG CCACAATGAA
201 TGCTGCGGCT GCCAAGATT ATATGAAAAC GGTGAGTTG AACAACTCTG
251 CCGGCAATGT CGATACTACA TCCAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCGG CGGAAAAATG GCGTTTTATA CGGGGATAGT CGATAAATT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAACCGGCT TTATTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```

a765.pep
1  MLRCRPSVL DSDGIFLKFN FLRSKPKEYI SFLPSFKRIL CLSAVISVLG

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1246

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51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FFRMLPYADA ANNTGCHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTGDEIAAI MGHEMTHALH EHGKKNVQOK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYRSLEEEA DEGGMLMAQ AGYHPAAVR
251 VWEKMNQEND QNGFIYAITs THPTNNARIE NLKRLLEPTVM PVYEHsVRNK
301 GRVKNRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

	10	20	30	40	50	60
m765.pep	MLRCRPKSVLDS	GI	FLKFNFLRSKPKYEIS	FLPSFKRILCLSAVIS	VLGACAVVADVYG	
a765	MLRCRPKSVLDS	GI	FLKFNFLRSKPKYEIS	FLPSFKRILCLSAVIS	VLGACTTVADVYG	
	10	20	30	40	50	60
	70	80	90	100	110	120
m765.pep	HDSATMNAAA	KDYMKTVELNKSAGNVDTT	SRTARRVQAV	FFRMLPYADA	ANNTSHKFDW	
a765	QDSATMNAAA	AEDYMKTVELNKSAGNVDTT	SKTARRVQAV	FFRMLPYADA	ANNTGCHKFDW	
	70	80	90	100	110	120
	130	140	150	160	170	180
m765.pep	KMTVFKNDEL	NAWAMPGGKMAFYTGIVDKL	KLTDEIAAIMGHEMTHALHEHGKKNVQ	Q		
a765	KMTVFKNDEL	NAWAMPGGKMAFYTGIVDKL	KLTDEIAAIMGHEMTHALHEHGKKNVQ	Q		
	130	140	150	160	170	180
	190	200	210	220	230	240
m765.pep	ILTNMAAQIG	TQIILDKKPD	TNPVLGLGMDILGT	YGLTLPYRSLEEEA	DEGGMLMAQ	
a765	ILTNMAAQIG	TQIILDKKPD	TNPVLGLGMDILGMYGITL	PYRSLEEEA	DEGGMLMAQ	
	190	200	210	220	230	240
	250	260	270	280	290	300
m765.pep	AGYHPAAAVR	VWEKMNQENDQNGFIYAIT	STHPTNNARIENL	KRLLEPTVMPVYE	QSVRNK	
a765	AGYHPAAAVR	VWEKMNQENDQNGFIYAIT	STHPTNNARIENL	KRLLEPTVMPVYE	HSVRNK	
	250	260	270	280	290	300
	310					
m765.pep	GRVKNRRRX					
a765	GRVKNRRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTG TG GATAAAC
101 CCATTCCTCA AGAACAGCCG GGAAAAATG AGGTTTGGG ATTTTTCGGC
151 TATTTTTCGG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCTTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCTG
301 GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTAAAGCAG TTACGAAACA
351 AAAAATCCGT TTGGAAAACA GGGCTGTTGC CGGAAATGG GCTTATCTC
401 AAAAAGGTTT TGACGGCAAA AACTGATGC GCGCCTATGA TTCCCCGAA
451 GCTGCCGCCG TCGCATTAAA AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGG GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQP GKIEVLEFFG
51  YFCVHCHHFD PLLLLGKAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

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101 GLKYQANSV FRAVYEQKIR LENRAVAGKW ALSQKGFDDG KLMRAYDSPE
 151 AAVALKMQK LTEQYGDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq
 1 A TGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCTCTCA AGAACAGTCG GGTAAAATTG AGGTTTGGGA ATTTTTCGGC
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAACTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTTGAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CGGCTGCCGT CAATTGTCTG
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCTGTG TTTAAAGCAG TTTACGAACA
 351 AAAAAATCCG TTGAAAAACA GGTCCGTTGC CGGAAAATGG GCTTTGTCTC
 401 AAAAAAGCCT TGACGGCAAA AACTGATGC GCGCTATGA TTCCCCGAA
 451 GCTGCCCGCG CCGCATTAAT AATGCAGAAA CTGACGGAAC AATACCGCAT
 501 CGACAGCAG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
 551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAAGAATT GGTGCGCAAA
 601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep
 1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPOEQS GKIEVLEFFG
 51 YFCVHCHHFD PLLKLKGKAL PSDAYLRTEH VVWQPEMLGL ARMAAVNLS
 101 GLKYQANPAV FRAVYEQKIR LENRSVAGKW ALSQKGFDDG KLMRAYDSPE
 151 AAAAAALMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLL	LSAVLSAQAY	ALTEGEDYLV	LDKPIPOEQS	GKIEVLEFFG	YFCVHCHHFD
m767	MKFKHLLPLL	LSAVLSAQAY	ALTEGEDYLV	LDKPIPOEQS	GKIEVLEFFG	YFCVHCHHFD
	70	80	90	100	110	120
g767.pep	PLLLKLGKAL	PSDYLRT	TEHVVRPE	MLGLARMA	AAVKLSGL	KYQANSV FRAVYEQKIR
m767	PLLLKLGKAL	PSDYLRT	TEHVVRPE	MLGLARMA	AAVKLSGL	KYQANPAV FRAVYEQKIR
	130	140	150	160	170	180
g767.pep	LENRAVAGKW	ALSQKGFDDG	KLMRAYDS	PEAAVALK	MQKLTEQY	GIDSTPTVIVGGKYR
m767	LENRSVAGKW	ALSQKGFDDG	KLMRAYDS	PEAAAAAL	KMQKLTEQY	RIDSTPTVIVGGKYR
	190	200	210			
g767.pep	VIFNNGFDGG	VHTIKELV	AKVREERK	QTPAVQKX		
m767	VIFNNGFDGG	VHTIKELV	AKVREERK	QTPAVQKX		
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq
 1 A TGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCTCTCA AAAACAGTCG GGCAAAATTG AGGTTTGGGA ATTTTTCGGC
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAATTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCCGT CAAGCTGTCA
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTTAAAGCAG TTTACGAACA
 351 AAAAAATCCG TTGAAAAACA GGTCCGTTGC CGAAAAATGG GCTTTGTCTC
 401 AAAAAAGCCT TGACGGCAAA AACTGATGC GCGCTACGA CTCTCCTGCG

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451 GCACGGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CCGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAAATGGCTT TGACGGCGGT GTTCATACGA TTAAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
1  MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPOKQS GKIEVLEFFG
51  YFCVHCHHFD PLLKLKGLAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
101 GLKYQANPAV FKAUYEQKIR LENRSVAEKW ALSQKGFDDG KLMRAYDSPA
151 AAAAAASKMQQ LTEQYRIDST PTVVVGKYYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

```

m767/a767    96.7% identity in 214 aa overlap

              10      20      30      40      50      60
a767.pep     MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPOKQSGKIEVLEFFGYFCVHCHHFD
              |||||
m767          MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPOKQSGKIEVLEFFGYFCVHCHHFD
              10      20      30      40      50      60

              70      80      90      100     110     120
a767.pep     PLLKLKGLALPSDAYLRTEHVVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVYEKIR
              |||||
m767          PLLKLKGLALPSDAYLRTEHVVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVYEKIR
              70      80      90      100     110     120

              130     140     150     160     170     180
a767.pep     LENRSVAEKWALSQKGFDDGKLMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGKYYR
              |||||
m767          LENRSVAGKWALSQKGFDDGKLMRAYDSPEAAAAALKMQKLTEQYRIDSTPTVIVVGKYYR
              130     140     150     160     170     180

              190     200     210
a767.pep     VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
              |||||
m767          VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
              190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
1  ATGAATATCA AACAAATGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCACGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATTACAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGTCAATTTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATATACGAA GCCCGCCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
251 GCACGGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
301 TATACAAATG TTGCCAATCA CGCGGTTAT GAAGACCTGC TCAAAAAGG
351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
1  MNIKQLITAA LIASAAFATQ AAPQKPVSAQ QTAQHSVWI DVRSEQEFSE
51  GHLHNAVNIPI VDQIVRRIYE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
101 YTNVANHGGY EDLLKKGMK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
1  ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATCCGCG CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGGCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATACACGAA GCCCGCCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC

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251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
 51 GHLHNAVNIP VDQIVRRIHE AAPDKTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKGMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAALIASAAFATQAAPQKPVSAQAQHSVWIDVRSEQEFSEGLHNAVNIP					
m768	MNIKHLITAALIASAAFAAQAPQKPVSAQAQHPAVWIDVRSEQEFSEGLHNAVNIP					
	10	20	30	40	50	60

	70	80	90	100	110	120
g768.pep	VDQIVRRIEAAAPDKDTPVNLVYCRSGRRAEALQELKKAGYTNVANHGGYEDLLKGMKX					
m768	VDQIVRRIEAAAPDKDTPVNLVYCRSGRRAEALQELKKAGYTNVANHGGYEDLLKGMKX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCGCG AAAAACCCTG ATCCGCGCGC CAAACCGCGC
 101 AACATTGATG CATTGATGAT GATGTCGCA GCGAACAGGA ATTTAGCGAA
 151 GGTCATTGTC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCGC
 201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC
 301 TATACGAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
 51 GHLHNAVNIP VDQIVRRIHE AAPDKTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKGMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAALIASAAFAAQAPQKPVSAQAQHSVWIDVRSEQEFSEGLHNAVNIP					
m768	MNIKHLITAALIASAAFAAQAPQKPVSAQAQHPAVWIDVRSEQEFSEGLHNAVNIP					
	10	20	30	40	50	60

	70	80	90	100	110	120
a768.pep	VDQIVRRIEAAAPDKDTPVNLVYCRSGRRAEALQELKKAGYTNVANHGGYEDLLKGMKX					
m768	VDQIVRRIEAAAPDKDTPVNLVYCRSGRRAEALQELKKAGYTNVANHGGYEDLLKGMKX					
	70	80	90	100	110	120

1250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq
 1 T TGATAATGG TTATTTTTTA TTTTATTTT TGTGGAAGA CATTATGCC
 51 T GCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
 101 C CGAAGaAAC ACCgtgCGAA CCGGATTGA GAAGCCGTCC CGAGTTCAGG
 151 C TTCATGAAG CGGAGGTCAA ACCGATCGAC AGGAGAAGG TACCGGGGCA
 201 G GTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
 251 A AAATCCCGA ATTGTTGTCG CGTGCCATGT ATTCGCGAGT GGTCTCAAAC
 301 A ATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
 351 G CAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
 401 A GGGCAGGGT GAAGGAGGCG GTTTCCTTATT ACCGGAATT GATTGCCGCC
 451 C AACCAGCAG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
 501 A GACAGCGAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
 551 A AGATCTGCC GCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
 601 T TGCGCGAAC GCGATGCGTG GAAGGTAAAC GCGGTTTCA GCGTTACCCG
 651 C GAACACAAT ATCAACCAAG CCCGAAACA GCAGCAGTAC GGCAATTGGA
 701 C TTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
 751 G AGAAAAAAT GGTGCTGAA AAACGGCTGG TACACGACGG CGGGCGGCGA
 801 C GTGTCGGG AGGGTTTATC CGGGGAATA GAAATCAAC GATATGACGG
 851 C AGGTGTTTC CGCGGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG
 901 C TGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
 951 C GCCAACCGG GCACGCCTTT ATTTCAACCG TTGGCAAACC CCGAGATGGC
 1001 A AACGCTGTC TTCGGCGGAG TGGGGCGGTT TGAAGAATAC GCGCCGGGCG
 1051 C GTTCCGACA ATACCCATTT GCAAATTTCC AATTGCTGG TGTTTTACCG
 1101 G AATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTAC CCGGAGCGCA
 1151 A CCCCAGCGA CCGTGGCGAC AATTCAACC GTTACGGCCT GCGCTTTGCC
 1201 T GGGGGCAGG AATGGGGCGG CAGCGGCTG TCTTCGCTGT TCCGCTCGG
 1251 C GTGGCGAAA CGGCATTATG AAAAACCCGG CTTCTTCAGC AGTTTTAAAG
 1301 G GGAAGGCG CAGGGATAAA GAATCGGACA CATCCTTGAG CCTTTGGCAC
 1351 C CGGCATTGC ATTTCAAAGG CATCACCGCG CGCCTGACGG TGTCGCACCG
 1401 C GAAACGTGG AGCAACGATG TGTTTAACGA ATACGAGAAA AACAGGGCGT
 1451 T TGTGCGAGT TAACAAAACG TTCTGA

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep
 1 L IMVIFYFYF CGKTEMPARN RWMLLP LLAS AAYAEETPCE PDLRSRPEFR
 51 L HEAEVKPID REKVPQVRE KGVLVQDGE TLLKNPELLS RAMYSVVSN
 101 N IAGIRVILP IYLOQARQDK MLALYAQIL AQAEGRVKEA VSHYRELIAA
 151 Q PDAPAVRMR LAAALFEDRQ NEAADQFDR LKTEDLPQL MEQVELYRKA
 201 L RERDAWKVN GGFVSTREHN INQAPKQQY GNWTFPKQVD GTAVNYRFGA
 251 E KKWSLKNW YTTAGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
 301 L AVFHERRY GNDAYSANG ARLYFNWQT PRWQTLSSAE WGRLEKTRRA
 351 R SDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
 401 W GQEWGSGSL SSLFRLGVAK RHYEKPGFFS SPKGERRRDK ESDTSLSLWH
 451 R ALHFKGITP RLTLSHRETW SNDVFNEYEK NRAFVEFNKT F*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq
 1 T TGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCCTGCACG
 51 A AACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
 101 A AGAAACACC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
 151 C ATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGCAGGT
 201 G CCGGAAAAA GGAAAAGTTT TGCAGATTGA CCGCGAAACC CTGCTGAAAA
 251 A TCCCGAATT GTTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
 301 A TTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
 351 G GATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
 401 G TAGGGTGAA GGAGGCGATT TCCCATTACC GGAATTGAT TGCCGCCCAA
 451 C CCGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCAGCAT TGTTGAAAA
 501 C CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCTG AAGGCGGAAA
 551 A CCTGCCGCC GCAGCTGATG GAGCAGGTGC AGCTGTACCG CAAGGCATTG
 601 C CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCACGC TCACCCGCGA
 651 A CACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
 701 T CCGGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
 751 A AAAAATGGT CGCTGAAAA CGGCTGGTAC ACGACGGCGG GCGGCGACGT
 801 G TCCGCGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
 851 G CGGTTCCCG CGGCATCGGT TTTGCCGACC GGCAGAAAGA TGCCGGGCTG
 901 G CAGTGTTC CAGAACGCGC CACCTACGGC AACGACGCTT ATTCTTACAC
 951 C AACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
 1001 C GTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
 1051 T CCGCAATAA CCCATTGCA AATTTCCAAT TCGCTGCTGT TTTACCGGAA
 1101 T GCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
 1151 C CGCGCAGCG GGGCGCAAT TTCAACCGTT ACGGCTGCG CTTTGCCTGG
 1201 G GGCAGGAAT GGGCGGCGAG CGGCCTGTCT TCGCTGTGCG GCCTCGGCGC

1251

1251 GCGGAAACGG CATTATGAAA AACCCGGCTT TTTCAGCGGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCAG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCAGGA
1401 AACCGGGAGT AACGATGTGT TCAACGAATA CGAGAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTT TGA

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

m769.pep

1 LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLRSRPEFRL
51 HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQAAQDDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151 PDAPAVRMRL AALFENRQN EAAADQFDR KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTRHNI NQAPKROQYG KWTFFPKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GRKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGSGSL SLLRLGAAK HYKPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYKN RAFVEFNKTF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

m769/g769 95.1% identity in 492 aa overlap

	10	20	30	40	50	59
g769.pep	LIMVIFYFCGKTFMPARNRWMLL-PLLASAAYAETPREPDLRSRPEFRLHEAEVKPI					
m769	LIMVIFY--FCGKTFMPARNRWMLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPI					
	10	20	30	40	50	
g769.pep	60	70	80	90	100	110 119
	DREKVPQVREK GKVLQVDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQAAQD					
m769	DREKVPQVREK GKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQAAQD					
	60	70	80	90	100	110
g769.pep	120	130	140	150	160	170 179
	KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAALFEDRQNEAAADQFD					
m769	KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAALFENRQNEAAADQFD					
	120	130	140	150	160	170
g769.pep	180	190	200	210	220	230 239
	RLKTEDLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNIHQAPKQOQYGNWTFPKQV					
m769	RLKAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNIHQAPKQOQYGNWTFPKQV					
	180	190	200	210	220	230
g769.pep	240	250	260	270	280	290 299
	DGTAVNYRFGAEKKWSLKNWYTTAGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV					
m769	DGTAVNYRLGAEKKWSLKNWYTTAGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA					
	240	250	260	270	280	290
g769.pep	300	310	320	330	340	350 359
	GLAVFHERRTYGNDAYSYANGARLYFNWQTPRWQTLSSAEWGRKNTRRARSDNTHLQI					
m769	GLAVFHERRTYGNDAYSYTNGARLYFNWQTPKWQTLSSAEWGRKNTRRARSDNTHLQI					
	300	310	320	330	340	350
g769.pep	360	370	380	390	400	410 419
	SNSLVFYRNARQYWTGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGSLSLRLGVA					
m769	SNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGSLSLRLGAA					
	360	370	380	390	400	410
g769.pep	420	430	440	450	460	470 479
	KRHYEKPGFFSSFKGERRRDKESTSLSLWHRALHFKGITPRLTLSHRETWSNDVFNEYE					

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m769      KRHYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
          420      430      440      450      460      470

          480      490
g769.pep  KNRAFVEFNKTFX
          |||||
m769      KNRAFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAAGAAACACC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGCAGGT
201 GCGGGAAAAA GGAAAAGTTT TGCAGATTGA CGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGAATTGAT TGTCGCCCAA
451 CCGGACGCGC CCGCGTCCG TATGCGTTTG GCGCGGCAT TGTGAAAAA
501 CAGGCAGAAC GAGCGGCGG CAGACAGTT CGACCGCTG AAGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACCGG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGCCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGCGGTCA ATTACCGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGCTGGTAC ACGACGCGG GCGGCGACGT
801 GTCCGCGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GGCACAAAGA TGCCGGGCTG
901 GCAGTGTTC ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGCGCGA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACCG CCGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACGTT ACGGCTCGC CTTTCCCTGG
1201 GGGCAGGAAT GGGCGGCGAG CGGCTGTCT TCGCTGTGC GCCTCGGCGC
1251 GCGGAAACGG CATTATGAAA AACC CGCTT TTTAGCGGT TTTAAAGGG
1301 AAAGGCGCAG GGATAAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCAG
1351 GCATTGCATT TCAAAAGCAT CACGCCGCGC CTGACGTTGT CGCACCAGCA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLLELLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLIQIDET LLKNPELLSR AMYSVVSN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NQAPKRQYQ KWTFFKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 QQEWGGGSL SLLRLGAAR HYEKPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDFVNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

m769/a769 99.8% identity in 490 aa overlap

```

          10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTFMPARNRWMLLLELLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTFMPARNRWMLLLELLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90      100     110     120
a769.pep  EKVPQVREKGVLIQIDETLLKNPELLSRAMYSVVSN IAGIRVILPIYLQQAQQDKM

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m769      |||||
           EKVPGQVREKGVQLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM
           70      80      90      100     110     120

a769.pep   130      140      150      160      170      180
           LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
           |||||

m769      130      140      150      160      170      180
           LALYAQGILAQADGRVKEAISHYRELIVAAQPDAPAVRMRLAAALFENRQNEAAADQFDRL

a769.pep   190      200      210      220      230      240
           KAENLPPQLMQVELYRKALRERDAWKVNGGFSVTRHNINQAPKRQQYQKWTFFPKQVDG
           |||||

m769      190      200      210      220      230      240
           KAENLPPQLMQVELYRKALRERDAWKVNGGFSVTRHNINQAPKRQQYQKWTFFPKQVDG

a769.pep   250      260      270      280      290      300
           TAVNYRLGAEEKWVSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
           |||||

m769      250      260      270      280      290      300
           TAVNYRLGAEEKWVSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL

a769.pep   310      320      330      340      350      360
           AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQISN
           |||||

m769      310      320      330      340      350      360
           AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQISN

a769.pep   370      380      390      400      410      420
           SLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAGWGQEWGSGLSLLRLGAAKR
           |||||

m769      370      380      390      400      410      420
           SLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAGWGQEWGSGLSLLRLGAAKR

a769.pep   430      440      450      460      470      480
           HYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTSLHRETRSNDVFNEYEKN
           |||||

m769      430      440      450      460      470      480
           HYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTSLHRETRSNDVFNEYEKN

a769.pep   490
           RAFEVFNKTFX
           |||||

m769      490
           RAFEVFNKTFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1   ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTCA AGCGCGGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTG GTTTACAGCG
401 ATAAATCGT CCAAGGATCG CCGAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGCGACGC GCATACCGCA AACCACGGG GTGCAAGCCG ATACTCCCG
501 CAAACTGCTT GCCGCGCCT GCATTATTC CAACCCGATA AAAATCCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1   MNRLLLLSAA VLPTACSGSE TDKIGRASTV FNMLGKNDRI EVEGFDDPDV
51  QGVACYISYA KGGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKRGTFGA FKSQRIVRY DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FSGGIPQTDG VQADTSGLL AGACIIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1   ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

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101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTC CAACCCGATA GAAATCTCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

```

m770.pep
1  MNRLLLLSAA VLLTACSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSQIVRY Y DPKRKTFA YL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

m770/g770 93.5% identity in 186 aa overlap

```

g770.pep
10 20 30 40 50 60
MNRLLLLSAAVLP TACSGETDKIGRASTVFNILGKNDR I EVEGFDDPDVQGVACYISYA
|||||
m770
10 20 30 40 50 60
MNRLLLLSAAVLL TACSGETDKIGRASTVFNILGKNDR I EVEGFDDPDVQGVACYISYA
|||||

g770.pep
70 80 90 100 110 120
KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKVEFKRGTFKSFQIVRY Y
|||||
m770
70 80 90 100 110 120
KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKVEFKHGASFAFKSRQIVRY Y
|||||

g770.pep
130 140 150 160 170 180
DPKRKFAYLVYSDKIVQGS PKNSLSAVSCFGSGIPQTDGVQADTSGKLLAGACIISNPI
|||||
m770
130 140 150 160 170 180
DPKRKTFA YLVYSDKIIQGS PKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI
|||||

g770.pep
KNPDKRX
:| |||
m770
ENLDRKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

```

a770.seq
1 ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCTGCTGA CTGCCTGCGG
51 CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTC CAACCCGATA GAAATCCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

```

a770.pep
1  MNRLLLLSAA VLLTACSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSQIVRY Y DPKRKTFA YL VYSDKIIQGS PKNSLSAVSC

```

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151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

a770.pep	10	20	30	40	50	60
	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA					
m770						
	10	20	30	40	50	60
	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA					
a770.pep	70	80	90	100	110	120
	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKVEVFKHGASFAFKSRQIVRY					
m770						
	70	80	90	100	110	120
	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKVEVFKHGASFAFKSRQIVRY					
a770.pep	130	140	150	160	170	180
	DPKRRTFAYLVYSDKIIQGSFKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
m770						
	130	140	150	160	170	180
	DPKRRTFAYLVYSDKIIQGSFKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
a770.pep	ENPKRXX					
m770	ENLDRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

1	ATGGATTAT	TATCGGTTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTGGC
51	GGTGCTGACG	ATGCTGCTTT	TGGCGGCAGT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCACCTT	CACGCCCGAA	AACATCCGCA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACCC	ACCGGAAAT	CTCGTTGAT	GCGGATATAC	GGCGCAGGCT
201	TCTGCCCGCG	CCGACCGTCA	TCCTGAAAA	CCTGACCATT	ACCGAACCCG
251	ACGGCGGCGG	GGTCGCCGTT	TCCGTCAAAG	AAACCAAAT	CGGATTGAGC
301	TGGAAAAACC	TGTGGTCGGA	TCGGATACAG	GTTGAAAAAT	GGGTGGTTTC
351	GGGTGCGGAT	CTTGCCCTGA	CGCGCGACAG	AAACGCGCCT	TGGAACATCC
401	AAGACCTGTT	CGACGGCGCG	AAACACTCCG	CCTCAGTCAA	CCGCATTATC
451	GTCGAAAAAC	GCACCGTCCG	CCTCAATTTC	CTGCAGCAAC	AGCTTATCCT
501	GAAGGAAATC	AGCCTCAACC	TGCAATCCCC	CGATTGCTCG	GGGCAGCAGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGAGGAA	AGCTGTCCGT	CCCGTGGAAA
601	AGCAGGGGGC	TGTTCTTTC	AGACGGCATC	GGCAGCGCCG	AAATCTCACC
651	GTTCCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATCACCATT
701	CCACCACCGG	CAGCCCTTCT	GTCCGCTTCA	ACGCCGCGCG	AGCGGATGCC
751	GCCGGCCTCG	GCCTGCGTGC	AGACACTTCC	TTCCGCAACC	TCCACCTGAC
801	CGCACAAATC	CCCGCACTGG	CACTCAAAAA	CAACAGCATC	AAAACCGGCA
851	CGGTCAACGG	CACGTTTACC	GCCGGCGGCG	AATATGCCCG	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAC	ACCGCGCCTT	CAAACCAATT
1001	TCTCCCTCGG	CTCGCCGTTG	GTTTGAGTTC	GGGACAACGG	GCTGGACGCC
1051	CCGCGCCTGC	ACATATCGAC	CCTTCAGGAT	ACCGTCGACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCATA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	ACCCGTTGCC
1201	GCAAAATTC	AATATACGCG	GGAAGCGGCA	CCGCACCTGG	AAGCCGCCGC
1251	CGCGCTGCAA	AAATTAAC	TCGCCCTTA	TCTTGACGAA	TTTCGGCAAC
1301	AAAACGGCAA	AATATTCCC	GACATCCTCG	GCAGGCTGTC	CGGCAACGTC
1351	GAGGCACACC	TCAAAATCGG	CAGCATCCAA	CTCCCCGGCT	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGACCATATC	GCGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAACACCC	GTCCCGCCAC	TTACCGCCTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	TGCGGTATC	GACCTGACCG	CAAGCGGCGA	AAACCGCAAA
1651	CAGCTTATCC	GCTCGCTGCA	AGGCAGCCTG	TCGCTGAATA	TTTCCACCGG
1701	CGCGTGGCAC	GGCATCGATA	TGGACAGCAT	TTTAAAAAC	GGCCTTCCG

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```

1751 GGA AATCTC GGCAGCACA CCCTTCTACC GATTCACGCT CAACAGCGAA
1801 ATTTCAGACG GCATCAGCCG CCACATCGAT ACCGAAGTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CCTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCGATTA
2001 CGGCAGGCTG ACCGGCGGCA TCAATTCGCG CAAAGAGAAA CAGAAAATCC
2051 TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
3051 TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

```

g771.psp
1 MDLLSVFHKY RLKYAVAVLT MLLLAUVGLH ASVYRTFTPE NIRSRLQOSI
51 AHTHRKISFD ADIRRRLLPR PTVILKNLTI TEPDGGRVAV SVKETKIGLS
101 WKNLWSDRIQ VEKVVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRRI
151 VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQGFESSGIL VWRKLSVPWK
201 SRGLFLSDGI GTPDISPFHF EASTSLDGHG ITISTTGSFS VRFNAGGADA
251 AGIGLRADTS FRNLHLTAQI PALALKNNNSI KTGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGSLSI PNLQNWNAEL NGTFDRQFVA
401 AKFKYTREGA PHLEAAAAAQ KLNLAFLYDE FRQONGKIFP DILGRLSGNV
451 EAHKIGISIQ LPGLQLDDME TYLHADKDHI ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QONASNIQIQ PLLQDLFGFH SFSNGDAVI DLTASGENRK
551 QLIRSLQSL SLNISNGAWH GIDMSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHD TELFSDSLYV TSNGYTNLDT QELSEDVLR NAVHPKNKPI
651 PLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDTLLE QWQWLKPKPE
701 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

```

m771.seq
1 ATGGATTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGCTGACG ATACTGCTTT TGGCGGCAGT CCGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCTGAA AACATCCGCA GCCGCCTACA ACAAGCATT
151 GCACACACAC ACCGGAATAT CTCGTTTGT GCGGACATTG AGCGCAGGCT
201 CCTGCCCCGG CCGACCGTCA TCGTGAATAA CCTGACCAT ACCGAACCCG
251 GCGGCGACCA GACTGCCGTT TCGTCCAAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGCAGAA CTGCGCTGA CCGCGCAGCG GAAAGGTGTT TGGAACATCC
401 AAGACCTGAT CGACAGCCAA AACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAAAC GCACCGTCCG CCTCAATTTC CTGCAAGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCTGCG GGGCAGCCGT
551 TTGAAAGTTT GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC TGTTCCTTTC AAACGGCATC GGGCCGCCCG AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTGCTGGA CCGACACGGC ATTACCATTT
701 CCACACCCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAATTC CCGCGCTGCG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTATAC GCCGGCGGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAA TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGCG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC CCGTCCCGCA
1101 ACCCGCTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCT GACACCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACC TGAATTCGG AAAAGTCCA CTTCGCGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAGTCA AGGCTTTTAC GCGGCGCATA CCGAAGGCGG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCTCG CAACAGAATG CAAGCAACAT
1551 CCAAAATCCA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTATC GACCTGACCG CGGGCGGCGA AACCCGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTCCAACGG
1701 TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAAACTGC CGACAATGCC GCACCCAGCA CACCTTCCA CCGATTACCG
1801 CTCAACAGCG AAATTCAGA CCGCATCAGC CGCCATATCG ATACCGAACT
1851 CTTCTCCGAC AGCCTCTATG TTACCAGCAA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCGGC ACGGTGGACA AACCGTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTCC CGCAAAGAGA
2051 AACAGAAAT CCTCGAAGAC ACCCTGCTGG AACATGGCA GTGGCTCAAA
2101 CCTAAAGAAC CGTA

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This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

m771.pep
 1 MDLLSVFHKY RLKYAVAVLT ILLLAAGVLH ASVYRTFTPE NIRSRLQOSI
 51 AHTHRRKISFD ADIQRRLPR PTVILKNLTI TEPGGDQTAV SVQETKIGLS
 101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
 151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
 201 SRGLFLSNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
 251 AGLGRLADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG
 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA
 401 AKFRYTHEDA PHLEAAVALQ KNLTPYLDD VRQONGKIFP DTLAKLSGDI
 451 EAHKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTEGGISI
 501 ANTRPATYRL QQNASNIQIQ PLLQLFGFH SFGNGDAVI DLTAGGETRK
 551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
 601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLTQELSED VLIRNAVHPK
 651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK
 701 PKEP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

m771/g771 90.3% identity in 704 aa overlap

	10	20	30	40	50	60
g771.pep	MDLLSVFHKYRLKYAVAVLTMLLLAAGVLHASVYRTFTPENIRSRLQOSIAHTHRRKISFD					
m771	MDLLSVFHKYRLKYAVAVLTMLLLAAGVLHASVYRTFTPENIRSRLQOSIAHTHRRKISFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g771.pep	ADIRRRLLPRPTVILKNLTITTEPDGGRVAVSVKTKIGLSWKNLWSDRIQVEKWVVSAD					
m771	ADIQRRLPRPTVILKNLTITTEPGDQTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
g771.pep	LALTRDRNGAWNIDLFDAKHSASVNRIIVENSTVRLNLFQQLILKEISLNQSPDSS					
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNLFQEQILKEINLNQSPDSS					
	130	140	150	160	170	180
	190	200	210	220	230	240
g771.pep	GQPFESSGILVWRKLSVPWKSRLFLSDGIGTPEISPFHFESTSLDGHGITISTTGSPS					
m771	GQPFESSGILVWGKLSVPWKSRLFLSNGIGPPEISPFHFESTSLDGHGITISTTGSPS					
	190	200	210	220	230	240
	250	260	270	280	290	300
g771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGTFTAGGEYARWDG					
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG					
	250	260	270	280	290	300
	310	320	330	340	350	360
g771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPVWSRDNGLDAPRLHISTLQD					
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD					
	310	320	330	340	350	360
	370	380	390	400	410	420
g771.pep	TVDRLPQPRFISRLDGSLSIPNLQNWNAELNGTFDRQPVAAKFKYTRGAPHLEAAALQ					
m771	TVNRLPQPRFISRLDGSLSVNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ					
	370	380	390	400	410	420
	430	440	450	460	470	480
g771.pep	KNLAPYLDEFROQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDH					
m771	KNLTPYLDDVRQONGKIFPDTLAKLSGDI EAHKIGKVQLPGLQLDDMETYLHADKGHI					

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	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771.pep	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMSILKNGLSGKISG----STPFYRFT					
m771	DLTAGGETRKEILIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDILLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDILLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

```

a771.seq
1   ATG GATTAT TATCGGTCTT CCACAATAC CGTCTGAAAT ATGCGGTAGC
51  CGTGCCTGACG ATACTGCTTT TGGCGGCAAT CGGGCTGCAC GCTTCCGTAT
101 ATCGCATCTT CACACCTGAA AACATCCGAA GCCGCCTCCA ACAAGCATT
151 GCCCATACGC ACCGGAATAT CTCGTTGAT GCGGATATAC AGCGCAGGCT
201 TCTGCCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
251 GCGGCGACCG GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTCCGGA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAAAC GCACCGTCCG CCTCAATTC CTGACGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCG GATTTCGTCG GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGAAAA
601 AGCAGGGGGC TGTTCCCTTC AGACGGCATC GGCACGCCCA AATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTGCTGGA CGGACACGGC ATTACCATTT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCGGCGCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAAATC CCTACGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTTACC GCCGCGCGCG AATATGCCCA ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGCG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCCTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTCCGGCAAC
1301 AAAACGGCAA AATATTTCCT GACACCCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACG TGAAAATCGG AAAAGTCCAA CTTCGCGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAGTTC AGGGCTTTAC GCGCGCCATA CCGAAGGCGG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1551 CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTATC GACCTGACCG CGGGCGGCGA AACCAGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCAACGG
1701 TGCAATGGAC GGTATCGACA TGGACAATAT CCGTAAAAAC GGCATTTCGG
1751 GCAAACTGTC CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTACAG
1801 CTC AACACGCG AAATTTGAGA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTTCTCCGAC AGCCTCTATG TTACCAAGCA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCAGT ACGGTGGACA AACCCTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTCT CGCAAGAGAA
2051 AACAGAAAT CCTCGAAGAC ACCCTGCTGG AACAATGGCA GTGGCTCAAA
2101 CCTAAGAAGC CGTAA

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This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

a771.pep
 1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQOSI
 51 AHTHRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
 101 WKNLWSDQIQ IEKVVSSAE LALTRDGKGW WNIQDLIDSQ KRQASVNRII
 151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
 201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTGSPS VRFNAGGADA
 251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQWNNAEL NGTFDRQTV
 401 AKFRYTHEDA PHLEAAVALQ KNLTPYLDD VRQONGKIFP DTLAKLSGDI
 451 EAHKIGKVQ LPGQLDDME TYLHADKGIH ALSRFKSGLY GGHTGGISI
 501 ANTRPATYRL QONASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
 551 ELIRSLQGS LSNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
 601 LNSEISDGI RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
 651 NKPIPLKITG TVDKPSITVD YGRLTGGIN S RKEQKILED TLEQWQWLK
 701 PKEP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

a771.pep	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPENIRSRLQOSIAHTRKISFD
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQOSIAHTRKISFD
a771.pep	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKVVSSAE
m771	ADIQRRLPRPTVILKNLTITEPGGDQTAHSVQETKIGLSWKNLWSDQIQIEKVVSSAE
a771.pep	LALTRDGKGWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNQSPDSS
m771	LALTRDGKGWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNQSPDSS
a771.pep	GQPFESSGILVWGKLSVPWKSRLGLFLSDGIGTPKISPFHFEASTSLDGHGITISTGSPS
m771	GQPFESSGILVWGKLSVPWKSRLGLFLSNGIGPPEISPFHFEASTSLDGHGITISTGSPS
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTLALRNNSIKIETVNGAFTAGGEYAQWDG
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
a771.pep	TVNRLPQPRFISRLDGSLSVFNLQWNNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
m771	TVNRLPQPRFISRLDGSLSVFNLQWNNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
a771.pep	KNLTPYLDDVRQONGKIFPDTLAKLSGDI EAHKIGKVQLPGLQLDDMETYLHADKGIH
m771	KNLTPYLDDVRQONGKIFPDTLAKLSGDI EAHKIGKVQLPGLQLDDMETYLHADKGIH

1260

	490	500	510	520	530	540
a771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
m771	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

g772.seq

1	GTGTTCCGCA	CGGTCTTGCG	GACTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGTCGGCAAG	TTCTTTCAGG	TTGTTGCGTA	TGGTTTTCGG	CGGTTGGCGG
101	AAGGCGAGTT	TCACCAAGTT	GGCGAAATGA	TCGAAATCGT	CCGCCTTGCC
151	GATACGGTGT	TTACCCGGAA	TCATGCGCAC	CACGCGGAA	TCGATTTTCG
201	GC GCGGGATC	GAACGATTCG	GGCGGCACGT	CAATCAGCAG	CTCCATATCG
251	AAAAAATATT	GCAGCATCAC	ACCCAAGCGA	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATGCGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCAATAT
351	CGGCGACATC	GTCCGCCACC	TCCGCCAGTT	TGAACAAAAG	CGGCGTGGAG
401	ATGTTATACG	GCAGGTTGCC	GACGATTTTC	TTTTTGCTTG	AGATGCCGTT
451	GAAATCAAAC	TGCAACACGT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGCGACGGT	TTTACAGACG	CATACGATGT	CGCGGTTCGAT	TTTGACAACG
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATTG	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA
651	CAATATCGCC	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC
701	TTGCGGGGCT	TGTGTTCTTT	CATCGTGTTT	CCTCTTCGGT	TGAAACCCCG
751	CCCTTAGGG	CGGCAGGATC	AGACTCTGTT	TGGCGGGGCG	GTAACCCCTT
801	CCAAATCAGG	ACGACACATA	GGGCGGTGCT	TTATGTGTCG	TCCTGTGTGT
851	TGGAACATAA	ATGTGTTTAC	AGTATCCGTT	TGATGTCGGC	ATTGTAA

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

g772.pep

1	VFGTVLRTDA	DCLQIIVVGK	FFQVVAYGFA	ALAEGEFHQF	GEMIEIVRLA
51	DTVFHRNHAH	HCGIDFRRGI	ERFGRHVNQO	LHIEKILQHH	TQATVVVAFR
101	RGNHALDHFF	LQHKVHIGDI	VRHLRQFEQK	RRGDVIRQVA	DDFLFA*DAV
151	EIKLQHVAFV	NHQFIRKRQR	FQTAYDVAVD	FDNVQAVQLF	RQRFNGCRQT
201	RADEFNHDIIR	LRAHGVNDIA	DNPRVLQKIL	PETLAGFVFF	HRVSSSVETP
251	PFRAAGSDSV	WAGRNPFQIR	TTHRAVLVVS	SCVLEHKCVY	SIRLMSAL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

m772.seq

1	ATGTTCCGCG	CGGTCTTGCG	GATTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGCCTGCAAG	CTCTTTCAGA	TTGTTGCGTA	TGGTTTTCGG	CGGTTGGTGG
101	AAGGCGAGTT	TCACCAAGTT	GGCAAAATGC	TCGAAATCGT	CCGCCTTGCC
151	GATGCGGTGT	TTACCCGGAA	TCATACGGAC	GACGCGGAA	TCCACTTTCG
201	GCGCAGGGTC	GAACGATTCG	GGCGGTACGT	CAATCAGCAT	TTCCATATCG
251	AAAAAATATT	GCAGCATCAC	GCCCAAGCGG	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATACGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCAATAT
351	CGAGGACATC	GTCCGCCACC	TCCGCCAGCT	TGAACAAAAG	CGGTGTGGAA
401	ATGTTGTACG	GGAGGTTGCC	GACGATTTTC	TTTTTGCTTG	CGATGCCGTT
451	GAAATCAAAC	TGCAATACAT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGCGACGGT	TTTACAGACG	CATACGATGT	CGCGGTTCGAT	TTTGACAACG
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATCG	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGGCG	ACGGCGTTGA
651	CAATATCGCT	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC

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701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CTTTTCGGT TGAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTTT
801 CCAAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTGC TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

m772.pep

```

1 MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GKMLEIVRLA
51 DAVFHRNHTD DGGIHFRRRV ERFGRVYNQH FHIKILQHH AQAAVVVAFR
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEQK RCGNVVREVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RADFNHDIIR LRAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLVVS SCVLKHKCVY SIRLMSAL*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

m772/g772 85.2% identity in 298 aa overlap

	10	20	30	40	50	60
g772.pep	VFGTVLRTDADCLQIIVGKFFQVAYGFAALAEGEFHFQF	GEMIEIVRLADTVFHRNHAH				
m772	MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g772.pep	HCGIDFRRGIERFGRHVNQQLHIEKILQHHTQATVVVAFRRGNHALDHFFLQHKVHIGDI					
m772	DGGIHFRRRVERFGRYVNOHFHIEKILQHHAQAAVVVAFRRGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
	130	140	150	160	170	180
g772.pep	VRHLRQFEQKRRGDVIRQVADDFLFAXDAVEIKLQHVAFVNHQFIRKRQRFQTAYDVAVD					
m772	VRHLRQLEQKRCGNVVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD					
	130	140	150	160	170	180
	190	200	210	220	230	240
g772.pep	FDNVQAVQLFRQRFGNCRQTRADFNHDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF					
m772	FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
	250	260	270	280	290	299
g772.pep	HRVSSSVETPPFRAAGSDSVWAGRNPFIQIRTHRAVLVSSCVLEHKCVYSIRLMSALX					
m772	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLVSSCVLKHKCVYSIRLMSALX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

a772.seq

```

1 ATGTTGCGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51 CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGGTTTTCGG GCGTTGGTGG
101 AAGCGGAGTT TCACGAGTTT GCGGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGGCCGAA TCCACTTTTCG
201 GCGCGGGGTC GAACGATTTC GCGGCGACGT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGCAGCATA AAGTGCATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAG CGGCGTGGA
401 ATGTTGTAGG GCAGGTTGCC GACGATTTTC TTTTTCCTG CGATGCCGTT
451 GAAATCAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTCAGACGG CATACGATGT CCGGTCGAT TTCGACAACG
551 TGCAAGCGGT TCAGCTTTT CGCCAAAGT TCGTAATCG CCGCCAAACC
601 CGGACCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAATTCTG CCCGAAACGC
701 TTGCGGGGCTT TGTGTTCTTT CATCGTGTTC CTTTTCGGT TGAACCCCG
751 CCGCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ACGGCACATA GGGCGGTGCT TTATGTGTGC TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

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This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

a772.pep
 1 MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GEMLEIVRLA
 51 DTVFHRNHAD DGRHFRRGV ERFGRHVNH FHIEEILQHH AQAQVVAFR
 101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV
 151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
 201 RTDFNHDIIR LRAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
 251 PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

m772/a772 95.6% identity in 298 aa overlap

	10	20	30	40	50	60
a772.pep	MFGAVLRIDADCLQIIVACKL	FQIVAYGFAALVEGEFHEF	GEMLEIVRLADTVFHRNHAD			
m772	MFGAVLRIDADCLQIIVACKL	FQIVAYGFAALVEGEFHEFG	KMLEIVRLADAVFHRNHTD			
	10	20	30	40	50	60
	70	80	90	100	110	120
a772.pep	DGRHFRRGVVERFGRHVNHQ	FHIEEILQHHQAQAVVAF	RRGNHTIDHFFLQHKVHIDDI			
m772	DGGIHFRRRVERFGRYVNHQ	FHIEKILQHHQAQAVVAF	RRGNHTLDHFFLQHKVHIDDI			
	70	80	90	100	110	120
	130	140	150	160	170	180
a772.pep	VRHLRQLEQKRRGNVVGQVAD	DLFACDAVEIKLQYIAFV	NHQFIRKRQRQTAYDVAVD			
m772	VRHLRQLEQKRCGNVREVAD	DLFACDAVEIKLQYIAFV	NHQFIRKRQRQTAYDVAVD			
	130	140	150	160	170	180
	190	200	210	220	230	240
a772.pep	FDNVQAVQLFRQRFGNRRQT	RTDFNHDIIRLRAHGVNDI	ADNPRVLQKILPETLAGFVFF			
m772	FDNVQAVQLFRQRFGNRRQT	RADFNHDIIRLRAHGVNDI	ADNPRVLQKILPETLAGFVFF			
	190	200	210	220	230	240
	250	260	270	280	290	299
a772.pep	HRVSFSVETPPFRAVESDSI	WEGRNSFQIRTAHRVLYVS	SCVLKHKCVYSIRLMSALX			
m772	HRVSFSVETPPFRAVESDSI	WEGRNSFQIRMAHRVLYVS	SCVLKHKCVYSIRLMSALX			
	250	260	270	280	290	

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

m773.seq
 1 ATGGGATTGG GTGCAACGAC TTTTGTGCGT TCGGGTGCTA TAGGCGGAGG
 51 TCTGTGCAGT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
 101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATTG
 151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
 201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAATCTAG
 251 CCGTATGGGG ATTGGAAACG CTGATTACGC GCAAATGGG AACTTGCCA
 301 ACGGGTGTGA AAACCTCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
 351 TATCCTGTCC CAATCCGAAG TCGGTATCAA GTGGGCAAG GGGATTGAAG
 401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGGCTT GTCTGCCAAT
 451 GCAAGGTTAC CTAAAAATTT TAAACATTT GATTATTTG ATCGTGGTAC
 501 AGGCACGGCA ATCAGTGCCA AAACCTGGA TACGCAAACT ACGGCACGCC
 551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
 601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGCGAGA
 651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAAACTAATA
 701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
 751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
1  MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TQASEGSRQL
51  FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA
101 TGVTSLTPK TADVQRNLS QSEVGKWK GIEGQGPWE DYVGKGLSAN
151 ARLPKNFKTF DYFDRGTGTA ISAKTLDTQT TARLSKPEQL YSTMKGIDK
201 TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEQRLQL QRVVEYGKSO
251 NI TVKITEIE *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101 CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAAT
201 GGAATGTGTA AACGGGAAAG TCAAAGCATT GGAGCATACG AAAATACACC
251 CTTCGGCAG GACATACGTC CAAAACTCG ACGACCGCAA ATTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATCAA AACGGCAGGT
401 TTTCTGCCCG AGCCGCCCTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGGAACCTG GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCCAACC CGG GAGTCA TATTCAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCAGCAGCT
651 GATACAGACC TATCCCGGCA GCCCGCGGCG AAAACGCGCC GCCGAGCCG
701 TACGCAAAAC ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRITYV QKLDRLKLE
101 HYLNTGEGSA SAHTVETAQN LYNQALKHYQ NGRFSAAAAL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEVIFKIGEC
201 QYRLQKQDIA RATWRSLIQT YPGSPAARKA AAARVRK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCCGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGCAGG CAGCCAAACC GAAATGTGCA
101 CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAAT
201 GGAACCTTA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT
251 CTTCGGCAG GGCATACGTC CAAAACTCG ACGACCGCAA GTTGAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTCGAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATAAA AGCGGCAAGT
401 TTTCTGCCCG TGCTCCCTG TTGAAGGGCG CGGACGGAGG CGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCCAACC CGG CCTGAAGCCA TGTTCAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCAGCAGCT
651 GATACAGACC TATCCCGGCA GCCCGCGGCG AAAACGCGCC GCCGAGCCG
701 TGCGCAAAAC ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDRLKLE
101 HYLNTGEGSA SAHTVETAQN LYNQALKHYK SGKFSAAASL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEAMFKIGEC
201 QYRLQKQDIA RATWRSLIQT YPGSPAARKA AAARVRK*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFIWLSVSASCASVLPVPEGSRTQENASDGIPYPVPTLQDRLDYLEGKI					
m774	MKIKLPLFIWLSVSASCASVSPVAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGKI					
	10	20	30	40	50	60
	70	80	90	100	110	120
g774.pep	VRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLDLDRKLKEHYLNTGEGGSASAHTVETAQN					
m774	VRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTGEGGSASAHTVETAQN					
	70	80	90	100	110	120
	130	140	150	160	170	180
g774.pep	LYNQALKHYQNGRFSAAAALLKGADGGDGGGSAQRSMYLLQSRARMGNCSVIEIGGRY					
m774	LYNQALKHYKSGKFSAAASLLKGADGGDGGGSAQRSMYLLQSRARMGNCSVIEIGGRY					
	130	140	150	160	170	180
	190	200	210	220	230	
g774.pep	ANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAARAAAARVRKR					
m774	ANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARAAAARVRKR					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

```

1  ATGAAGACCA AATTACCGCT TTTATCATT TGGCTGTCCG TATCCGCCGC
51  CTGTTCTTCC CCTGTTTCCC GCAATATTC AAGATATGCG CTCGAACCGC
101 AGGCAGAGGC AGGTAGTTCG GACGCTATTC CCTATCCCGT TCCCACTCTG
151 CAAGACCGTT TGGATTATCT GGAAGGCACA CTCGTCCGCC TGTCGAACGA
201 AGTGGAAACC TTAACCGGCA AAGTCAAAGC ACTGGAGCAT GCGAAAACAC
251 ACCCTTCCAG CAGGGCATA GTCAAAAAC TCGACGACCG CAAGTTGAAA
301 GAGCATTACC TCAATACCGA AGGCGGCAGC GCATCCGCAC ATACCGTCGA
351 AACCGCACAA AACCTCTACA ATCAGGCACT CAAACACTAT AAAAGCGGCA
401 GGTTTTCTGC CGCTGCCTCC CTGTTGAAAG GCGCGGACGG AGGCGACGGC
451 GGCAGCATCG CGCAACGCAG TATGTACCTG TTGCTGCAAA GCAGGCGCGC
501 TATGGGCAAC TGCGAATCCG TCATCGAAAT CCGAGGGCGT TACGCCAACC
551 GTTTCAAAGA CAGCCCAACC GCGCCTGAAG CCATGTTCAA AATCGGCGAA
601 TGCCAATACA GGCTTCAGCA AAAAGACATT GCAAGGGCGA CTTGGCGCAG
651 CCTGATACAG ACCTATCCCG GCAGCCCGGC GGCAAAACGC GCCGCGCGAG
701 CCGTGCGCAA ACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

```

1  MKTKLPLFII WLSVSACSS PVSRIQDMR LEPQAEAGSS DAIPYPVPTL
51  QDRLDYLEGT LVRLSNEVET LNGKVKALEH AKTHPSSRAY VQKLDLDRKLK
101 EHYLNTGEGS ASAHTVETAQ NLYNQALKHY KSGRFSAAAS LLKGADGGDG
151 GSIAQRSMYL LLQSRARMGN CESVIEIGGR YANRFKDSPT APEAMFKIGE
201 CQYRLQKDI ARATWRS LIQ TYPGSPAAR AAAARVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKTKLPLFIIWLSVSACSSPVSRIQDMRLEPQAEAGSSDAIPYPVPTLQDRLDYLEGT					
m774	MKIKLPLFIIWLSVSASCAS-VSPVAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGK					
	10	20	30	40	50	

1265

```

      70      80      90      100     110     120
a774.pep  LVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKDDRKLKEHYLNTEGGSASAHTVETAQ
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      IVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKDDRKLKEHYLNTEGGSASAHTVETAQ
          60      70      80      90      100     110

      130     140     150     160     170     180
a774.pep  NLYNQALKHYKSGRFSAAASLLKGADGGDGGSIQRSMYLLQSRARMGNCESVIEIGGR
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      NLYNQALKHYKSGKFSAAASLLKGADGGDGGSIQRSMYLLQSRARMGNCESVIEIGGR
          120     130     140     150     160     170

      190     200     210     220     230     239
a774.pep  YANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAKRAAAVRRRX
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      YANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAKRAAAVRRRX
          180     190     200     210     220     230

```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```

m790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAGTC CTTAACGATG TCCAAGGCGA TACGACCATC AACAACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ATGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTTCG
551 CCCCTTCGCA GTACACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGAGA CTTGCTGGTG GTCGAGCCGC GTATGTGCCC
651 TGCGGACGAA GACATCGCGC TGATTGAACT GTCCGACAAG CGGCTGGTTCG
701 TCGCGCACCT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
751 GGCAGGCCGT CTGAAGCCTT TGACCTGCCC GAAGGCAGCA CGATTTTAGG
801 TGTGGTCTGT GAGTCAAAAA ACGGTTTATG TCCGCCGCGC AGGCAAGAAG
851 GCGTGTTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTATGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

```

m790.pep
1  MARRSKTFEE AAAEVEERFG HRGIKLEFE GTAKPCVINC PKHGNQTCR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTOAYNEMT KSVAGSNSIV LNDVQGDTTI NNHHTHTNNH SDADGKALSM
151 RLTPRPLLSL RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMCPADE DIALIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEAFDLP EGSTILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGMI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```

a790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATATC CTTAACGATG TCCAAGGCGA TACGACCATC AACAACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ACGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTTCG
551 CCCCTTCACA ATATACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
651 TGCGGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTTCG
701 TCGCGCACCT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG

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1266

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751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGCTG GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTAT TCGGATTACC GCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MAFRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDTTI NNHHTHTNH SDADGKALSM
151 RLTPRPLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIKGDLLV VEPRMRPADE DIVLIELSDK RLVV AHLVID IAGRMLIYOT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

```

a790/m790    98.2% identity in 342 aa overlap

          10      20      30      40      50      60
a790.pep    MARRSKTFEEAAEEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCSRYSNMFIGSSW
m790         MARRSKTFEEAAEEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCSRYSNMFIGSSW
          10      20      30      40      50      60

          70      80      90     100     110     120
a790.pep    GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSII
m790         GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSIV
          70      80      90     100     110     120

          130     140     150     160     170     180
a790.pep    LNDVQGDTTINNHHTHTNHSDADGKALSMRLTPRPLSDRQAAAFARTGKLTGSFDLFA
m790         LNDVQGDTTINNHHTHTNHSDADGKALSMRLTPRPLSDRQAAAFARTGKLTGSFDLFA
          130     140     150     160     170     180

          190     200     210     220     230     240
a790.pep    SVVAPSQYTF AVAMPDTSMS PVIKGDLLVVEPRMRPADE DIVLIELSDKRLVV AHLVID
m790         SVVAPSQYTF AVAMPDTSMS PVIKGDLLVVEPRMCPAEDIALIELSDKRLVV AHLVID
          190     200     210     220     230     240

          250     260     270     280     290     300
a790.pep    IAGRMLIYOTGRPSEALDLPESVILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGTI
m790         IAGRMLIYOTGRPSEAFDLPEGSTILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGMI
          250     260     270     280     290     300

          310     320     330     340
a790.pep    SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
m790         SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAX
          310     320     330     340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTA CTGTTT
51  TGGTTTGT TTGGTTTTT GTGTATTGG AGTGGGCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGCT CTTTGGATTC TTG CAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGCGGATG GAGAAGTCAT
201 CCGTATGTAT GGGGAGCAGC GGCGCGAATT TACAAAATC GGCGATTTC
251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTGGG GGGTGGATGT TTGGGGTGT GCCCGGCTG CCGTCGCGAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

```

```

401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTTC ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC ATAAGAATGT CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAAT GCATTATGAG CGGTTTGTTT GGAATAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCAGATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CGCGGCAGCA GCTACCGCGG TGCGGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTGCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTGG ATGTTACTAA
1101 AAGAGAAAAA GTCGTCATAC AGCTGCCCGG CGGCAGCGCG GTTGCCTTG
1151 ACAGGCGCGC CTTGGGTTT GCGGCCGAG CGGTCGATAA TGAGAAAATG
1201 GGGGAGGACC GTATCCGCGG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GGTGACGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TCGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCC GGGGAAAGGG
1501 CGGAACGGCT CGGTTTGAC ACCTAAAAAT TCAGACGGCA GATATCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAA ATGGTTTCCA
1601 TCGTATTTT GATGCTATC GGTGTCGGT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCGGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GCGCGAGGCA TATAGTGAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGC ACGTGATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAATG CAACCTTTG TGCGAGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATAT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCG TAAACCGGT ACGACCAACG ACAATAAGA
2001 TGCGTGGTTT GTCGGTTTA ACCCTGATG GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAATGC CTGAAGGTG GGTACGACG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

```

g791.pep
1  MVNYYSAMIK KILTTCEGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWGV ARAAVGNVVS GSVQSGASTI TQOVAKNFYL SSEKTETRFK
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR OKYILNNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFVKYTTV
301 RTDHQKAATE ALRKALRNFD RGSSRYGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVNV DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELF ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRLAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGKGKGG MKMPEGVVSS NGEYMKERM VTDPLMLDN
751 SGIAQPQSRK AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

```

m791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTC
51  TGTTTGGTT TTTGGGTTT GTGATTATGG AGTGGGTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGCGT CTTTGGATT TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTAT TCAGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GCGGATTTC
251 CAGAGGTGTT GCGGAATGCG GTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGATTTGGG GGGTGGATGT TTGGGGTGT GCCCGCGTGC CCGTCGCGAA
351 TGTGCTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGCGGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

```

1268

```

451 AATGAGGTGT TGCTTGCCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC AATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC AATAAGATGT CCGAGATTGT
601 ACTTTGGCCG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAC TGCATTACGAG CGGTTTGTTT GGAAATCGA
801 TCAGAGTGGG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CGCGGCAGCA GCTACCGCGG TGCGGAAATC TATATCGATT
1001 TAGATTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTGCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCCG CTGCGGTTT GCGCCCGCG CGGTCAATAA TGAAAAAATG
1201 GGGGAGGACC GTATCCGCG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGCGGTTGG GCGGTGTTT AAGAGCGGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCCGC GGCATTATCT AAGGGGATGA
1451 CC GCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CC GACCGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCGGTATTTT GATGTCATC GGTGTGCGTT ACGCGCAACA GTATATCCGG
1651 CGTTTTCGGT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GGCAGGAGCA TATAGCGTAT
1751 TTGCGAACCG CGGATATAGG GTTCTTCGCG ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAATG CAACCTTTGG TGGCTGGGCA
1851 AAATGCGCCG CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACCG ATATTGCCGG TAAACCGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCG GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCGCG TTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGCG CTGAAGGTGT GGTACGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAA
2251 AGCGGTATG CGCCGCAACC TTCCCGACGG GCAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAAGAAAC GCCGTGCTT CCGAGTAATA CTGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

m791.pep

```

1  MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWG ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHOKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDV EETVSQYLSG
351 LYTVDMKMPA VVLDVTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPQLQG ALGSLDARTG AVRALVGGYD
451 FHSKTFNRVAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDRIY
601 DRDGRLLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVVVDYMR FALKGKQKKG MKMPEGVVSS NGEYMKERM VTDPLGLTDN
751 SGIAPOPSRR AKEDDGAAE GGRQAADDEV RQDNQETPVL PSNTGSKQQQ
801 LDSLF*

```

g791/m791 97.3% identity in 805 aa overlap

```

              10      20      30      40      50      60
g791.pep      MVNYYSAMIKKILTTFCGLFFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
              |||
m791           MVNYYSAMIKKILTTFCGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
              10      20      30      40      50      60

              70      80      90      100     110     120
g791.pep      SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVVDVWGVARAAVGNVVS
              |||
m791           SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVVDVWGVARAAVGNVVS
              70      80      90      100     110     120

```

1269

	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPKAPSAYNPIVNPERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPKAPSAYNPIVNPERAKLRQKYILNNMLE					
	190	200	210	220	230	240
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFRDGSSEYGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
m791	RADHQKVATEALRKALRNFRDGSSEYGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
	310	320	330	340	350	360
	370	380	390	400	410	420
g791.pep	VVLDVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIIRGAVIRVKNNGGRW					
m791	VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIIRGAVIRVKNNGGRW					
	370	380	390	400	410	420
	430	440	450	460	470	480
g791.pep	AVVQOEPLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQOEPLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPKGPNPNSVWTPKNSDGRYSGYITLQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPKGPNPNSVWTPKNSDGRYSGYITLQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
	550	560	570	580	590	600
g791.pep	GVGYAQYIRRFGRFSELPAISLMAAGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQYIRRFGRFSELPAISLMAAGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
	610	620	630	640	650	660
g791.pep	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
m791	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
	610	620	630	640	650	660
	670	680	690	700	710	720
g791.pep	TTNDNKDAWFGFNPVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKGKQK					
m791	TTNDNKDAWFGFNPVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKGKQK					
	670	680	690	700	710	720
	730	740	750	760	770	780
g791.pep	MKMPEGVSSNGEYMKERMVTDPLMLDNSGIAPQPSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVSSNGEYMKERMVTDPLMLDNSGIAPQPSRRAKEDDGGAAEGGRQADDEV					
	730	740	750	760	770	780
	790	800				
g791.pep	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```

1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51  TGGTTTGGTT TTTGGGTTTT GTGTATTGGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGTGCCG CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGCAATT TACAAAAATC GGCATTTC
251 CAGAGGTGTT GCGGAATCGG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCTGTGCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG
601 ACTTTTGGCG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCGCTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCCGGAT
751 CAGGCGTTGA ATGAGGAACT GCATTACGAG CGGTTTGTTT GGAATAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCGCATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTCGAT CGCGGCAGCA GCTACCGCGG TGCGGAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCCCGCC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCGCGCG CGGTCAATAA TGAAAAAATG
1201 GGGGAGGACC GTATCCGCAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCAGA GCTGTGCGCG CGCTGGTTCG CGGTATGAT
1351 TTTTACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTGGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTTCGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTTCGC ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAAATG CAACCTTGG TGCCCGGGG
1851 AAATGCCCTT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGC GTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTCAAGCAG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGCGACGGC AGCGCGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep

```

1  MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWG ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVIQLPGRR VTLDRRALGF AARAVNNEKM
401 GEDRIIRGAV IRVKNNGGRW AVVQEPILQG ALVSLDARTG AVRALVGGYD
451 FHSKTFNRVA QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRLAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVVVDYMR FALKGKQKKG MKMPEGVVSS NGEYMKERM VTDPLGLTLDN
751 SGIAFPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

a791/m791 99.9% identity in 805 aa overlap

10 20 30 40 50 60

1271

a791.pep	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLOHYQPKMPLTIY
m791	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLOHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
m791	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAVGNVVS
	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAGLGPAPSAYNPVNPRAKLRQKYILNNMLE
	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFVYTTV
	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
m791	RADHQKVATEALRKALRNFDGSSYRGAENYIDLSKSEDEETVSQYLSGLYTVDKMVP
	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
m791	VVLDTVKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
m791	AVVQEPLLQALVSLDAKTGAVRALVGGYDFHSTFNRAVQAMRQPGSTFKPFVYSAALS
	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
m791	KGMTASTVVNDAPISLPKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI
	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
m791	GVGYAQQYIRRFGRSSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
m791	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
m791	TTNDNKDAWFGFNPDPVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKG
	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
m791	MKMPEGVVSSNGEYYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV
	MKMPEGVVSSNGEYYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV

1272

730 740 750 760 770 780

790 800

a791.pep RQDMQETPVLPSNTGSKQQQLDSLFX
|||||

m791 RQDMQETPVLPSNTGSKQQQLDSLFX
790 800

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

```

1 ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51 CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCCGAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTGT
251 CCggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCTAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGGAAAGAGG GGCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAAC
451 AGGATTTTCG AACTGTATTT AAACCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAAACCG GcgcgaGACC
551 TGACCAAACA GCAGgcggcG aaactgacgg tactcgtccc cgccccgttt
601 taCtactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcaggggtt cggcaaatTA ccccaagcg aaacggactg
701 attgttcag atatggaaat gccgcctgaa ctgggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

```

1 MFRIVKWLIA LPVGIFIFFN AYVYGNIIY RAVAPHRTAF MSMRMKQFEQ
51 EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKKP AADLTQQAQ KLTVLVPAPF
201 YYSDHPSKR LRNKTNIIVL RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

```

1 ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51 CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGGCAGCG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCAAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCTAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTTAC CGACAAAGAC
451 AGGATTTTTG AACTGTATTT AAACCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCCGCGTCCC GGTATTTTAA TCAAATACCC GCCGCAAAGC
551 TGACCAAACA GCAGGCGGCA AAACGACGG CGCGCGTCCC CGCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAAA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

```

1 MFRIVKWLIA LPVGIFIFFN AYVYGNIIY RAVAPHRTAF MSMRMKQFEQ
51 EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQAQ KLTARVPAPL
201 YYADHPKSKR LRNKTNIIVL RMGSAELPES DTD*

```

g792 / m792 90.4% identity in 230 aa overlap

```

10 20 30 40 50 60
g792.pep MFRIVKWLIALPVGIFIFFNAYVYGNIIYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR
|||||
m792 MFRIVKWLIALPVGIFIFFNAYVYGNIIYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR
10 20 30 40 50 60

70 80 90 100 110 120
g792.pep WVPYNRISTNLKKALIASDVRFAGHGGFDGDGIQNAIRNRNSGEVKAGGSTISQQLAK

```



```
m792      WMPYKRISTNLKKALIASEDARFAGHGFGFDWGGIQNAIRNRNSGKVKAGGSTISQQLAK  
          70           80           90           100           110           120  
  
g792.pep   NLFLNLSRNYLRKGEEAAITAMMEAVTDKNRI FELYLNSIEWHYGVFGEAASRYFYKKP  
          130           140           150           160           170           180  
m792      NLFLNLSRSYIRKGEEAAITAMMEAVTDKDRI FELYLNSIEWHYGVFGEAASRYFYQIP  
          130           140           150           160           170           180  
  
g792.pep   AADLTQQQA AKLTVLVPAPFFYS DHPKSRLRNKTNI VLRRMGSA NYPKAKRTDCSRYGN  
          190           200           210           220           230           240  
m792      AAKLTQQQA AKLTARVPAPIYYADHPSKSLRNKTNI VLRMGSAL PESDSTD X  
          190           200           210           220           230  
  
g792.pep   AAXTGVRTAYVFWDLX
```

```
a792.seq
1 ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51 CT'TTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGTGAAGCA GTTTGAACAG
151 GAAGGTGCGC ATGTGCGCAT GGATTACCGC TGATGCCCT ACAACGCAT
201 TTCCACCAAC CTCAAAAAG CCTGATTGC TTCCGAAGT GCCCGTTTCG
251 CCGGGCACGG CGGCTTCGAT TGGGGCGGCA TCAAAAACGC CATAGGCGC
301 AACCGGAACA CGCGCAAAAT GAAGGCGGGC GGTGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCCGAAAG
401 GCAGAAGAC GGCAGTATCC GACGATGAG AAGCCGTTC ACACGAAGAC
451 AGGATTTTTG AACTGTATT AAACCTCAAT GAATGGCACT ACGGCGTTTT
501 CGCGCGGGAA GCGCGGTCCT GGTATTTTTA TCAAAATACC CGCGCCAGCG
551 TGACCAAAAC GCAGCGGCGA AAACGACGG CGCGCGTCCC CGCCCGCTC
601 TACTACCGCG ACCATCCGAA AAGCAAACGG CTCGCAACA AAACCAATAT
651 CTGTGCTCAGA CGCATGGGTT CGGCAGAGT GCCTGAAAGC GACACGGCAT
701 GA
```

```
a792.pap
1 MFRIIKWLIA LPVGIFIFNN AVYVGNIIY RAVAPHRTAF MSMRMKQFEQ
51 EGRDVALDYR WMPYKRISTN LKALIASD ARFAGHGDF WGGIGNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFNLSRSY IRKGEEAAIT AMMEAVTDKD
151 RI FELYLNSI EWHVGVFGAE AASRYFYQIP AAKLTQKQAA KLTARVPAPL
201 YYADHPKSKR LRNKNTVILR RMSAELPES DTD*
```

	10	20	30	40	50	60
a792.pep	MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
m792	MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
	10	20	30	40	50	60
a792.pep	70	80	90	100	110	120
	WMPYKRISTNLKALIASEDARFAGHGGFDWGGIQNAIRNRNRSGBKVKAGGSTISQQLAK					
m792	WMPYKRISTNLKALIASEDARFAGHGGFDWGGIQNAIRNRNRSGBKVKAGGSTISQQLAK					
	70	80	90	100	110	120
a792.pep	130	140	150	160	170	180
	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNLSIEWHYGVFGAEAAASRYFYQIP					
m792	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNLSIEWHYGVFGAEAAASRYFYQIP					
	130	140	150	160	170	180
a792.pep	190	200	210	220	230	
	AAKLTKQAAAKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSAELPESDIDX					
m792	AAKLTKQAAAKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSAELPESDIDX					
	190	200	210	220	230	

g793.seq

1274

```

1  ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC TGCTGATTG CCCGCGGGCT GTATCTGCAG
151 ACGGTAAAGT ATAACCTTTT GAAAGAACAG GGCACAAACC GGATTGTGCG
201 GACTCAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC TGTCCGAGCT
351 TGTTCGATGT CCGGTCGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
401 AGTCGTTTAT TTGGATCAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AAACCTTGT TTTGAAAAG AATTAAACG
501 CCATTACCGG ATGGGCAACC TGTTTGACA CGTCATCGGA TTTACCGATA
551 TTGACGCAAG AGGTCAGGAA GGTTCGAAAC TTTCGCTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTTGTTTTG CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCACCAGCA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCAAGTA CCATCAGGCA AAAGCCGGA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGACCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAAACG ATATGATCGA ACCTGGTTCG GCAATCAAAC CGTTCTGTAT
951 TCGCAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCCGGA CCGTCTCCCG TGCGCGATGA TACCCATGTT
1051 TACCCCTCTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCAACGTCGG
1101 CACAAGCAAA CTGCTGCGC GTTTCGGCGC CGAAGAAATG TATGACTTCT
1151 ATCATGAATT GGGCATCGGT GTGCGTATGC ACTCGGGCTT TCCGGGGGAA
1201 ACTGCAAGTT TGTTGAGAAA TTGGCGCAGG TGGCGGCCCA TCGAACAGGC
1251 GACGATGCTT TTCGTTACG GTCTGCAATT GAGCCTGCTG CAATTGGCGC
1301 GCGCCTATAC CGCACTGACG CACGACGGCG TTTGCTGCC GCTCAGCTTT
1351 GAGAAGCAGG CGGTTCGCC GCAAGGCAAA CGCATATTC AAGAATCGAC
1401 CGCGCGCGAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGGCGGCA
1451 CCGGTACGGC GGGTGGCGTG GACGGTTTCG ATGTCGGCGC TAAACCGGCG
1501 ACGGCGCGCA AGTTCGTCAA CGGGCGTTAT GCGGACAACA AACACGTCGC
1551 TACCTTTATC GGTTTTGCCC CCGCCAAAAA CCCCCGTGTG ATTGTGGCGG
1601 TAACCATCGA CGAACCAGCT GCCACGGCT ATTACGGCGG CGTAGTGGCA
1651 GGGCCGCCCT TCAAAAAAAT TATGGCGGCG AGCCTGAACA TCTTGGGCAT
1701 TTCCCGACC AAGCCACTGA CCGCCGACG CGTCAAAACA CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

```

g793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAMAVLFA CLIARGLYLO
51  TVTYNFKLEQ GDNRIVRTQA LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 DMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYP MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 YGEDGAEVVL RDRQGNIVDS LDSPRNKAPQ NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPQ RADSEQRRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
351 YPSLDVRGIM QKSSNVGTSK LSAFSGAEEM YDFYHELIGI VRMHSGFPGE
401 TAGLLRNWRR WRPIEQATMS FGYGLQLSLL QLARAYALT HDGVLLPLSF
451 EKQAVAPQWK RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFVDVGARTG
501 TARKFVNTRY ADNKHVATFI GFAPAKNPRV IVAVTIDEPT AHGYVGVVA
551 GPFPKKIMGG SLNILGISPT KPLTAAVKT PS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

```

m793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAAAGT ATAACCTTTT GAAAGAACAG GGCACAAACC GGATTGTGCG
201 GACTCAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTTCGATGT CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AAACCTTGT TTTGAAAAG AATTAAACG
501 CCATTACCGG ATGGGCAACC TGTTTGACA CGTCATCGGA TTTACCGATA
551 TTGACGCAAG AGGTCAGGAA GGTTCGAAAC TTTCGCTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCAAGTA CCATCAGGCA AAAGCCGGA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TCGCAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA

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1001 C GCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGGATAC CCATGTTTAC
1051 C CCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 A AGCAAACTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 A TGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 G CAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 G ATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 C CTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 A AACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCCG
1401 G CGCGAGGTA CGCAATCTGA TGGTTCCGT AACCGAGCCG GCGCGCACCG
1451 G TACGGCGGG TCGGTGGAC GGTTCGATG TCGCGCGGAA AACCGGCACG
1501 G CGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 C TTTATCGGT TTTGCCCCCG CCAAAATCC CCGTGTGATT GTGGCGGTAA
1601 C CATTGACGA ACCGACTGCC CACGGTTATT ACGCGCGCGT AGTGGCAGGG
1651 C CGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 C CCGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

```

m793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKFSIWIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLYAYE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRP RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRRW RPIEQATMSF GYGLQLSLQ LARAYTALH DGVLLPVSE
451 KQAVAPQGRK IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*

```

g793/m793 98.5% identity in 582 aa overlap

```

g793.pep      10      20      30      40      50      60
                MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ
                |||
m793           10      20      30      40      50      60
                MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ
                |||

g793.pep      70      80      90      100     110     120
                GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVPKDMKEMPSAAQLERLSELVDV
                |||
m793           70      80      90      100     110     120
                GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV
                |||

g793.pep      130     140     150     160     170     180
                PVDVLRNKLEQKGKFSIWIKRQLDPKVAEEVKALGLENFVFEKELKRHPYMGNLFAHVIG
                |||
m793           130     140     150     160     170     180
                PVDVLRNKLEQKGKFSIWIKRQLDPKVAEEVKALGLENFVFEKELKRHPYMGNLFAHVIG
                |||

g793.pep      190     200     210     220     230     240
                FTDIDGKGQEGLELSLEDSLYGEDGAEVVLDRQGNIVDSLSPRNKAPQNGKDIILSLD
                |||
m793           190     200     210     220     230     240
                FTDIDGKGQEGLELSLEDSLHGEDGAEVVLDRQGNIVDSLSPRNKAPKNGKDIILSLD
                |||

g793.pep      250     260     270     280     290     300
                QRIQTLYAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR
                |||
m793           250     260     270     280     290     300
                QRIQTLYAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR
                |||

g793.pep      310     320     330     340     350     360
                AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDDTHVYPSLDVRGIM
                |||
m793           310     320     330     340     350
                AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRD-THVYPSLDVRGIM
                |||

g793.pep      370     380     390     400     410     420
                QKSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMS
                |||
m793           370     380     390     400     410
                QKSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMS
                |||

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1276

```

          430      440      450      460      470      480
g793.pep    FGYGLQLSLLQLARAYTALTHDGVLLPLSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE
             |||||:|||||:|||||:|||||:|||||:|||||
m793        FGYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE
          420      430      440      450      460      470

          490      500      510      520      530      540
g793.pep    PGGTGTAGAVDGFVDGAKTGTARKFVNNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
             |||||:|||||:|||||:|||||:|||||:|||||
m793        PGGTGTAGAVDGFVDGAKTGTARKFVNNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          480      490      500      510      520      530

          550      560      570      580
g793.pep    AHGYYGGVVAGPPFFKKIMGSSLNILGISPTKPLTAAAVKTPSX
             |||||:|||||:|||||:|||||:|||||:|||||
m793        AHGYYGGVVAGPPFFKKIMGSSLNILGISPTKPLTAAAVKTPSX
          540      550      560      570      580

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

```

a793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CCGAACGGTG
251 CGGTTTTGGC GTTGAGTGC GCGACGGAGT CCTGTGTTGC CGTGCCTAAG
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCGGAGCT
351 TGTTCGATGT CCGGTTGATG TTTTGAGGAA CAGACTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGST TGCCGAAGAG
451 GTCAAAAGCT TGGGTTTGGA AAACCTTGTA TTTGAAAAAG AATTAAGACG
501 CCATTACCCG ATGGGCAACC TGTTCGACCA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTCGGAAC TTTGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGGACCGGC AGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCGCGCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCGGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCTTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACGT TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGCGGAC
1251 GATGCTTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCGCGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GGCGGCACCG
1451 GTACGGCGGG TGCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAC ACATCGCTAC
1551 CTTTATCGGT TTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGCGGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```

a793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVIG FTDIDKGQGE GLELSLEDLS
201 HGEDGAEEVL RDRQGNIVDS LDSPRNKAPK NGKDIIISLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPQ RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTOPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFEHELIGIV RMHSGFPGET
401 AGLLRNWRWW RPIEQATMSF GYGLQLSLLQ LARAYTALTH DGVLLPVSFE
451 KQAVAPQGR IFEKSTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNRYA DNKHIAFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAVKTP S*

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a793/m793 100.0% identity in 581 aa overlap

1277

a793.pep	10	20	30	40	50	60
	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
m793	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
	10	20	30	40	50	60
a793.pep	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
a793.pep	130	140	150	160	170	180
	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
m793	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
	130	140	150	160	170	180
a793.pep	190	200	210	220	230	240
	FTDIDGKGQEGLESLSDSLHGEDGAEEVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793	FTDIDGKGQEGLESLSDSLHGEDGAEEVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
a793.pep	250	260	270	280	290	300
	QRIQTLAYEELNKAVEYHQAKAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQAKAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
a793.pep	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
	310	320	330	340	350	360
a793.pep	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMYDFYHELIGVIRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	KSSNVGTSKLSARFGAEEMYDFYHELIGVIRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
	370	380	390	400	410	420
a793.pep	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALHDGVLLPVSEKQAVAPQKRIKKESTAREVRNLMVSVTEP					
m793	GYGLQLSLLQLARAYTALHDGVLLPVSEKQAVAPQKRIKKESTAREVRNLMVSVTEP					
	430	440	450	460	470	480
a793.pep	490	500	510	520	530	540
	GGGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	GGGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
	490	500	510	520	530	540
a793.pep	550	560	570	580		
	HGYGGVVAGPPFKKINGGSLNILGISPTKPLTAAAVKTPSX					
m793	HGYGGVVAGPPFKKINGGSLNILGISPTKPLTAAAVKTPSX					
	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

```

1  gtgcgtttca ATCATTTCAT AATGGTAACG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAC AAGCCGGTCC GCCGCCCGCG CGTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTCACCTAT GAATTCCTCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCGG CATACCCGTC
301 AATCCCGCGT CCACGATGAA GCTCGTTACC GCGTTTGCCG CCTTCAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTCA ATCAGGAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 CAAAGGCATC CGCAATATCA CGGGCGCCT GATGCTCGAC CACAGCTGT

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1278

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551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTTCCGCG
601 TTTATGACGC CCCCAATCC GACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CT'TTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTCCGTCAA AAAACTGATG CGCGCATCTT TTTCGGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCGCTGGC TGCTCGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCTGCT TCCTCAAAC CCGCGCGGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCCAAATG TTGGAACGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT GCCCATCGCG GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCCGGCGGC
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

```

g794.pep
1  VRFNHFMIVT IIIYVISPAN KPVRRPGVPT YPALPYNCFF YVTDSPMNF
51  KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRAGIPV
101 NPA STMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLT GNLYWAGSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRLMLD HSLWGEVGSF DHEADSGSP
201 FMT'PPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILT MNKRSNLLIA
351 RSVFLKLGDD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGTILNRNF KQSGGLRLRK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVAKNIISGG
501 DGWLDALMC KERRA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

```

m794.seq
1  GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51  CCTTGCAAAC AAGCCGGCCC GCCGCCACAG CGTCCCCTAT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAA
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGTTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGGCG CCTTCAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTAT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CTGCTTGAT GCTCAAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCCGAAGT CGGCAGCCCC GACGATTTCC AAGCCGACAG CGGTTCCGCC
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCCGA TATTTTCGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGCGCG CGGACGGATT TCAGACGTA TCGGCATAGC
951 CGACACGCCG GAAGGCGCGC AGACATTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCTGCT TCCTCAAAC CCGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGCCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCCAAATG TTGGAACGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

```

m794.pep
1  VRLNHFMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51  KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRSDVPV

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101 NPASTMKLVT AFAAFKTFGS NYRWATEFES NGTVNDGTLD GNLYWAGSGD
 151 PVFNQENLLD AQKOLREQGI LNTGHLMLD HSLWGEVGSF DDFEADSGSP
 201 FMTPPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
 251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
 301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSNLI
 351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
 401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLTRNRF KQSGGLLRLK
 451 TGTNNVRAL AGYWLGDKPM AVVVIINSGR AVSLPDLDN FVANNIISGG
 501 DGWLDKLMC KERRA*

g794/m794 95.5% identity in 515 aa overlap

	10	20	30	40	50	60
g794.pep	VRFNHFIMVTIIIVISPAKPVRRPGVPTYPALPYNCFYVTDSPMNFPKTAASLLLL					
m794	VRLNHFIMIAIIIVISPAKPARRHVSPTYPALPYNCFYVTDLPNMFPKTAASLLLL					
	10	20	30	40	50	60
g794.pep	ASLAHAHALDTGRIPONEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFKTFGS					
m794	ASLAHAHALDTGRIPONEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFKTFGS					
	70	80	90	100	110	120
g794.pep	NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRLRDKGIRNITGRMLMD					
m794	NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQKOLREQIILNITGHLMLD					
	130	140	150	160	170	180
g794.pep	HSLWGEVGSFDDFEADSGSPFMTPPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
m794	HSLWGEVGSFDDFEADSGSPFMTPPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
	190	200	210	220	230	240
g794.pep	QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
m794	QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
	250	260	270	280	290	300
g794.pep	NRWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSNLIARSVFLKLGGD					
m794	NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSNLIARSVFLKLGGD					
	310	320	330	340	350	360
g794.pep	GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVARTARMAQMLETAYFSPFA					
m794	GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVARTARMAQMLETAYFSPFA					
	370	380	390	400	410	420
g794.pep	QDFIDTLPIAGTDGTLNRNRFKQSGGLLRLKTGTNNVRALAGYWLGDKPMVAVVVIINSGR					
m794	QDFIDTLPIAGTDGTLNRNRFKQSGGLLRLKTGTNNVRALAGYWLGDKPMVAVVVIINSGR					
	430	440	450	460	470	480
g794.pep	AVSLPDLDNFVAKNIISGGDGWLDKLMCKERRAX					
m794	AVSLPDLDNFVANNIISGGDGWLDKLMCKERRAX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

a794.seq

1 GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTT
 51 CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTCCCACT TATCCGGCTT
 101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
 151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
 201 GCTCGATACA GGTCCGATTC CGCAAACGA AATCGCCGTA TATGTCCAAG
 251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGGTC

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301 AACCCGCGCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTT CGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGCGGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGCGGAAGT CGGCAGCCCC GACGATTCG AAGCCGACAG CGGTTCGCGG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTATGGT
651 GCGCGCGGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATAC CGCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAACTGATG CGTGCATCTT TTTCCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTG GGCAAGCCTG
851 TCGGTGTCGG GATGTCGCG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCGG GAAGCGCGCG AGACGCTTGC CGTTGCACAC TCAAGCCGCA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCGCTCT TCCTCAAACT CGGCGCGGAC GGCAAACTGC CCGCGGTTTC
1101 CGAACAGGCA GCGTCTGCCG TCCGGCGTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGTT CAGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAAATGAT GCGCAAAATG TTGGAAACGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGCCTTTACG CAACCGCTTC AAACAAGCG CCGGCGCTGT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGGAT GCGGTGGTCG TCATCATCAA CAGCGGCGCG GCCGTTTCCC
1451 TGTGCCCGCA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGCG
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

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This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

```

a794.pep
1  VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCF YVTDLPMNFP
51  KTAASLLLL ASLAHALDT GRIPONEIAV YVQELDSGK IIDHRSDVPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFES NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLA VQRQLREGGI RNITGHLMLD HSLWGEVSGP DDFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILD MNKRSNLI
351 RSVFLKLGDD GLPAVSEQA ASAVRELA VSGIDVADLV ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLRLK
451 TGTLLNVRL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDKLMC KERRA*

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a794/m794 98.6% identity in 515 aa overlap

	10	20	30	40	50	60
a794.pep	VRLNHFIMIAIIIYVISPAN					
m794	VRLNHFIMIAIIIYVISPAN					
	70	80	90	100	110	120
a794.pep	ASLAHALDTGRIPONEIAVYVQELDSGKIIDHRSDVPVNPASTMKLVTAF					
m794	ASLAHALDTGRIPONEIAVYVQELDSGKIIDHRSDVPVNPASTMKLVTAF					
	130	140	150	160	170	180
a794.pep	NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRQLREGGIRNITGHLMLD					
m794	NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQKQLREGGILNITGHLMLD					
	190	200	210	220	230	240
a794.pep	HSLWGEVSGPDDFEADSGSPFMTPPNPTMLSAGMVMVRAERNAADSTDILTDPPLPHIFA					
m794	HSLWGEVSGPDDFEADSGSPFMTPPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
	250	260	270	280	290	300
a794.pep	QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
m794	QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
	310	320	330	340	350	360
a794.pep	NHWLLGGGRISDGIGISDTPGAQTLAVAHSKPMKEILDMNKRSNLIARSVFLKLGDD					

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|||||
m794      NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTDMNKRSDNLIARSVFLKLGGD
          310      320      330      340      350      360

          370      380      390      400      410      420
a794.pep  GKLPAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
          |||||||
m794      GKLPAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
          370      380      390      400      410      420

          430      440      450      460      470      480
a794.pep  QDFIDTLPIAGTDGTLNRNFKQSGGLRLKTGT LNNVRALAGYWLGDKPMVAVVVIINSGR
          |||||||
m794      QDFIDTLPIAGTDGTLNRNFKQSGGLRLKTGT LNNVRALAGYWLGDKPMVAVVVIINSGR
          430      440      450      460      470      480

          490      500      510
a794.pep  AVSLLPDLDNFVANNIISGGDGWLDKLMCKERRAX
          |||||||
m794      AVSLLPDLDNFVANNIISGGDGWLDKLMCKERRAX
          490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2699>:

g900.seq

```

1   ATGccgTCTG AAATGCCGTC TGAAACGTGG CAGGCGGAGG TTCGGACGGC
51  ATTGGGTTTA TTTCAACGGG CGGATGCCGA CCGCATCGCG TACTTTATCC
101 AACAAATTCGC GCGCTTCTTT GCGCGCTTTT TCGCGCctg cctGCAAAAT
151 CTCTTCGATT TGCGAAGGAT TAGAGGTCAA TCGGTTGTAG CGTTCGCGCA
201 GTTCTGCCAA TTCGGCGTTG ATTTTCGCCG CCGAAAGTTT TTTCCGCTCG
251 CCCCAGCCA AGCCGTCGGC AAGCATTGTC GTAAATTCCG CCGTTTCAGA
301 CGGCGTGGAG AAGGCTTTAT AGATTTCAAA CAAAGGGCTT TCGTCGGGCT
351 GTTTCGGCTC GCCCGGCTCT TTCATGTTGG TAATGATTTT GTTGACCGAT
401 TTTTGGGTTT TTTTGTCTGT TTCCCAAAGC GGAATGGTAT TGCCGTAGGA
451 TTTGGACATT TTGCGTCCGT CCAAACCGAC CAAGAGTTCG ACGTTTTCGT
501 CGATTTTCAC TTCGGGCagg GTGaagagtt cTTGGAaacc gtgggtgaag
551 cgGCCggcAa tgtcgcgcgc cATTTCgacg tgttgGATTT GGTGCGGCCC
601 GACGGGGACT TCGTTGGCGT TGAACATCAA AATGTCGCA GTCATCAGAA
651 TCGGATAACT GAACAAACC ATTTCCACAC CGAAATCGGG GTCTTCCTGC
701 CCGTTTTCCG CATTGGCTTG AACGGCGGCT TTGTAGGCGT GGGCGCGGTT
751 CATCAAACCC TTGGCGGTGA TGCAGGTCAG AATCCAGTTC AACTCCATCA
801 CTTGCGGAAT GTCGCTTTGG CGGTAGAAGG TGGTGCCTC GGGGTGAGT
851 CCGCAGGCAA GCCAAGTGGC GGCAACGGCt tgGGTGGATT GGTGAATCAT
901 CTCCTGCTCG TGGCATTGTA TGATGCCGTG GTAATCGCG AGGAAGAGGA
951 AGGATTCGGT ATCGGGGTTT TCGCGCGCGC GGACGGCGGG CGCGATGGCG
1001 CCGACGTAGT TGCCAGATG CGGGGTGCCG GTGGTGGTTA CGCCGGTCAG
1051 AACTCGTTTT TTGCTCATAA AAATGTCCTT ACGGCAGCAA TGCCGTCTGA
1101 AAGGGAaaa. gatgCGCGA TTATACCGA TTTGCCACAT ACATCCAGCC
1151 GacaACagac TTTTCATAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng:

g900.pep

```

1   MPSEMPSETW QAEVRTALGL FORADADRIA YFIQQFARFF ARFLRACLQN
51  LFDLRRIRGQ CVVAFQFCQ FGVDfRRRKf FRLAPSQAVG KHLRKfRRfR
101 RRGEgFIDfK QRAfVGLfRL ARLfHVGNdf VDRfLGfFFvV fPKRNGIaVG
151 FGHfASvQTD QEfDVfVDFH FGQGEfFLET VGEaAGNVAR HfDVLdLVAP
201 DGDFvGVeHQ NVGSHQNRIT EQTHfHTEIG VFLPVfRIGL NGGFvGVGAfV
251 HQTLGGDAGQ NPVQLHHfGN VALAVEGGAL GVESAGKPSG GNGLGGLVNH
301 LLLVAFDDAV VIGEEEGfGf IGVLRRADGG ADGADvVAQM RGAGGGYAGQ
351 NSFFAHKNVL TAAMPsEREK DAPIIPDLPH TSSRQQTfPY *

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

m900.seq

```

1   ATGCCGTCGT AAACGCGGCA GCGGAGGTT CCGACGGCAT CGGGTTCATT
51  TCAACGGGCG GATGcCGACC GCATCgG.TA CTTTGTCCAA TAATTCGCGT
101 GCTTCTTTAC GCGCTTTCGC CCGCCTGCC TGCAAATCT CTTCGATTG

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1282

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1 51 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
2 01 CCGCGTTGAT TTTCGCGGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
2 51 CCGTCGGCAA GCATTTTCGT AAATTCACC GTTTCAGACG GCGTGGAGAA
3 01 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TCGGCTCGC
3 51 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATT TTGGGTTTTT
4 01 tTGTCGTTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
4 51 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
5 01 CCGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTGAAGCG GCCGCGCATG
5 51 TCGCGCGCCA TTTCGACGTG TTGGATTGG TCGCGCCCGA CgGGCaCTTC
6 01 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
6 51 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCCTGCCC GTTTTCTGCA
7 01 TTTGCCTGCA CGGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCTT
7 51 GGCAGTGATG CAGGTCAGAA TCCAGTTCAA TTCCATCACT TCgGAGTGT
8 01 GCGTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTTCGAGTCC GCAGGCAAGC
8 51 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
9 01 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTCGGTAT
9 51 CGAGGTTTTG CGCCGCGCGG ACGGCGGGG GATGGCGCC GACGTAGTTG
10 01 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
10 51 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
11 01 TGTGCCGATT ATACCGGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
11 51 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

m900.pep

```

1 MPSETRQAEV RTASGSFQRA DADRIXYPVQ *FACFFTRFR RACLQNLFDL
51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVPKR NGVAVGFGHF
151 ASVQTDQEFV VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVHQNIGS HQNRITEQTH FHTAIRVFLP VFCICLHGGF VGMGAVHQT
251 GSDAGQNFVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHLRLV
301 AFDDTVVIGE EEEFGIEVL RRADGGADGA DVVAQMRDAG GGYAQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QQTFFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

m900/g900

	10	20	30	40	50
m900.pep	MPSETRQAEVRTASGSFQRADADRIXYPVQX*FACFFTRFRACLQNLFDLRRVGGQ				
g900	MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRACLQNLFDLRRIRGQ				
	10	20	30	40	50
	60	70	80	90	100
m900.pep	LVVAFARFGEFGVD FRRQKFFGFT PRQAVGKHFRKFHRFRRRGE GFVDFKQWAFVGLFRL				
g900	CVVAFQAQFCQFGVD FRRRKFFRLAPSQAVGKHLRKFRFRRRRGE GFIDFKQRAFVGLFRL				
	70	80	90	100	110
	120	130	140	150	160
m900.pep	ARLFHIGDDFVDRFLGFFVVPKRNKVAVGFGHFASVQTDQEFVDFIDFHFGQGEFPEA				
g900	ARLFHVGNDFVDRFLGFFVVPKRNKGIAGVGFHFASVQTDQEFVDFVDFHFGQGEFLET				
	130	140	150	160	170
	180	190	200	210	220
m900.pep	VVEAAGDVARHFDVLDLVAPDGHFVGVHQNIGSHQNRITEQTHFHTAIRVFLPVFCICL				
g900	VGEAAGNVARHFDVLDLVAPDGHFVGVHQNIGSHQNRITEQTHFHTAIGVFLPVFRIGL				
	190	200	210	220	230
	240				

```

      240      250      260      270      280      290
m900.pep  HGGFVGMGAVHQTLGSDAGQNPVQFPHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH
          :|||:|||||:|||||:||||:|||||
g900      NGGFVGVGAVHQTLGGDAGQNPVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH
          250      260      270      280      290      300

      300      310      320      330      340      350
m900.pep  LRLVAFDDTVVIGEEEEFGFIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVL
          | |||:|||||
g900      LLLVAFDDAVVIGEEEEFGFIEVLRRADGGADGADVVAQMRGAGGGYAGQNSFFAHKNVL
          310      320      330      340      350      360

      360      370      380
m900.pep  AASMPSEREKDVPIIPDLPPTSSRQQTFFPYX
          :|||:|||||
g900      TAAMPSEREKDAPIIPDLPHPTSSRQQTFFPYX
          370      380      390

```

a900.seq	(partial)					
1	GAGGTCGGA	CGGCATTGGG	TTTATTTCAA	CGGGCGGATA	CCGACCGCAT	
51	CACGTACTTT	GCCCAATAAT	TCGCGTGCTT	CTTTACGCGC	TTTTTGC GCG	
101	CCTGCCTGCA	AAATCTCTTC	GATTTGC GAA	GGGTGCGGCG	TCAGCTCGTT	
151	GTAGCGTTTCG	CGCGGTTTCGG	CGAGTTCGGC	GTTGATTTTC	GCCGCCAAAA	
201	GTTTTTTTGC	CTCGCCCCAA	GCCAAGCCGT	CGGCAAGCAT	TTTTCGTAAAT	
251	TCTGCCGTTT	CAGACGGCGT	GGAGAAAGCT	TTGTAGATTT	CAAACAGAGG	
301	GCTTTCGTCG	GGCTTCTTCG	GCTCGCCCCG	CTCTTTTCATA	TTGGTGATGA	
351	TTTTTGTGAC	CGATTTTTCG	GTTTTTTTGT	CGTTTTCCCA	AAGCGGAATG	
401	GTGTTGCCGT	AGGATTTTGA	CATTTTTCGT	CCGTCCAAC	CAACCAGAG	
451	TTCGACGTTT	TCGTGATTT	TCACTTCGGG	CAGTGTGAAG	AGTTCGCGGA	
501	AGCGGTGGTT	GAAGCGGCCG	GCAATATCGC	GTGCCATTTC	AACGTGTTGG	
551	ATTTGGTCGC	GACCGACTGG	AACTTCATGG	GCATTGAACA	TGAGAATGTC	
601	GGCAGTCATG	AGGATAGGTT	AGCTGTACAA	ACCCATTTC	ACGCCGAAT	
651	CGGGGTCTTC	CTGCCCCGTT	TCCGCATTTC	CCTGCACCGC	GGCTTTGTAG	
701	GCGTGGGCGC	GGTTCATCAA	ACCCTTGGCG	GTGATGCAGG	TCAGAATCCA	
751	GTTCAATTTC	ATCACTTCGG	GAATGTCGCT	TTGACGGTAG	AAGGTGGTGC	
801	GCTCGGGTCC	GAGTCCGCAG	GCAAGCCAAG	TGGCGGCCAAC	GGCTTGGGTG	
851	GATTGGTGAA	TCATCTCCGG	CTCGTGCAT	TTGATGATAC	CGTGGAATC	
901	GGCGAGGAAG	AGGAAGGATT	CGGTATCAGG	GTTTTGCGCC	GCGCGGACGG	
951	CGGGGCGGAT	AGCACCGACG	TAGTTGCCCA	GATGCGGGAT	GCCGGTGGTG	
1001	GTTACGCCGG	TCGAACCTCG	TTTTTTGCTC	ATAAAAATGT	CCTTGC GCGCA	
1051	TCAATGCCGT	CTGAAAGGGA	AAAAGATGCG	CCGATTATAC	CCGATTGCGC	
1101	ACCTACATCC	AGCCGACAAC	AGACTTTTCC	ATATTAAT		

a900.pap	(partial)				
1	EVRTALGLFQ	RADTDRTITYF	AQ*FACFFTR	FLRACLQNLF	DLRRVGGQLV
51	VAFARFGEF	VDFFRRQKDF	LAPSQAVGKH	FRKFCVFRRR	GESFVDFKQR
101	AFVGLLRAL	LFHIGDDFVD	RELGFVVVF	KRNGVAVGFG	HFASVQTNQE
151	FDVFVDHFH	QCEEFPEAVV	EAGNIACHF	NVLDLVATDV	NFMGIEHNV
201	GSHEDRVAV	THFHAIGVF	LPVFRICLHG	GFVGVGAVHQ	TLGGDAQGNP
251	VQFHHFGNVA	LTVEGAGLV	ESAGKPSGGN	GLGLVNHLLR	LVAFDDTVVI
301	GEEEEGFGIR	VLRRADGGAD	STDVVAQMRD	AGGGYAGQNS	FFAHKNVLAA
351	SMPSEREKDA	PIIPDLPTS	SRQTFPY*		

```
m900.pep      MPSETRQAEVVRTASGSFORADADRIXYFVQXFACFFTRFRRACLQNLFDLRRVGGQLVVA  
              ||||| :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||  
a900          EVRTALGLFLQRADTDRIITYFAQXFACFFTRFLRACLQNLFDLRRVGGQLVVA  
               |         |        |       |      |      |      |      |  
              70        80        90       100     110     120
```

m900. pep	FARFGFEGVD	FRRQKFFG	FTPRQAVG	GKHF	FRKFR	FRRRGES	FVDFKQ	WAFVGL	FRLARLF
a900	FARFGFEGVD	FRRQKFFC	LAPSQAVG	GKHF	FRKFCR	FRRRGES	FVDFKQ	RAFVGL	LLRLARLF
	60	70	80	90	100	110			
m900. pep	130	140	150	160	170	180			
a900	HIGDDFVD	RFLGFFV	FPKRN	GVAVG	FGHFA	SVQTDQ	EFDVFI	DFHFG	QGEFPEAV
	120	130	140	150	160	170			
m900. pep	190	200	210	220	230	240			
a900	AGDVARH	FDVLDL	VAPDGH	FVGVEH	QNI	GSQNR	ITEQT	HFHT	IRVFLP
	180	190	200	210	220	230			
m900. pep	250	260	270	280	290	300			
a900	VGMGAVH	QTLGSD	AGQNPV	QFHHF	GSVAL	AVEGG	ALGVES	SAGKPS	GGNGLG
	240	250	260	270	280	290			
m900. pep	310	320	330	340	350	360			
a900	AFDDTVV	IGEEEE	GFIEVL	RRADG	GADG	ADVVAQ	MRDAG	GGGYA	QNSFFA
	300	310	320	330	340	350			
m900. pep	370	380							
a900	PSEREK	DVPIIP	DLPTSS	RQQT	FPYX				
	360	370							

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

```
m901.pep
  1  MPDFSMSNLA VAFSITLAAG LFTVLXSLGV MFSKTPNPRV LSFGLAFAGG
 51  AMVVYSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP
```

101 NPHETLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
 251 YGLTGMMAVI AVSLVLFHF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq
 1 ATGCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCTTTT CCATTACGTT
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTTCCTA
 1 01 AAACGCCCAA TCCGCGCGTG TTGTCGTTTG GTTTGGCATT TGCCGCGCGT
 1 51 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
 2 01 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
 2 51 CATTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
 3 01 AACCCGCATG AAACCTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
 3 51 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGCGCGTTT GCGATTACTG
 4 01 CGCACAATTT CCCCAGAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAT
 4 51 CCAGCAGTCG GGATGCCCTT GGCTTGGCG ATTGCCATCC ATAATATTCC
 5 01 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGGCCAC CGCAGCCGTA
 5 51 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTTGGGG
 6 01 GCGGCTTTGG GCTATTGGT TTGCGAGCCG TTTTGTGCGC CTGCCGTGTT
 6 51 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGT TTGGCGTTGG
 7 01 ACGAGCTGCT GCCGCGTGCC AAACGCTATT CAGACGGCCA TGAAACCGTT
 7 51 TACGGCCTGA CAATGGGCAT GCGCGTGATT GCCGTCAGCC TGGTATTGTT
 8 01 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep
 1 MPDFSMSNLA VAFSITLAAG LFTVLGSGLV MFSKTPNPRV LSFGLAFAGG
 51 AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP
 1 01 NPHETLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 1 51 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG
 2 01 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
 2 51 YGLTGMMAVI AVSLVLFHF*

m901/a901 98.9% identity in 269 aa overlap

m901.pep	10	20	30	40	50	60
	MPDFSMSNLA VAFSITLAAG LFTVLGSGLV MFSKTPNPRV LSFGLAFAGG AMVYVSLTEI					
a901	MPDFSMSNLA VAFSITLAAG LFTVLGSGLV MFSKTPNPRV LSFGLAFAGG AMVYVSLTEI					
	10	20	30	40	50	60
m901.pep	70	80	90	100	110	120
	FSKSSEAF AEIYDKDHAF AA ATMAFLAGMG GIALIDRLVP NPHETLDAQD PSFQESKRRH					
a901	FSKSSEAF AEIYDKDHAF AA ATMAFLAGMG GIALIDRLVP NPHETLDAQD PSFQESKRRH					
	70	80	90	100	110	120
m901.pep	130	140	150	160	170	180
	IARVGMMAAF AITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
a901	IARVGMMAAF AITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
	130	140	150	160	170	180
m901.pep	190	200	210	220	230	240
	RSRKKTWVAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA					
a901	RSRKKTWVAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA					
	190	200	210	220	230	240
m901.pep	250	260	270			
	KRYSDGHETV YGLTGMMAVI AVSLVLFHF					
a901	KRYSDGHETV YGLTGMMAVI AVSLVLFHF					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

```

g902.seq
1  ATGCCGTCGG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCTATTG CGCCGCCGCA TTGTCCAAGC GGTGATTTC
151 ACGCCGCGCC TGTTCGCCGT CGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG
251 GCGCGGATGT GGTTCAAAAT GCGGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCTGCC TTGCGCGCGC CGCCTATCA TGATGCCGTC GCGGCGGTT
401 TGTTCGAGGA cggCGGCGGC TTTTgcggc GAagtGATGT CGCGTTGac
451 cCaggCCGGG ATGTTcAGAc ggCTTTTGGT CTCGGcgatg agttCGTAAC
501 gcGCCTCGCC TTGTACATT TCGTGcgcg CGcgcccggtg aacggcaaGg
551 gcggcaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg
601 atcgtcgtcg tgccaacca AacggGTTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCCGTC
701 ATCagcGCGC TACCGGCTTG GACGTGCAC ACTTTcTtgg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTg taacgcgcg
801 ca tCCGCCAT CtgttcggGg TCGTCGCCG CAATCTGCAC GGCAACGATG
851 CCGccttcac cggcaAAAtc actgcggtg cAGGTTTTTC CGGTATTcCT
901 GAGCGTCGGA TCGCTGGCCA GCATTTCGCA CACCGCCCA CCTGCGCCAA
951 ACGCCCGACA GAGCGGCGG AAGGGTTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCga TGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

```

g902.pep
1  MPSEPERRHG NTALPFPIAA RPTVGFSKPK FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQVN GGSAPCQTQG
101 RR *NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAAlF GDFGDGGQVL
201 IVVVPTQTGF EGNgyARRLD HRLQNGGNQR LVLHORATGL DVAHFLGGAA
251 HlDVDDLrPE SDVVTRRlRH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

```

m902.seq
1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATT TGGCGGTAGG
51  CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCTG ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TgTCTgTTCG CCGTcGGGCA TTTCTGCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG TATGCGCGCG
251 ATGTGGTTCA AAATAGCGGC GCGCATTCT GCCAAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTCGGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGGCGGC GGTTTGTTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAAGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC GATGAGTTCT TAACGCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTGCCTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTCGCGCAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT TCGCACCCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGcGCaAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCGC ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

1 TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51 CGCACGCCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA

1288

```

1 01 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTACAGACG
1 51 TGTCTGTTTCG CCGTCGGGCA TTTCTGTCGAT GTACCAGCCT ATGTGTTTGC
2 01 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
2 51 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAAACTCA AGGCAGGCGG
3 01 TAAACACCG TGTTCCGGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
3 51 TGCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTGTTGTTG
4 01 AGGACGGCTT GGGCTTTTTCG CGGCGAGGTA ATGTGCGCGT TGACCCAGAC
4 51 CCGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
5 01 CGCCTTTGTA CATTGCGTG CGCGTGCCTC CGTGGACGGC AAGGCGGGCA
5 51 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
6 01 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCCGCCGCTT
6 51 TGACCACCGC CTCCAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
7 01 GCGTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
7 51 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAAACG GCGGCATCCG
8 01 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
8 51 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
9 01 CGGGTCGCTG GTCAGCATTT CGCACACCGC CCAACCTGCG CCAAAATCTC
9 51 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CCGCGCAAGT
10 01 GCGATGGGGT TGTCGATAAA ATAGCCGCGC ATGTGCATAA TGGATCCGCG
10 51 TTTCAAAAAA GTACGCCATT GTACATTTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

a902.pep

```

1 LHFQRIIKCS EGIWAVGARPTVGFFGKSEK ITCKHVLLRR RTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCQTQGRR
1 01 *NTVFGVMFQ IAEEPRASLR AAPYHNAVCG GLFEDGLGFL RRGNAVDPD
1 51 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGNAAIFGD FGDDGQVLMV
2 01 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
2 51 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
3 01 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRCDCGVVDK IAADVHNGSA
3 51 FQKSTPLYIF *

```

m902/a902 94.7% identity in 360 aa overlap

	10	20	30	40	50	60
m902.pep	LHFQRIIKCSEGIWAVGARPTVGFFGKSEKITCKHVLLRRRTVQAVDFTTCLFAVGHFVD					
a902	LHFQRIIKCSEGIWAVGARPTVGFFGKSEKITCKHVLLRRRTVQAVDFTTCLFAVGHFVD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m902.pep	VPAYVFACDAHTGGVAVKRVYGVADVVQNSGGAFQQTQGRRQNTVFGIMFQIAEEPRPALR					
a902	VPAYVFACDAHTGGVAVKRVHGSDVVQNSGGTFCQTQGRRXNTVFGVMFQIAEEPRASLR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m902.pep	AAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASVDG					
a902	AAPYHNAVCGGLFEDGLGFLRRGNVAVDPDRDVQTAFGFGNQVVSRAFAFVHLRTRASVDG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m902.pep	KGGDAAI FGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGLDI					
a902	KGGNAAI FGDFGDDGQVLMVVVPTQTGFEGNGYARRFDHRLQNGGNQRLVLHQRATGLDI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m902.pep	ADFFSGTAHVVDVDKLRPKADVTRGIRHLLRIASGNLHGNNAFIGKIAAVQGFSSISER					
a902	ADFFSGTAHVVDVDKLRPKADVTRGIRHLLRIASGNLHGNNAFIGKIAAVQGFSSISER					
	250	260	270	280	290	300
	310	320	330	340	350	360
m902.pep	RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF					


```

a902      |||||
          RVAGQHFHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
          310      320      330      340      350      360

m902.pep    X
            |
a902        X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcG gatgaggCAA GCCCCTGCTT
51 TCCTATTTCCT GAGGTGGAAaT TGGTGGGTGA aGaaacggct aaATTCCGgt
101 tTGCCTCaa ccaTGCCTTG tgccAAACAC ATTTTGtttc cGcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAatcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCGGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAaccctga tgccggGCTA TctgcgctcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTC CCACCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgttcc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAC GTCTGCTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTCCG CTTCAACCGC CTGTTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAAACTGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAAGT ACTGTACAAC GGCGTAAAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTCGCAGTA CGGCAGATT TAAGTTGAAA
1051 TATAAACACG GCACCGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG ACAAACTGGC
1251 TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTTAAA
1351 CAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGGTTATCGG GCCAAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGCA GATAAAGCTT GCGCGCAACC TGCATTACGA TATATTACC
1501 GGCCGTGCAT TGAAAAGCC cgaatatttt CAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51 LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAAFO NKFPTRSNDL LNLRDLEQGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DGHKKEGGSN NYAVHYSAPP
251 GKWTWAFNHN GYRYHQAIVSG LSEVYDYNKG SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTRE TKSYYDDAEL TVQRRKTTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTPFQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGKY WRNDLSWQFK
451 PGHQLYLGLAD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIFT
501 GRALKKPEYF QTKKWVTGFO VGYSF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

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m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAAATGT
51 CCGTTTCGAG CAACCATTTG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AAACACCGTG TACTCGGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

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1290

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1 51 CGCAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
2 01 AACTGGGATG TGTTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
2 51 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
3 01 CAaCCACAGA ATATGGATTC GGAATTTCTG AAATTACGGG TATCAGCAGG
3 51 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
4 01 AGGGCAGTAT TAGTGCATTC AATAACAAAT TTCCCTTATA TAGGAACAAA
4 51 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAGAAC TCGCTCGTTT
5 01 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
5 51 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCAGT
6 01 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
6 51 TGCAGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTtTATG
7 01 TTTCATATGG ACGCGGTTTG GCGCACAAAA CGGACTTGAC TGATGCCACC
7 51 GGTACGGAAA CTGAAAGCGG ATCCAGAAAGT TACAGCGTGC ATTATTCGGT
8 01 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
8 51 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
9 01 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
9 51 TAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
10 01 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
10 51 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
11 01 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
11 51 AAGAAAACGG CGGCGATATT CTTCCAGGTA CATCTCGTAT GAAAATCATT
12 01 ACTGCCAGTT TGGACGCAGC CGCCCCATT AyTTTAGGCA AACAGCAGTT
12 51 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
13 01 CCCAAGATAA ATTGTCAATC GGCAGCCGCT ACACCGTTCG CGGATTTGAT
13 51 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
14 01 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
14 51 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
15 01 GTGTCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
15 51 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
16 01 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

m903.pep

```

1 MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTIV
51 RKPSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEKRDG KSAEGSISAF NNFPLYRNK
151 IILNRDVEQG LENLRLPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTDAT
251 GTETESGSR S YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSSLAAERM LWRNRLHKT S VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRLAYLN RWQLDGKLSY KRGTMGRQSM PAPEENGDI LPGTSRMKII
401 TASLDAAAPF XLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYL ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTINTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

          10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTIV RKPSFLPSVL
          |:::| |:::| |:::| |:::| |:::|
g903      MATQVGGANSDEASPCFP ISEVELVGEETAKFRFALNHA
          10      20      30

          70      80      90     100     110     120
m903.pep  MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG
          :| | | | |:::| |:::| |:::| |:::| |:::| |:::|
g903      LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGYTTTRILAAPQDLNSGKQLTLMPGYLR
          40      50      60      70      80      90

```

[illegible]

a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTTAACTG	ATGCAAATGT
51	CCGTTTCGAG	CAACCATTGG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAATTTT	CTTTTCTTCC	TTCTGTGCTC	ATGAAGAAAA	CAGCTTTTAA
201	AACCTGGGATG	TGTTTAGGTT	CCAATAATTT	GACGAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGCGTACC	TCACTTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATTG	GGGAATTCTG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	AGGCGAGTAT	TAGTGCGATT	AATAACAAAT	TTCCCTTATA	TAGGAACAAA
451	ATTCTCAATC	TTCCGCGATG	AGAGCAGGGC	TTGGAAAAAC	TGCGTCGTTT
501	GCCGAGTGTT	AAAACAGATA	TTCAGATTAT	ACCGTCCGAA	GAGAAGGCCA
551	AAAGCGATTT	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTTCAGT

1292

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601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTTATG
701 TTTTCATATGG ACGCGGTTTG GTGCACAAAA CGGACTTGAC TGATGCCACC
751 GGACCGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCGCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACGG CGGCGGTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCCGATG TGGATGCAGC GGCCCGGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTG AAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCCAAGACAA GTTGTCTATC GGCAGCGGCT ACACCGTNG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

a903.pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTA
51  RKFSFLPSVL MKETAFTKGM CLGSNNLSRL OKAAQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEKRDG KSAEGSISAF NNFPLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFVVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSLAERML LWRNRFHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRAYLN RWQLDGKLSY KRGTMGRQSM PAPEENGGGT IPGTSRMKII
401 TAGLDAAAPF MLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

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m903/a903 98.4% identity in 547 aa overlap

	10	20	30	40	50	60
m903.pep	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTV	RKFSFLPSVL
a903	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTAR	KFSFLPSVL
	70	80	90	100	110	120
m903.pep	MKETAFKTM	CLGSNNLSRL	QKAAQILIV	RGYLTSQAI	IQPQNMDSG	ILKLRVSAGEIG
a903	MKETAFKTM	CLGSNNLSRL	QKAAQILIV	RGYLTSQAI	IQPQNMDSG	ILKLRVSAGEIG
	130	140	150	160	170	180
m903.pep	DIRYEKRDG	KSAEGSISAF	NNKFPLYRN	KILNLRDVE	QGLLENLRL	PSVKTDIQIIPSE
a903	DIRYEKRDG	KSAEGSISAF	NNKFPLYRN	KILNLRDVE	QGLLENLRL	PSVKTDIQIIPSE
	190	200	210	220	230	240
m903.pep	EEGKSDLQI	KWQONKPIR	FSIGIDDAG	GKTTGKYQG	NVALSFDN	PLGLSDLFVVS
a903	EEGKSDLQI	KWQONKPIR	FSIGIDDAG	GKTTGKYQG	NVALSFDN	PLGLSDLFVVS
	250	260	270	280	290	300
m903.pep	AHKTDLTD	ATGTETESG	SRSVHYSV	PKWLFSFN	HNGHRYHE	ATEGYSVNYD
a903	VHKTDLTD	ATGTETESG	SRSVHYSV	PKWLFSFN	HNGHRYHE	ATEGYSVNYD

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	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKT SVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
a903	YQSSLAERMLWRNRFHKT SVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQQFFYA					
a903	RWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIITAGLDAAAPFMLGKQQFFYA					
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

g904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTGCGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTGCGGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATAACGGAA ATGCCGTTGA TTTGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACGAGCC GCAGCGGCGC GCGCGGCCGG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACCAATT CCGTCGGGAA
451 CGGGCCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCGCGCG CTGCCGAAGC CGCGCGGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TTTTCGTTCAA CACGCgggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTACAG CAGTTTTTCA GGATGCAGCA AATCGCGGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CCTTTGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCCCAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAGGAT ACCGCTCGGA ATCAGGCGCA AAATGTTTTT TTTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

g904.pep

```

1  MMQHNRFFAV GAGDDGDRR AADFFNPFQI CFGIGRQCVV AFHADSRFAP

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1	ATGATGCAGC	ACAATCGTTT	CTTCTCGGTC	GGGGCCG ₉ TG	GAGACGATGG
51	CGACCGGCGC	GCCGCAGACT	TCTTCAATCC	GTTTCAAATA	TGCTTTGGCG
101	TTTTCGGGCA	ATGCGCCGTA	GTCCTTCACG	CCGAAAGTGG	ATTCGCGCCA
151	GCCGGGCATG	GTTTCGTAAA	TCGGCTTGCA	GGTTTCCACC	GCATCGGAAC
201	CGCAAGGCAG	GATGTCGGTT	TTGCCGCCCT	CGGGCAATTC	ATAGCCGACG
251	CAGATATTGA	TGTTTTC AAC	GCCGTCAGT	ACATCGAGTT	TAGTAATACA
301	CATACCGGAA	ATGCCGTTGA	TTTGATGGA	CGGTTTCAGG	GCGTCCGCGAT
351	CAAACCAGCC	GCAGCGGCGT	GCGCGTCCGG	TTACCGAACC	GAATTCTGTG
401	CCGCGTTCTG	CCAAACCTAC	GCCTACTTCG	TCGAACAATT	CGGTCCGGAA
451	CGGGCCCGAA	CCGACGCGCG	TGGTATAGGC	TTTGACGATG	CCCAAAACAT
501	AATCCAGCAT	TTGAGGACCT	ACGCCCCGCG	CTGCCGAAGC	TGCGCCCGCC
551	AGACAGTTTG	ACGAGGTAAC	GAAGGGATAA	GTGCCGTAGT	CGATGTCCAA
601	CAACGCACCT	TGCGCGCCTT	CAAACACGAG	TTTTTCCGCG	TTTTTGTTTT
651	TCTCGTTCAA	CACGCGGGAC	ACGTCGGTAA	TCATCGCGCG	ATAGCGCGGC
701	GCGACTTTTT	CGATAACCGC	CATCACGTCT	TCCGCTTTAA	CCGGCTCGGC
751	ATTGTGCAGA	TGTTGCAGTT	GGACATTGTA	ATAGGCAAGG	ACGGCATCCA
801	GTTTTTCACG	CAGTTTyTCA	GGATGCAGCA	AATCGGCGCG	GCGAATGGCG
851	CGGCGTGCCA	CTTTGTCTTC	GTAGGCAGGG	CCGATGCCGC	GGCCGGTCGT
901	CGCGAATTTG	CCTTTGCCCG	GCG .ATcTTC	GCGGGCTTGG	TCGAGCGCGA
951	TGTGGTAAGG	CAGGATCAGC	GCGAGGCTCG	GCGCGATTTT	CAGACGGCCT
1001	TCGACGTTTT	TCACGCCTGC	CGCGTTCAAC	TCGTGATTTT	CGCCCAACAG
1051	GGCTTCGGGG	GAGACGACAA	CGCCCGAACC	GATGAAGCAG	TCCAAACTTT
1101	CATGCAGGAT	GCCGCTCGGA	ATCAGGCGCA	AAATGGTTTT	TTTGCCGCCG
1151	ACAACCAAGG	TATGGCCCGC	ATTGTGGCCG	CCTTGGAAGC	GCACCaGCC
1201	GCCGGCTTTC	TCCGCCAGCC	AGTCAACGAT	TTTACCTTTA	CCCTCGTCGC
1251	CCCACGTGTC	CGCGATTAsT	ACAACATTTT	TAGCCATAGC	CATATAACCT
1301	ATCGATATTA	A			

1	MMQHNRRFSV	GAGGDDGDRR	AADFFNPFI	CFGVFGQCAV	VLHAESGFAP
51	AGHGFVNRLA	GFHRIGTARQ	DVGFAAVGQF	IADADIDGFN	AVHYIEFSNT
101	HTGNAVLDLG	AFQGGGIKPA	AAACASGYRT	EFVS AFCQTY	AYFVEQFGRE
151	RARTDARGIG	FDDAQNIIQH	LRTYARACRS	CARQTVGRGN	EGISAVVDVQ
201	QRTLRAFKQQ	FFAVFVFLVQ	HAGHVGNHRR	NARRDFFDNR	HHVFRFNRLG
251	IVQMLQLDIV	IGKDGIOFFT	QFXRMQQIGF	ANGAACHFVF	VGRADAAAGR
301	ADFAFAAXIF	AGLVERDVVR	QDQRAGRDGF	QTAFDVFHAC	RVQLVDFAAQ
351	FGGGDDNART	DEAVQTFMQD	AARNQAQNGF	FADNQGMAR	IVAALAEHHA
401	AGFFRQPVND	FTFTLVAPLC	ADXYNIFSHS	HITYRY*	

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m904.pep	MMQHNRFFSVGAGGDDGDRRAADFFNP	QICFGVFGQCAVVLHAESGFAPAGHGFVNRLA				
	:	:	: : :			
g904	MMQHNRFFAVGAGGDDGDRRAADFFNP	QICFGIGRQCVVAFHADSRFAPAGHGFVNRF				
	10	20	30	40	50	60
	70	80	90	100	110	120

1295

m904 . pep	GFHRIGTARQDVGF	AAVGGQFIADAD	IDGFNAVHYIEFS	NTHTGNAV	DL	DGAFOGGGIKPA
g904	GFHRIRTARQDVGF	AAAWQFVADAD	IDGFNAVHYIEFG	NAHTGNAV	DL	DGAFOGGGIKPA
	70	80	90	100	110	120
m904 . pep	130	140	150	160	170	180
	AAACASGYRTEFV	SAFCQTYAYFVE	QFGRERARTDAR	GIGFDDAQNI	I	QHLRTYARACRS
g904	AAARAAGYRTEFV	SALRQTCAYFVE	QFGRERARTDAR	GIGFDDAQNI	I	QHLRTYARACRS
	130	140	150	160	170	180
m904 . pep	190	200	210	220	230	240
	CARQTVGRGNEGI	SAVVDVQORTL	RAFKQQFFAVF	VFLVQHAGHV	GNHRRNARRD	FFDNR
g904	RAGETVGRGNEGV	SAVVDVQORTL	RAFKQQFFAVF	VFLVQHAGHV	GNHRRNARRD	FFDNR
	190	200	210	220	230	240
m904 . pep	250	260	270	280	290	300
	HHVFRFNRLGIV	QMLQLDIVIGK	DGIQFFTOFXR	MQQIGGANGA	ACHFVFVGR	ADAAAGR
g904	HHVFRFNRSQV	MLQLDIVIGK	DGIQFFTOFXR	MQQIGGANGA	ACHFVFVGR	ADAAAGR
	250	260	270	280	290	300
m904 . pep	310	320	330	340	350	360
	ADFAFAARIFAG	LVERDVVRQDQ	RARRDQTA	FDVFHACRV	QLVDF	FAQQGFGDDNART
g904	ADFAFAARCFAG	LVERDVVRQDQ	RARRDQTA	FDVFHACRV	QLVDF	FAQQGFGGNDNART
	310	320	330	340	350	360
m904 . pep	370	380	390	400	410	420
	DEAVQTFMQDA	ARNQAQNGFFA	ADNQGMA	RIVAAL	EAHHAAGFF	RQPVNDFTFTLVAPLC
g904	DEAIQSFVQD	TARNQAQNGFF	AADDQGM	A	EAHDAAGFF	RQPVNDFTFTLVAPLC
	370	380	390	400	410	420
m904 . pep	430					
	ADXYNIFSHSH	ITYRYX				
g904	ADYYNIFSHSH	ITYRYX				
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

```

1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTG GAGACGATGG
51  CGACCGGCGC ACCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGTA ATGCGTCGTA GCTTTTCACG CCGAAAGTGG ATTCGCTCCA
151 ACCGGGCATG GTTTCGTAAA TCGGCTTGCA GGCTTCTACC GCATCAGAGC
201 CGCAAGGCAG GATGTCGGTT TTGCGCCGCT CGGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATACA
301 CATAACGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTTCTG CCAACCTGCT TCCGACTTCG TCGAACAATT CCGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTGACGATG CCCAAACAT
501 AATCCAGCAT TTGAGGCCTT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGGCAGTTGG ACGAAGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGC GCGCCTT CAAACAGCAG TTTTTCGCGG TTTTGTGTTT
651 TTTTCGTTCA CACGCGGGAC ACGTCGGTAA TCATCGGCGT AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCAGCTCT TCCGCTTTCA CCGACTCGGC
751 ATTGTGCAGA TGTGTCAGTT GGACGTTGTA ATAAGCAAAG ACGGCATCCA
801 GTTTTTTACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCTG
901 GCCGATTTTG CCTTGCCGCG GCGATGCTTC TCGGCTTGG TCGAGCGCGA

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1296

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9 51 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
10 01 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
10 51 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT
11 01 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTGCGCGCCG
11 51 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGGGAAG GCACCACGCC
12 01 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
12 51 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
13 01 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

a904.pep

```

1 MMQHNRFFAV GAGGDDGDRR TADFFNPFQI CFGIGR*CVV AFHAESGFAP
51 TGHGFVNRLA GFYRIRAARQ DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVDLDG AFQGGGIKPA AAACASGYRT EFVS AFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNNRR NARRDFFDNR HHVFRFHLRG
251 IVQMLQLDVV ISKDGIOFFT QFFRMQOIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF SGLVERDVIR QDQAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMR IVAALEAHHA
401 SGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITXRY*

```

m904/a904 91.3% identity in 436 aa overlap

	10	20	30	40	50	60
m904.pep	MMQHNRFFSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA					
a904	MMQHNRFFAVGAGGDDGDRRTADFFNPFQICFGIGRXCVAFAHAESGFAPTGHGFVNRLA					
	10	20	30	40	50	60
m904.pep	GFHRIGTARQDVGF AAVGQFIADADIDGFNAVHYIEFSNTHGTGNAVDLDGAFQGGGIKPA					
a904	GFYRIRAARQDVGF AAVGQFVADADIDGFNAVHYIEFGNTHGTGNAVDLDGAFQGGGIKPA					
	70	80	90	100	110	120
m904.pep	GFHRIGTARQDVGF AAVGQFIADADIDGFNAVHYIEFSNTHGTGNAVDLDGAFQGGGIKPA					
a904	GFYRIRAARQDVGF AAVGQFVADADIDGFNAVHYIEFGNTHGTGNAVDLDGAFQGGGIKPA					
	70	80	90	100	110	120
m904.pep	AAACASGYRTEFVS AFCQTYAYFEVQFGRERARTDARGIGFDDAQNIQH LRTYARACRS					
a904	AAACASGYRTEFVS AFCQTCSD FVEQFGRERARTDARGIGFDDAQNIQH LRAYARACRS					
	130	140	150	160	170	180
m904.pep	AAACASGYRTEFVS AFCQTYAYFEVQFGRERARTDARGIGFDDAQNIQH LRTYARACRS					
a904	AAACASGYRTEFVS AFCQTCSD FVEQFGRERARTDARGIGFDDAQNIQH LRAYARACRS					
	130	140	150	160	170	180
m904.pep	CARQTVGRGNEGISA VVDVQORTLRAFQKQFFAVFVFLVQHAGHVGNNRRNARRDFFDNR					
a904	RAGEAVGRSNEGISA VVDVQORTLRAFQKQFFAVFVFLVQHAGHVGNNRRNARRDFFDNR					
	190	200	210	220	230	240
m904.pep	CARQTVGRGNEGISA VVDVQORTLRAFQKQFFAVFVFLVQHAGHVGNNRRNARRDFFDNR					
a904	RAGEAVGRSNEGISA VVDVQORTLRAFQKQFFAVFVFLVQHAGHVGNNRRNARRDFFDNR					
	190	200	210	220	230	240
m904.pep	HHVFRFHLRGIVQMLQLDIVIGKDGIOFFTQFFRMQOIGGANGAACHFVFGVGRADAAAGR					
a904	HHVFRFHLRGIVQMLQLDVVISKDGIOFFTQFFRMQOIGGANGAACHFVFGVGRADAAAGR					
	250	260	270	280	290	300
m904.pep	HHVFRFHLRGIVQMLQLDIVIGKDGIOFFTQFFRMQOIGGANGAACHFVFGVGRADAAAGR					
a904	HHVFRFHLRGIVQMLQLDVVISKDGIOFFTQFFRMQOIGGANGAACHFVFGVGRADAAAGR					
	250	260	270	280	290	300
m904.pep	ADFAFAAXIFAGLVERDVVRQDQAGRRDFQTAFDVFHACRVQLVDFAAQQGFGGDDNART					
a904	ADFAFAARCFSG LVERDVIRQDQAGRRDFQTAFDVFHACRVQLVDFAAQQGFGGDDNART					
	310	320	330	340	350	360
m904.pep	ADFAFAAXIFAGLVERDVVRQDQAGRRDFQTAFDVFHACRVQLVDFAAQQGFGGDDNART					
a904	ADFAFAARCFSG LVERDVIRQDQAGRRDFQTAFDVFHACRVQLVDFAAQQGFGGDDNART					
	310	320	330	340	350	360
m904.pep	DEAVQTFMQDAARNQAQNGFFAADNQGMRIVAALAHHAAGFFRQPVNDFTFTLVAPLC					
a904	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHAAGFFRQPVNDFTFTLVAPLC					
	370	380	390	400	410	420
m904.pep	DEAVQTFMQDAARNQAQNGFFAADNQGMRIVAALAHHAAGFFRQPVNDFTFTLVAPLC					
a904	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHAAGFFRQPVNDFTFTLVAPLC					
	370	380	390	400	410	420

1297

m904.pép ADXYNIFSHSHITYRYX
 || ||||| ||||
 a904 ADYYNIFSHSHITXRYX
 430

g906.seq not found yet
 g906.pép not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

m906.seq
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51 GTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
 101 T'GAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CCGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGA AAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAACAAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

m906.pép
 1 MKYIVSISLA MGLAACSFEG FKNPWDAA FWEKKNYANP YPGSASAALD
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPENK
 101 KYEWPREEGK TK*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

g907.seq (partial)
 1 ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTgcaAC GCCGCCGCCT
 51 GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG
 101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
 151 TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
 201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGGCA AGATTCTGTC
 251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
 301 AGCCGGGCGG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
 351 aagcgggtac cgagctcgaa tcatatca..

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

g907.pép (partial)
 1 MKKPTDLPV NLQRRRLCA AGALLISPLA HAGAOREETL ADDVASVMRS
 51 SVGSVNPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
 101 SRAGLDTQIV LGLIEVESGY RARIIS...

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

m907.seq
 1 ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
 51 GTTGTGTGCC GCCGGTGCGT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
 101 CGCAACGTGA GGAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
 151 TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
 201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGGCA AGGTTCGTCC
 251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
 301 AGCCGGGCGG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
 351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
 401 TGCAGGTTAT GCCGTTkTGG AAAAACTACA TCGGCAAACC GGCGCACAAAC
 451 CTGTTGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
 501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTTA
 551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
 601 CGCAACCGCT GGCAGTGGCG TTGA

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

m907.pép
 1 MRKPTDLPV NLQRRRLCA AGALLSPLA HAGAOREETL ADDVASVMRS
 51 SVGSVNPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
 101 SRAGLDTQIV LGLIEVESAF RQYAISGVA RGLMQVMPXW KNYIGKPAHN

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151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

	10	20	30	40	50	60
g907.pep	MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAOREETLADDVASVMRSSVGSVNPRL					
	: :					
m907	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAOREETLADDVASVMRSSVGSVNPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
g907.pep	VFDNPKEGERWLSAMSARLARFVPEDEGERRLLVNIQYESSRAGLDTQIVLGLIEVESGY					
	: :					
m907	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	70	80	90	100	110	120
g907.pep	RARIIS					
m907	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

1	ATGAAAAAAC	CGACCGATAC	CCTACCCGTC	AATCTGCAAC	GCCGCCGCCT
51	ATTGTGTGCT	GCCGGCGCGC	TGTTGCTCAG	CCCGCTGGCA	CAAGCCGGCG
101	CGCAACGTGA	AGAAACGCTT	GCCGACGATG	TGGCTTCCGT	GATGAGGAGC
151	TCTGTCGGCA	GCATAAATCC	GCCGAGGCTG	GTGTTGACGA	ATCCGAAAGA
201	GGCGGAGCGT	TGGCTGTCCG	CGATGTCTGC	TGGTTGGCA	AGGTTCGTCC
251	CCGATGAGGA	GGAGCGGCGC	AGGCTGCTGG	TCAATATCCA	GTACGAAAGC
301	AGCCGGGCGC	GTTTGGATAC	GCAGATTGTG	TTGGGGCTGA	TTGAGGTGGA
351	AAGCGCGTTC	CGCCAGTATG	CAATCAGCGG	TGTCGGCGCG	CGCGGCCTGA
401	TGCAGGTTAT	GCCGTTTGG	AAAACTACA	TCGGCAAACC	GGCGCACAAAC
451	CTGTTGACGA	TCCGCACCAA	CCTGCGTTAC	GGCTGTACCA	TCCTGCGCCA
501	TTACCGGAAT	CTTGAAAAAG	GCAACATCGT	CCGCGCACTC	GCCCGTTTTA
551	ACGGTAGCCT	CGGCAGCAAT	AAATATCCGA	ACGCCGTTTT	GGGCGCGTGG
601	CGCAACCGCT	GGCAGTGGCG	TTGA		

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

1	MKKPTDTLPV	NLQRRRLCA	AGALLSPLA	QAGAOREETL	ADDVASVMRS
51	SVGSINPPRL	VFDNPKEGER	WLSAMSARLA	RFVPDEEERR	RLLVNIQYES
101	SRAGLDTQIV	LGLIEVESAF	RQYAISGVGA	RGLMQVMPFW	KNYIGKPAHN
151	LFDIRTNLRY	GCTILRHYRN	LEKGNIVRAL	ARFNGSLGSN	KYPNAVLGAW
201	RNRWQWR*				

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAOREETLADDVASVMRSSVGSVNPRL					
	: :					
a907	MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAOREETLADDVASVMRSSVGSINPPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	: :					
a907	VFDNPKEGERWLSAMSARLARFVPEDEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m907. pep	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
a907	RQYAISGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180
	190	200				
m907. pep	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
a907	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

g908. seq

```

1   ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAC TG CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTTACGATG ACTGATTTAT
151 CAAAACGCTC CGCATTGAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTTTTCCTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatt Ttagcttcgc tgaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

g908. pep

```

1   MKKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPVNTQTAT LFPPIREQVK PDSIVYTDY RSYDVLVDSE FSHFSFAETS
151 PSYQSQTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

m908. seq

```

1   ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAC TG CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTGAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTTTTCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTATATAC GGATTGTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAACCTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

m908. pep

```

1   MRKSRLSOYK QXKLIELFVT GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51  QNSPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPVNTQTAT LFPPIREQVK PDSIFYTDY RSYDVLVDRE FSHFSFAETS
151 PSYQSQTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

g908/m908

	10	20	30	40	50	60
g908. pep	MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAYDFHRLRLXLIYQNGPHLEMF					

1300

m908	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAYYFHRLRLLIYQNSPHLEMF
	10 20 30 40 50 60
g908.pep	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPIIREQVK
m908	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPIIREQVK
	70 80 90 100 110 120
g908.pep	PDSIVYTDYRSYDVLVDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
m908	PDSIFYTDCYRSYDVLVDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
	130 140 150 160

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2739>:

a908.seq

```

1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAATAAAC TCATTGAGCT
51  ATTTGTGCGCA GGTGTAAGT CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTGGA AATGTTTAT GCGGAAGTAG AAGCAGATGA
201 AAGTTATTTT GCGGACAAAC GCAAAGGCAA ACGCGGTTCG GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTGTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTAGCCATT TTAGCTTCGC TGAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2740; ORF 908.a>:

a908.pep

```

1  MRKSRLSQYK QNKLIELFVA GVTARTAAEL VGVNKNNTAAY YFHRLRLLIY
51  QNSPHLEMF GEVEADESYF GGQRKGKRG GAAGKVAVFG LLKRNGKVY
101 VTPNTQTAT LFPIIREQVK PDSIVYTDY RSYDVLVDV FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

m908/a908 98.2% identity in 166 aa overlap

m908.pep	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAYYFHRLRLLIYQNSPHLEMF
a908	MRKSRLSQYKQNKLIELFVAGVTARTAAELVGVNKNNTAAYYFHRLRLLIYQNSPHLEMF
	10 20 30 40 50 60
m908.pep	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPIIREQVK
a908	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPIIREQVK
	70 80 90 100 110 120
m908.pep	PDSIFYTDCYRSYDVLVDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
a908	PDSIVYTDYRSYDVLVDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
	130 140 150 160

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2741>:

g909.seq (partial)

```

1  atgcgtaaaa ccgtacttat cCTgaccatc tccgcccggc ttttgcggg
51  ctgcacatgG gaaacttatt aagacggcag cggcaaaacc gccgtccgtg
101 caaaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcggctcg

```

1301

151 aaaaaggtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg
 201 caacccaaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga
 251 aaccgagttt ccgggcgagg gacggggggg ggcgggtgaa cagggcagaa
 301 acggggggagg ggaagcgatc ggcgagg..

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS
 51 KKVDCDEYGG ERRAVLNRQK RGKPTRRAA TLGKPSFRAR DGGGRVNRAE
 101 TGEGRKSAR..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCC TTTGTGCGG
 51 CTGCGCGTGG GAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTACC
 201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AACCAAAGTT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

1 MRKTFLEFLTA AAALLSGCAW ETYQDNGKT AVRQKYPAGT PVEYQDGSYS
 51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQPKFQNR *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTAALLSGCAWETYQDNGKTAVRQKYPAGTPVEYQDGSYSKNMNYNQYRP					
		:	:	:	:	:
g909	MRKTVLILTI SAALLSGCTWETYQDGSgKTAVRAKSTGTPLCWQDGRGSKKVDCEYGG					
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVLPNQTGNNADEEHRQHWQPKFQNRX					
			::	::		:
g909	ERRAVLRNQKRGKPTRRAATLGKPSFRARDGGGRVNRAETGEGKRSAR					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

1 ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCC TTTGTGCGG
 51 CTGCGCGTGG GAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTACC
 201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AGCCCAAATT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

1 MRKTFLEFLT AAALLSGCAW ETYQDNGKT AVRQKYPAGT PVEYQDGSYS
 51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQPKFQNR *

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTAALLSGCAWETYQDNGKTAVRQKYPAGTPVEYQDGSYSKNMNYNQYRP					
		:	:	:	:	:
a909	MRKTFLEFLTAAALLSGCAWETYQDNGKTAVRQKYPAGTPVEYQDGSYSKNMNYNQYRP					
	10	20	30	40	50	60

1302

	70	80	90
m909.pep	ERHAVLPNQTGNNADEEHRQHWQPKFQNRX		
a909	ERHAVLPNQTGNNADEEHRQHWQPKFQNRX		
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```
g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```
g910.pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```
m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATTGG GGTAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```
m910.pep
1  MKKLLLAADV SLSAAAFAG DSAERQIYGD PHFEQNRKA VKMLEQRGYQ
51  VYDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

```
g910/m910

          10      20      30      40      50      60
g910.pep  MKKLLLAADVSLNAATAFAGDSAERQIYGDPHFEQNRKAVKMLEQRGYQVYDVDADDYW
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m910      MKKLLLAADVSLSAAAFAGDSAERQIYGDPHFEQNRKAVKMLEQRGYQVYDVDADDDHW
          10      20      30      40      50      60

          70      80      90
g910.pep  GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m910      GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
          70      80      90
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```
a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATTGG GGCAAACCTG TTTTGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

```
a910.pep
```

1 MKKLLLVAVV SLAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
51 VHDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

m910/a910 95.7% identity in 94 aa overlap

	10	20	30	40	50	60
m910.pep	MKKLLLAADVSLSAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDADDDHW					
a910	MKKLLLVAVVSLAATAFAGDSAERQIYGDYPYFEQNRTKAVKMLEQRGYQVHDVDADDDHW					
	10	20	30	40	50	60
	70	80	90			
m910.pep	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
a910	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

g911.seq

1	ATGAAAAAGA	ACATATTGGA	ATTTTGGGTC	GGACTGTTTC	TCTTGATCGG
51	CGCGGCGGCG	GTTGCCTTTC	TCGCTTTCCG	CGTGGCGGGC	GGCGCGGCGT
101	TCGGCGGTTT	GGACAAAAC	TACGCCGTTT	ATGCCGATT	CGGCGACATC
151	GGCGGTTTGA	AGGTCAATGC	CCCCGTCAA	TCCGCAGGCG	TATTGGTTCG
201	GCGCGTCGGC	GCTATCGGGC	TTGACCCGAA	ATCCTATCAG	GCGAGGGTGC
251	GCCTTGATT	GGACGGCAAG	TATCAGTTCA	GCAGTGACGT	TTCCGCGCAA
301	ATCCTGACTT	CGGGACTTTT	GGGCGAACAG	TACATCGGGC	TGCAGCAGGG
351	CGGCGATACG	GAAAACCTTG	CTGCCGGCGA	CACCATCTCC	GTAACCAAGT
401	CTGCAATGGT	TCTGGAAAAC	CTGATCGGTA	AATTCATGAC	CAGCTTCGCC
451	GAGAAAAACG	CTGAGGGCGG	CAATGCGGAA	AAAGCCGcag	aAtaa

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

g911.pep

1	MKKNILEFWV	GLFVLIGAAA	VAFLAFRVAG	GAAFGGSDKT	YAVYADFGDI
51	GGLKVNAPVK	SAGVLVGRVG	AIGLDPKSYQ	ARVRLDLGK	YQFSSDVSAQ
101	ILTSGLLGEQ	YIGLQQGGDT	ENLAAGDTIS	VTSSAMVLEN	LIGKFMTSFA
151	EKNAEAGNAE	KAAE*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

m911.seq

1	ATGAAGAAGA	ACATATTGGA	ATTTTGGGTC	GGACTGTTTC	TCCTGATTGG
51	CGCGGCGGCG	GTTGCCTTTC	TCGCTTTCCG	CGTGGCGGGC	GGTGCAGGCGT
101	TCGGCGGTTT	GGACAAAAC	TACGCCGTTT	ATGCCGATT	CGGCGACATC
151	GGCGGTTTGA	AGGTCAATGC	CCCCGTCAA	TCCGCAGGCG	TATTGGTTCG
201	GCGCGTCGGC	GCTATCGGAC	TTGACCCGAA	ATCCTATCAG	GCGAGGGTGC
251	GCCTTGATT	GGACGGCAAG	TATCAGTTCA	GCAGCGACGT	TTCCGCGCAA
301	ATCCTGACTT	CGGGACTTTT	GGGCGAGCAG	TACATCGGGC	TGCAGCAGGG
351	CGGCGACACG	GAAAACCTTG	CTGCCGGCGA	CACCATCTCC	GTAACCAAGT
401	CTGCAATGGT	TCTGGAAAAC	CTTATCGGCA	AATTCATGAC	GAGTTTTCGC
451	GAGAAAAATG	CCGACGGCGG	CAATGCGGAA	AAAGCCGCCG	AATAA

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

m911.pep

1	MKKNILEFWV	GLFVLIGAAA	VAFLAFRVAG	GAAFGGSDKT	YAVYADFGDI
51	GGLKVNAPVK	SAGVLVGRVG	AIGLDPKSYQ	ARVRLDLGK	YQFSSDVSAQ
101	ILTSGLLGEQ	YIGLQQGGDT	ENLAAGDTIS	VTSSAMVLEN	LIGKFMTSFA
151	EKNADGGNAE	KAAE*			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

10	20	30	40	50	60
----	----	----	----	----	----

1304

```

g911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          |||||
m911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
g911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          |||||
m911      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
g911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNAEGGNAEKAAEX
          |||||
m911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNAEGGNAEKAAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1   ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCCTGATTGG
51  CGCGCGGCGG GTTGCCTTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTC GGACAAAAC TACGCCGTTT ATGCCGATT CGGCGACATC
151 GCGCGTTTGA AGGTCAATGC CCCCCTCAAA TCCGCAGGC TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGCGCA CACCATCTCC GTAACCAATT
401 CTGCAATGGT TCTGGAAAAC CTTATCGGCA AATTCATGAC GAGTTTTCGC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1   MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFFGGSDKT YAVYADFGDI
51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

          10      20      30      40      50      60
m911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          |||||
a911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
m911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          |||||
a911      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
m911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNAEGGNAEKAAEX
          |||||
a911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNAEGGNAEKAAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1   gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51  CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```


q912. pep

1	VKSSFISAL	GIGILSIGMA	FASPADAVGO	IRONATQVLT	ILKSGDAASA
51	RPKAEAYAVP	YFDFORMTAL	AVGNPWRITAS	DAQQALAKE	FQTLIRITYS
101	GTMLKFKNAT	VNVKDNPIVN	KGGKEIVVRA	EVGIPGQKPV	NMDFTTYQSG
151	GKYRTYNVAI	EGTSLVTVYR	NQFGEIHKAK	GIDGLIAELK	AKNGGK*

m912.seq

1	ATGAAAAAAT	CCTCCCTCAT	CAGCGCATTG	GGCATCGGTA	TTTTGAGCAT
51	CGGCATGGCA	TTTGCCGCCC	CTGCCGACGC	GGTAAGCCAA	ATCCGTCAAA
1 01	ACGCCACTCA	AGTATTGAGC	ATCTTAAAAA	ACGGCGATGC	CAACACCGCT
1 51	CGCCAAAAAG	CCGAAGCCTA	TGCGATTCCC	TATTTTCGATT	TCCAACGTAT
2 01	GACCGCATTG	CGGTCGGCA	ACCCTTGGCG	CACCGCGTCC	GACGCGCAAA
2 51	AACAAGCGTT	GGCCAAAGAA	TTTCAAACCC	TGCTGATCCG	CACCTATTCC
3 01	GGCACGATGC	TGAAATTAAA	AAACGCCAAC	GTCAACGCTA	AAGACAAATCC
3 51	CATCGTCAAT	AAAGGCGGCA	AAGAAATCAT	CGTCCGCGCC	GAAGTCGGCG
4 01	TACCCGGGCA	AAAACCGGTC	AACATGGACT	TCACCACCTA	CCAAAGCGGC
4 51	GGTAAATACC	GTACCTACAA	CGTCGCCATC	GAAGGCGGAA	GCCTGGTTAC
5 01	CGTGTACCGC	AACCAATTCTG	CGCAAAATTAT	CAAAAGCGCA	GGCGTGGACG
5 51	GACTGATTGC	CGAGTTGAAA	GCCAAAAACG	GCGGCAAAATA	A

m912.pcp

1	MKKSSLSIAL	GIGILSIGMA	FAAPADAVSQ	IRQNATQVLS	ILKNGDANTA
51	RQKAEAYAIP	YFDFQRM TAL	AVGNPWRTAS	DAQQALAKE	FQTLLIRTYS
1 01	GTMLKLKNAN	VNVKDNPIVN	KGGKEIIVRA	EVGVPQGKPV	NMDFTTYQSG
1 51	GKYRTYNVAI	EGASLVTVYR	NQFG EIIKAK	GVDGLIAELK	AKNGGK*

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

q912/m912

```

      10          20          30          40          50          60
g912.pep    VKKSSFISALGIGILSIGMAFASPADAVGQIRONATQVLTLTKSGDAASARPKAEAYAVP
             :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
m912        MKKSSLISALGIGILSIGMAFAAPADAVSQIRONATQVLSILKNGDANTARQKAEAYAIP
             10          20          30          40          50          60

      70          80          90         100         110         120
g912.pep    YFDFORMTALAVGNPWRTASDAQKQALAKEFOTLLIRTYSGTMLKFKNATNVNKDNPIVN
             |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
m912        YFDFORMTALAVGNPWRTASDAQKQALAKEFOTLLIRTYSGTMLKLKNANNVNKDNPIVN
             70          80          90         100         110         120

      130         140         150         160         170         180
g912.pep    KGGKEIVRAEVGIPGQKPVNMDFTTYSGGKYRTYNVAIEGTSLVTVYRNQFGEIIKAK
             |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
m912        KGGKEIIVRAEVGVPGQKPVNMDFTTYSGGKYRTYNVAIEGASLVTVYRNQFGEIIKAK
             130         140         150         160         170         180

      190
g912.pep    GIDGLIAELKAKNGGKK

```

1306

m912
 :|||
 GVDGLIAELKAKNGGKX
 190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

a912.seq

```

1  ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTGAGCAT
51  CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAACCAA ATCCGTCAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
151 CGCCAAAAAG CCGAAGCCTA TCGGATTCCC TATTTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAA
251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAT AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGCGCGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAATACC GTACCTACAA CGTCGCCATC GAAGCGCGCA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGGTGGACG
551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A
  
```

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

a912.pep

```

1  MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQATQVLS ILKSGDANTA
51  RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRITYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTYR NQFGEI IKAK GVDGLIAELK AKNGSK*
  
```

m912/a912 98.0% identity in 196 aa overlap

m912.pep	10	20	30	40	50	60
	MKKSSLISALGIGILSIGMAFAAPADAVSQIRQATQVLSILKNGDANTARQKAEAYAIP					
a912	MKKSSFISALGIGILSIGMAFAAPADAVNQIRQATQVLSILKSGDANTARQKAEAYAIP					
	10	20	30	40	50	60
m912.pep	70	80	90	100	110	120
	YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRITYSGTMLKLKNANVNVKDNPIVN					
a912	YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRITYSGTMLKLKNANVNVKDNPIVN					
	70	80	90	100	110	120
m912.pep	130	140	150	160	170	180
	KGGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNQFGEI IKAK					
a912	KGGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNQFGEI IKAK					
	130	140	150	160	170	180
m912.pep	190					
	GVDGLIAELKAKNGGKX					
a912	GVDGLIAELKAKNGSKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

g913.seq

```

1  atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCTGCAATT GCAGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
151 GCGCGCGCGG GCTACGCAA AGTTACGCCG AAACCCGTCC GCGCGGCGT
201 GTCCAATTTT TTAAACAACC TGCGCGACGT GGTCAATTTC GGCAGCAATA
251 TCTTGCGTTT GGAcatCAAA cgcgcAAGcg aAGACctcgT CCGcgtcggc
301 atCAATACCA CCTTCGTTT GGgcgGGCTC ATTGATATTG CCGGcgcGGg
351 cggcgttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
401 GctgGAAAAa cagcaATTAT TTCGTgttgc CCGtcttagg cccgtccacc
  
```

```

4 51 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
5 01 tatcgttttc catacccctg ccggacgctg GGgcacgact gCCGCTGCCG
5 51 CCGTcagtag gcgcgaaggc ctcctcgatt tgaccgacag Tctggacgaa
6 01 gccgccatCG ACAAATACAG CTACACGCGc gacctctata tgAAAGTCCG
6 51 CGcagcGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
7 01 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
7 51 CCGCCCGTTC ACGAAGATTG CGTATCCGAA ACACAGGCAG AAGCAGCAGG
8 01 GGAAGCCGAA ACGCAACCTG GAACACAACC CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:

g913.pep

```

1 MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
51 AARGYRKVTP KPVVRAGVSNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
1 01 INTTFGLGGL IDIAGAGGVP DNKNTLGDTF ASWGWNKSNY FVLPVLGPST
1 51 VRDALGTGIT SVYPPKNIVF HTPAGRWTG AAAAVSTREG LLDLTDLSLE
2 01 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDIDEL VESAETGAAE
2 51 PAVHEDSVSE TQAEAGEAE TQPGTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

m913.seq

```

1 ATGAAAAAAA CCGCCTATGC CTTCTCTCTG CTGATCGGGT TCGCTTCCGC
51 CCCTGCATTT GCCGAAACCC GCCCGCCGGA CCCTTATGAA GGCTACAACC
1 01 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCTT
1 51 GCCGCGCGCG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGCGGT
2 01 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCACTTC GGCAGCAATA
2 51 TCTTGCCTT GGACATCAAA CGCGCAAGCG AAGACCTGT CCGCGTCGGC
3 01 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGCGCGGGC
3 51 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCCTCGTGGG
4 01 GATGGAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
4 51 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCAAGAA
5 01 TATCGTCTTC CGCACCCTTG TCGGACGCTG GGGCACGACT GCCGTATCCG
5 51 CCGTCAGTAC GCGCGAAGGC CTgCTCGATT TGACCGACAG TCTGGACGAA
6 01 GCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
6 51 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGgTACGAA GATAACATCG
7 01 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGCGCGGGC GGAAACTGCC
7 51 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
8 01 CGAAACGCAA CCTGGAACAC AACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

m913.pep

```

1 MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
51 AARGYRKVAP KPVVRAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWNKSNY FVLPVLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWTG AVSAVSTREG LLDLTDLSLE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

g913/m913

```

          10      20      30      40      50      60
g913.pep  MKKTAYAILLLIGFASAPAF AETRPADPYEGYNRAVSKFNDQADRYIFAPAARGYRKVTP
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m913      MKKTAYAFLLLLIGFASAPAF AETRPADPYEGYNRAVSKFNDQADRYIFAPAARGYRKVAP
          10      20      30      40      50      60

          70      80      90     100     110     120
g913.pep  KPVVRAGVSNFFNNLRDVVSF GSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGVP
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m913      KPVVRAGVSNFFNNLCDVVSF GSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP
          70      80      90     100     110     120

```

1308

	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYPPKNI VFHTPAGRWGTT					
m913	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNI VFRTFPVGRWGTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDIDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAETGAAEPAVHEDSVSETQAEAAAGEAETQPGTQPX					
m913	VESAETGAAETAVQEDSVSETQAEAAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

```

a913.seq
1   ATGAAAAA CCGCCTATGC CTTCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCACTTC GGCAGCAATA
251 TCTTGCCTT AGACATCAA CGCGCAAGCG AAGACCTGT CCGCGTCGGT
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCTTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCACGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTGGAAC ACAACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

```

a913.pep
1   MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
51  AARGYRKVAP KPVVAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPVLPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDSLDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQPGTQP*

```

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLLLIGFASAPAF AETRPADPYEGYNRAVFKFNDQADRYIFAPAARGYRKVAP					
a913	MKKTAYAFLLLIGFASAPAF AETRPADPYEGYNRAVFKFNDQADRYIFAPAARGYRKVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPVVAGVSNFFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
a913	KPVVAGVSNFFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNI VFRTFPVGRWGTT					
a913	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNI VFRTFPVGRWGTT					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pép	AVSAVSTREGLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pép	SAETGAAETAVQEDSVSETQAEAAEAEETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAEAEETQPGTQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACCG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTG
451 t aggcTTCGA CGATTTTTTG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GTGAAGGTA TGGAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAA TCCCGATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCGGTAA TGACGGCTTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCAATTGT TCGGGCGTGg tgTtttGgcC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAg cgTCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPADF RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLV
201 SPVMTAFAPK PMVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACCG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CCGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTCGTAGG CTTGACGAT TTTTTCACCA AAAGGATGCC GGACAACGTC
501 TTCGCCGGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTTGATGT TTTTGGGCAG GTCGATTG
601 CTGGTGTGCG CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TCGGGTCAG
651 GAACATTTTC ATTTGTTCCG GCGTGGTGTT TTGCGCTTCG TCGAGGATGA
701 TGTATGCGCC GTTGAAGCTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPADF RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 IRCRKFDXCI GWTDKETDTE TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

1310

151 DSXASTIFCT KGCRTTSSPV KWKYSPSTL CSFSRASFP DLMFLGRSIW
 201 LVSPVMTAFA PKPMVRNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPAFADRISDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
m914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCRKFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEAIRCRKFDXCIGWTDKETDTD					
	70	80	90	100	110	120
	120	130	140	150	160	170
g914.pep	-ELGFRLCFSLPDPFCIGFQTALEQCSCSADSXASTIFCTRGCRRTSSPVKWKYSPATP					
m914	TELGFRLCFSLPDPFCIGFQTALEQCSCSADSXASTIFCTKGCRRTSSPVKWKYSPSTL					
	130	140	150	160	170	180
	180	190	200	210	220	230
g914.pep	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
	240					
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTGTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCAGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTATCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAATGTC AGTCGTGTTC TGCCGATTCC
451 TAGGCTTCGA CGATTTTTTG CACCAAAGGA TGCCGGACAA CGTCTTCGCC
501 GGTAAGGTG TGGAAATACA GCCCTTCCAC GCCGTGCAGT TTCTCACGCG
551 CATCTTTTAA TCCCGATTG ATGTTTTTGG GCAGGTCGAT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCGCCGAAG CCGATGCGGG TCAGGAACAT
651 TTTCATTTGT TCGGGCGTGG TGTTTTGCGC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAG CGTCTGCGG CGCATATAG
  
```

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGSNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCEDEA
101 IRCRKFD*CI GWTDKETDTE LGFRICFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTKG CRTTSSPVKV WKYSPSTPCS FSRASFPDL MFLGRSIWLV
201 SPVMTAFAPK PMVRNIFIC SGVVFCASSR MMYAPLSVLP RI*
  
```

1311

m914/a914 98.4% identity in 244 aa overlap

	10	20	30	40	50	60
m914.pep	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLES GGNTVKIDLFGSNSTMYVC					
a914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLES GSNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD					
a914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--					
	70	80	90	100	110	
	130	140	150	160	170	180
m914.pep	TELGFRICFSLPDPFCIGFQTALECSADXSASTIFCTKGCRTTSSPVKVKYSPSTL					
a914	TELGFRICFSLPDPFCIGFQTALECSADXSASTIFCTKGCRTTSSPVKVKYSPSTP					
	120	130	140	150	160	170
	190	200	210	220	230	240
m914.pep	CSFSRASFPDLMFLGRSIWLVPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
a914	CSFSRASFPDLMFLGRSIWLVPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	180	190	200	210	220	230
m914.pep	LPRIX					
a914	LPRIX					
	240					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915.seq

```

1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
51  CCGGCagcg gaAGaggcac cgccgCCTTT ACCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

g915.pep

```

1  MKKTLAIVA VFALSACRQA EEAPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915.seq

```

1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGC.tg
51  CCGGCAGGCG GAAGAGGGAC CGCCGCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TtTGTTCTC
201 CACCATCAAG CAGATGTTG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG

```

1312

451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2780; ORF 915>:

m915.pep

```

1 MKKTLAIVA VSALSXRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

m915/g915

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g915	MKKTLAIVAVFALSACRQAEAPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
	:					
g915	DQPVWFSTVKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
	:					
g915	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

a915.seq

```

1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCAGA TTTTCTTGAA CGGCAACCC GATCAGCCCG TTTGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCTGGT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

a915.pep

```

1 MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

m915/a915 99.4% identity in 164 aa overlap

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSXRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a915	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
a915	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pcp	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccact cgcCGTCctg actgctTtgc tgcttgacgc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaAA
101  accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151  ACCGTGCGCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201  GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCCG
251  GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAg
301  GCAGGTGCGT ATCAGAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351  TCTCAACCCCT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401  AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451  GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAgTG
501  GGATTGCGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
551  TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACAT
601  TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651  CGCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCGG
701  GCTTTATCGA TGATTGCGG CGCGCGGATA CCTGCGTAAC AATCGGTTTC
751  GCGCGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801  GGAAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGGG ATTTGGGTGG
851  ATTCTTTCTG GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901  TACATCAACG ACTTCTCTGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951  cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTGT ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCGGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CCGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKKNQ IKVTYDVYDS DETLESKVLV GKSGYDIVAP SNAFVGRQIK
101  AGAYQKIDKS MIPNYKHLNP EMRLMDGVD PDHEYAVPFY WGTNTFAINT
151  ERVKKALGTD KLPDQWDLV FNPEYTFKLK QCGISYLDLS AEIYPMVLNY
201  LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCTVTIGF
251  GGDNLNIAKRR AEEAGGKEKI RVMMPKEGVG IWVDSFVIPK DAKNVANAHK
301  YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351  SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGACGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101  ACCAAAACGT ATTGAAAATT TACAACTGGT CGGAATATGT CGATCCGGAA
151  ACCGTGCGCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201  GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251  GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAg
301  GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351  CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401  AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451  GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAgTG
501  GGATTGCGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551  TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601  TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651  CGCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCGG
701  GCTTTATCGA TGATTGCGG CGCGCGGATA CCTGCGTAAC AATCGGTTTC

```

1314

```

751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTGAAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

m917.pep

```

1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51 TVADFEKNG IKVTYDVYDS DETLESKVLK GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLDPNQWDLV FDPEYTSKLG QCGISYLD SA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
	10	20	30	40	50	60
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
g917	EMMRLMDGVDPDHEYAVPFYWGNTFAINTERVKKALGTDKLPDNQWDLVFNPEYTPKLG					
	130	140	150	160	170	180
m917.pep	190	200	210	220	230	240
	QCGISYLD SA AEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
g917	QCGISYLD SA AEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	250	260	270	280	290	300
	RGDTCVTIGFGGDLNIAKRR AEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
g917	RGDTCVTIGFGGDLNIAKRR AEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
	250	260	270	280	290	300
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPSGEDLKNSFIMVPIRPA					
	310	320	330	340	350	360

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m917.pep ALKFMVRQWQDVKAGKX
 |||||
 g917 ALKFMVRQWQDVKAGKX
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

a917.seq
 1 ATGACCAAAC ATCTGCCCTT GGGCGTCTTG ACTGCTTTGC TGCTTGCAGC
 51 GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA
 101 ACCGAAACGT ATTGAAAATT TACAACTGGT CGGAATACGT CGATCCGGAA
 151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
 201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCTG
 251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
 301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
 351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACC
 401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
 451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAAGT
 501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
 551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
 601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
 651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCGG
 701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
 751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CCGGCGGCAA
 801 GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
 851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
 901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
 951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
 1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
 1051 AGCTTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
 1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

a917.pep
 1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
 51 TVADFEKKNG IKVTYDVYDS DETLESKVL T GKSQYDIVAP SNAFVGRQIK
 101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
 151 ERVKKALGTD KLPDQWDLV FDPEYTSKLK QCGISYLSA AEIYPMVLNY
 201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
 251 GGD LNIARR AEEAGGKEKI RVMPKPEGVG IWVDSFVIK DAKNVANAHK
 301 YINDFLDPEV SAKNGNFVY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
 351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

m917/a917 99.7% identity in 376 aa overlap

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG					
a917	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKKNG					
	10	20	30	40	50	60
m917.pep	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
a917	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLK					
a917	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLK					
	130	140	150	160	170	180
m917.pep	QCGISYLSAAAEIYPMVLNLYLGNPNSSNTEDIREATALLKKNRPNIKRF TSSGFIDDLA					
a917	QCGISYLSAAAEIYPMVLNLYLGNPNSSNTEDIREATALLKKNRPNIKRF TSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	QCGISYLSAAAEIYPMVLNLYLGNPNSSNTEDIREATALLKKNRPNIKRF TSSGFIDDLA					
a917	QCGISYLSAAAEIYPMVLNLYLGNPNSSNTEDIREATALLKKNRPNIKRF TSSGFIDDLA					

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a917      QCGISYLDAAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRTSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pép  RGDTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKKEGVGIWVDSFVIPKDAKNVANAHK
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      RGDTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKKEGVGIWVDSFVIPKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pép  YINDFLDPEVSAKNGNFVITYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      YINDFLDPEVSAKNGNFVITYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360

           370
m917.pép  ALKFMVRQWQDVKAGKX
           ||||||||||||||
a917      ALKFMVRQWQDVKAGKX
           370

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The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccat
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATT TGCCAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGCG cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtagcgt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACGCCCg ACCTCTCCCG ATTCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTGAAaggAA GCCGCTTCTT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGCGcgcgTT GACGGCAAag cccCCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTTCATGCAC AtccaaggCT CGGGCCGCTT
801 GAAAACCCcg tcgggcaaat acatCCGCaT cgggTacgcc gacAAAAACG
851 AACatccgTa tgtttccatc ggACGetaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcata aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCGAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCCGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGTTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

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This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

```

g919.pép
1  MKKHLRSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIQTGXN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGSRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAGS GNEGFPVGALG
351 TPLMGEYAGA IDRHYYTLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

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1	ATGAAAAAAT	ACCTATTCCG	CGCCGCCCTG	TACGGCATCG	CCGCCGCCAT
51	CCTCGCCGCC	TGCCAAAGCA	AGAGCATCCA	AACCTTTCCG	CAACCCGACA
1 01	CATCCGTCAT	CAACGGCCCG	GACCGGCCGG	TCGGCATCCC	CGACCCCGCC
1 51	GGAAACGACGG	TCGGCGGGCG	CGGGGCCGTC	TATACCGTTG	TACCGCACCT
2 01	GTCCTTGCCC	CACTGGGCGG	CGCAGGATTT	CGCCAAAAGC	CTGCAATCCT
2 51	TCCGCCTCGG	CTGCGCCAAT	TTGAAAAACC	GCCAAGGCTG	GCAGGATGTG
3 01	TGCGCCCAAG	CCTTTCAAC	CCCCGTCCAT	TCCTTTCAGG	CAAAACAGTT
3 51	TTTTGAACGC	TATTTACGCG	CGTGGCAGGT	TGCAGGCAAC	GGAAAGCCTTG
4 01	CCGGTACGGT	TACCGGCTAT	TACGAAACCG	TGCTGAAGGG	CGACGACAGG
4 51	CGGACGGCAC	AAGCCCGCTT	CCCGATTTAC	GGTATTCCCG	ACGATTTTAT
5 01	CTCCGTCCCC	CTGCGTCCCG	GTTTGCGGAG	CGGAAAAGCC	CTTGTCGCGA
5 51	TCAGGCAGAC	GGGAAAAAAC	AGCGGCACAA	TCGACAATAC	CGGCGGCACA
6 01	CATACGCGCG	ACCTCTCCCG	ATTCCCCATC	ACCGCGCGCA	CAACAGCAAT
6 51	CAAAGCGCAGG	TTTGAAGGAA	CGCGCTTCT	CCCCTACCAC	ACGCGCAACC
7 01	AAATCAACGG	CGGCGCGCTT	GACGGCAAAG	CCCGCTACT	CGGTTACGGC
7 51	GAAGACCCTG	TCGAACTTTT	TTTTATGCA	ATCCAAGGCT	CGGGCCGTCT
8 01	GAAAACCCCG	TCCGGCAAAT	ACATCCGCAT	CGGCTATGCC	GACAAAAACG
8 51	AACATCCyTA	CGTTTCCATC	GGAAGCTATA	TGGCGGATAA	GGGCTACCTC
9 01	AAACTCGGAC	AAACCTCCAT	GCAGGGCATT	AAGTCTTATA	TGCGGCAAAA
9 51	TCCGCAACGC	CTCGCGGAAG	TTTTGGGTCA	AAACCCAGC	TATATCTTTT
10 01	TCCCGCAGCT	TGCCCGGAAG	AGCAATGAC	GCCCTGTCCG	CGCACTGGGG
10 51	ACGCCGCTGA	TGGGGGAATA	TGCCGGCGCA	GTCGACCGGC	ACTACATTAC
11 01	CTTGGGTGCG	CCCTTATTTG	TCGCCACCGC	CCATCCGGTT	ACCGCAAAAG
11 51	CCCTCAACCG	CCTGATTATG	GCGCAGGATA	CCGGCAGCGC	GATTAAAGGC
12 01	GCGGTGCGCG	TGGAATTATT	TTGGGGATAC	GGCGACGAAG	CCGGCGAACT
12 51	TCCCGGCAAA	CAGAAAATCA	CGGGATATGT	CTGGCAGCTC	CTACCCAACG
GTATGAAGCC CGAATACCG CCGTAA					

m919.pep

1	<u>MKKYLFRAAL</u>	<u>YGIAAAILAA</u>	<u>CQSKSIQTFF</u>	<u>QPDTSVINGP</u>	<u>DRPVGIPDPA</u>
51	GTTVGGGGAV	YTVVPHLSLP	HWAAQDFAKS	LQSFRLGCAN	LKNRQGWQDV
101	CAQAPQTPVH	SFQAKQFFER	YFTPWQVAGN	GSLAGTVTGY	YEPVLKGGDDR
151	RTAQARFFIY	GIPDDFISVP	LPAGLRSGKA	LVRIRQTGKN	SGTIDNTGGT
201	HTADLSRFFI	TARTTAIKGR	FEGSRFLPYH	TRNQINGGAL	DGKAPILGYA
251	EDPVELFFMH	IQSGRLKPT	SGKYIRIGYA	DKNEHPYVSI	GRYMADKGYL
301	KLQGTSMQGI	KSYMRRONPQR	LAELVLQONPS	YIFFRELAYS	ANDGPVGALG
351	TPLMGEYAGA	VDRHYITLGA	PLFVATAHPV	TRKALNRLLIM	SDQTGSAIKG
401	AVRVDYFWGY	GDEAGELAGK	QKTTGYVWOL	LPNGMKPEYR	P*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N.gonorrhoeae*
ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF
919.ng) from *N. gonorrhoeae*:
m919/g919

	10	20	30	40	50	60
m919.pap	MKKYLFRALYGIAAAAILAACQSKSIQTFFPQDTSVINGPDRPGIPDPAGTTVGGGAV					
	: : : : : : : : : : : :					
g919	MKKHLLRSALYGIAAAAILAACQRSISQTFFPQDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pap	YTVVPHLSLPHWAAQDFAKSLQSFLRGCANLKNRQGWDVCAQAQFQTPVHSFOAKQFFER					
	: : : : : : : : : : :					
g919	YTVVPHLSMPHWAAQDFAKSLQSFLRGCANLKNRQGWDVCAQAQFQTPVHSFOAKRFFER					
	70	80	90	100	110	120

1318

	130	140	150	160	170	180
m919.pap	YFTPWQVAGNGSLAGTVTGYEVLKGDGRRRTAQARFPIYGIPDDFISVPLPAGLRSGKA					
	:					
g919	YFTPWQVAGNGSLAGTVTGYEVLKGDGRRTERARFPIYGIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pap	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	:					
g919	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pap	DGKAPILGYAEDFVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
g919	DGKAPILGYAEDFVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pap	KLGQTSMQGIKSYMQRNPQRLAEVLGQNPYSIYFFRELAGSSNDGPVAGLGTPLMGEYAGA					
	:					
g919	KLGQTSMQGIKAYMRNPQRLAEVLGQNPYSIYFFRELAGSGNEGFPVAGLGTPLMGEYAGA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pap	VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVVDYFWGYGDEAGELAGK					
	:					
g919	IDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pap	QKTTGYVWQLLPNGMKPEYRFX					
g919	QKTTGYVWQLLPNGMKPEYRFX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGCCCG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGCGGCGG CGGGCCGTT TATACGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATT CGCCAAAAGC CTGCAATCCT
251 TCCGCTCGG CTGCGCCAAT TTGAAAACC GCCAAGGCTG CGAGGATGTG
301 TGCGCCCAAG CCTTCAAAC CCCCGTCCAT TCCGTTCAAG CAAAACAGTT
351 TTTTGAACGC TATTTACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATCCCG ACGATTTTAT
501 CTCGTCCTCC CTGCTGCCG GTTTCGGAG CGGAAAAGCC CTGTGCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCCA ATTCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CCGACTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGTTT ACCCGCAAAG

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1319

1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
 1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGGACGAAG CCGGCGAACT
 1251 TGCCGCGAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCAACG
 1301 GTATGAAGCC CGAATACCG CCGTAA

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:
 a919.pep

```

      1 MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
    51 GTTVGGGGAV YTVVPHLSLP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
   101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
   151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
   201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
   251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
   301 KLGQTSMOGI KAYMQONPQR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
   351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
   401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap
      10      20      30      40      50      60
m919.pep MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          |||||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
      10      20      30      40      50      60

      70      80      90     100     110     120
m919.pep YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCQAQAFQTPVHVSQAKQFFER
          |||||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCQAQAFQTPVHVSQAKQFFER
      70      80      90     100     110     120

      130     140     150     160     170     180
m919.pep YFTPWQVAGNGSLAGTVTGYIEPVLKGDGRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
          |||||
a919      YFTPWQVAGNGSLAGTVTGYIEPVLKGDGRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
      130     140     150     160     170     180

      190     200     210     220     230     240
m919.pep LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
          |||||
a919      LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m919.pep DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
          |||||
a919      DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
      250     260     270     280     290     300

      310     320     330     340     350     360
m919.pep KLGQTSMOGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
          |||||
a919      KLGQTSMOGIKAYMQONPQRLEAELGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
      310     320     330     340     350     360

      370     380     390     400     410     420
m919.pep VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          |||||
a919      VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
      370     380     390     400     410     420

      430     440
m919.pep QKTTGYVWQLLPNGMKPEYRPX
          |||||
a919      QKTTGYVWQLLPNGMKPEYRPX
      430     440

```

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCGAATAT CAGCCTACTT TCCCGTCAAA AAACAAAGCA
151 GGCTGGAAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTCCGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCT GGAAATCGTC
301 CCGCTGGACA ATCcgccgca caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtgttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
401 TTGacggctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaagtgg acatcatCCC
501 CTTGCgcaa GGCTTttgga aAgcGAGTGT CGAATAcaaa gccgAtttcc
551 CCGATcaaAG CCTGTGccga AAACAggcga ACTAcCaac TTtaaccttc
601 caaatcgccc attctCacca tTAa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YOYRSNRPVK DGSYLVTAEY QPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCACGCC CACCGmGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCGT TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAAH HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYOYRSNRPV KDGSYLVIAE
101 YOPTFWSKKK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
```


g920/m920

```

g920.pep      10      20      30
               PMQLVTEKGKENMIQRGTYNQYRSNRPVK
               |||||
m920          GGEYLKADLGYGFEFLEPIAKDRLHIFSKPMQLVTEKGKENMIQRGTYNQYRSNRPVK
               40      50      60      70      80      90

g920.pep      40      50      60      70      80      90
               DGSYLVTAIEYQPTFRSKNKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT
               |||||
m920          DGSYLVIAIEYQPTFWSKKKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT
               100     110     120     130     140     150

g920.pep      100     110     120     130     140     150
               KPVGQNLEIVPLDNPAIHVGXRFKVRVLFERGEPLPNATVTATFDGFDTSDRSKTHKTEA
               |||||
m920          KPVGQNLEIVPLDNPANIHVGXRFKVRVLFERGEPLPNATVTATFDGFDTSDRSKTHXHEA
               160     170     180     190     200     210

g920.pep      160     170     180     190     200
               QAFSDTTDGEGEVDIIPLRQGFWKASVEYKADFPDQSLCRQANYTTLTFQIAHSHHX
               |||||
m920          QAFSDSTDDKGEVDIIIXLRQGFWKANVEHKTDFPDQSVCKQANYSTLTFQIGHSHHX
               220     230     240     250     260

```

```

a920.seq
1      TGAAGAGAAA  CATTGACACT  GCTCGCCGTT  TCCGCCCTAT  TTGCCGCATC
51     CGCCCCACGCC  CACCGCGTGT  GGGTCGAAAC  CGCCCACACG  CACGGCGGCG
101    AATACCTTAA  AGCCGACTTG  GGCTACGGCG  AATTTCCGAG  ACTCGAACC
151    ATCGCCAAAG  ACCGCTTGCA  CATCTTCAGC  AAACCGCATG  AGCTGGTTAC
201    CGAAAAAGGC  AAGGAAAACA  TGATTCAACG  CGGCACATAC  AACTACCAGT
251    ACCGAAGCAA  CCGTCCCGTT  AAGGACGGCA  GTTACCTCGT  CATCGCCGAA
301    TATCAGCCTA  CTTTCTGGTC  AAAAAACAAA  GCAGGCTGGA  AACAGCGCGG
351    CATCAAAACA  ATGCTTGAGC  CAACTATTG  CGAACAAAC  CGAATGTTCT
401    GCAAAACAT  CGTCAACGTC  GGACACGAAA  CGCGGGACAC  GCCTATCATC
451    ACCAAACCGG  TCGGACAAAA  CTTGGAATC  GTCCCCTGCG  ACAATCCCGC
501    CAACATTCAC  GTAGGCGAAC  GCTTCAAAGT  CCGCGTTCGT  TTCCGTGGCG
551    AACCGCTGCC  CAATGCCACC  GTTACCGCCA  CCTTTGACGG  CTTCGACACC
601    AGCGACCGCA  GCAAAACGCA  CAAAACGAA  CGCAGGCTT  TCTCCGACAC
651    CACAGACGAC  AAAGGCGAAG  TGGACATCAT  CCCCTTGCG  CAAGGCTTCT
701    GGAAGGCCAA  TGTCGAACAC  AAAGCCGACT  TCCCCGATCA  AAGCGTGTGC
751    CAAAACACAG  CGAACTACTC  GACTTTAACC  TTCCAAATCG  GCCATTGCGA
801    CCATTAA

```

a920.pap

1	*KKTLLTLLAV	SALFAASAHA	HRVWVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKDRRLHIFS	KPMQLVTEKG	KENMIQRGTY	NYQYRSNRPV	KDGSYLVIAE
101	YQPTFWSKNK	AGWKQAGIKQ	MPDASYCEQT	RMFGKNIVNV	GHSADTAII
151	TKPVGQNLEI	VPLDNPAHII	VGERFKVRVL	FRGEPLPNAT	VTATFDGFD
201	SDRSKTHKTE	AQAFSDTDD	KGEVDIIPLR	QGFVKANVEH	KADFPDQSV
251	QKQANYSTLT	FOIGHSHH*			

m920/a920 97.0% identity in 267 aa overlap

1322

	10	20	30	40	50	60
m920.pep	MKKTLTLLSVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGFEPELEPIAKDRLHIFS					
a920	XKKTLTLLAVSALFAASAHHRVWVETAHTHGGEYLKADLGYGFEPELEPIAKDRLHIFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m920.pep	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKXKAGWKQAGIKE					
a920	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m920.pep	MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
a920	MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m920.pep	FRGEPLPNATVTATFDGFDTSDRSKTHXKEAQAFSDSTDDKGEVDIIXLRQGFWKANVEH					
a920	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
	190	200	210	220	230	240
	250	260	269			
m920.pep	KTDFFDQSVQCQKQANYSTLTTFQIGHSHHX					
a920	KADFFDQSVQCQKQANYSTLTTFQIGHSHHX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCcggtt TcCGCACTAT TTGCCACATc
51  cgCaCACCCC CACCgCGTCT GGGTCGAAAC CgcccACACg cAcgCGGCGG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGccAAAG ACCgctTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGT AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGCAGCAA CCGTCCCCTC AAAGACGGCA GCTACCTCGT TACCGCCGAA
301 TATCAGCCTA CTTTCCGGTC AAAAAACAAA GCAGGCTGGA AACAGGCTGG
351 CATCAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGTATGTTCTG
401 GTAAAAACAT TGTCACGTG GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCCTGCG ACAATCCCGC
501 CAACATTCAAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCTA CATTTGACGG CTTGCACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCCCAAGCCT TCTCCGACAC
651 CACCGACGGC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTTT
701 GGAAAGCGAG TGTCGAATAC AAAGCCGATT TCCCCGATCA AAGCCTGTGC
751 CAAAACAGG CGAACTACAC AACTTTAACC TTCCAAATCG GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLTLLAV SALFATSAHP HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVTAE
101 YQPTFRSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDTTDG KGEVDIIPLR QGFWKASVEY KADFFDQSLC
251 KQQANYTTLT FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCCACGCC CACCGCGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCCTT AAGGACGGCA GTTACCTCGT CATCGCCGAA

```

```

301 TAATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGCACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTGGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAACAGG CGAATACTC GACTTTAACC TTCCAAATCG GTCATTGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

m920-1.pep

```

1 MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRTGY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDSTDD KGEVDIPLR QGFWKANVEH KTDFFDQSV
251 QKQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

m920-1.pep	10	20	30	40	50	60
	MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLG YGEFPELEPIAKDRLHIFS					
g920-1	MKKTLTLLAVSALFATSAHPRVWVETAHTHGGEYLKADLG YGEFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
m920-1.pep	70	80	90	100	110	120
	KPMQLVTEKGKENMIQRTGYNYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE					
g920-1	KPMQLVTEKGKENMIQRTGYNYQYRSNRPVKDGSYLVIAEYQPTFRSKNKAGWKQAGIKE					
	70	80	90	100	110	120
m920-1.pep	130	140	150	160	170	180
	MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
g920-1	MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
m920-1.pep	190	200	210	220	230	240
	FRGEPLPNATVTATFDGFDTSRSKTHKTEAQAFSDSTDDKGEVDIPLRQGFWKANVEH					
g920-1	FRGEPLPNATVTATFDGFDTSRSKTHKTEAQAFSDTDGKGEVDIPLRQGFWKASVEY					
	190	200	210	220	230	240
m920-1.pep	250	260	269			
	KTDFFDQSVCKQKQANYSTLTTFQIGHSHHX					
g920-1	KADFFDQSLCQKQANYTTLTFQIGHSHHX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

a920.seq

```

1 TGAAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51 CGCCACAGCC CACCGCTCT GGTGCGAAAC CGCCACACG CACGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAACAAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGCACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTGGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAACAGG CGAATACTC GACTTTAACC TTCCAAATCG GCCATTGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

```

a920.pep
  1 *KKTLTLLAV SALFAASAH HRVWVETAHT HGGEYLKADL GYGEFPELEP
 51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVAIE
101 YQP TFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKP VQONLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSVC
251 QKQANYSTLT FQIGHSHH*

m920-1/a920    98.9% identity in 267 aa overlap

              10      20      30      40      50      60
m920-1.pep    MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
a920           XXXKTLTLLAVSALFAASAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
              10      20      30      40      50      60

              70      80      90     100     110     120
m920-1.pep    KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVAIEYQPTFWSKNKAGWKQAGIKE
a920           KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVAIEYQPTFWSKNKAGWKQAGIKQ
              70      80      90     100     110     120

              130     140     150     160     170     180
m920-1.pep    MPDASYCEQTRMFGKNIVNVGHESADTAITKPVQONLEIVPLDNPANIHVGERFKVRVL
a920           MPDASYCEQTRMFGKNIVNVGHESADTAITKPVQONLEIVPLDNPANIHVGERFKVRVL
              130     140     150     160     170     180

              190     200     210     220     230     240
m920-1.pep    FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
a920           FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
              190     200     210     220     230     240

              250     260     269
m920-1.pep    KTDFFPDQSVCCQKQANYSTLTFQIGHSHHX
a920           KADFPDQSVCCQKQANYSTLTFQIGHSHHX
              250     260

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

```

g921.seq
  1 ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
 51 Ccagtctatt tatGtgccca cattgacggA aatccccgTg aatccccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCTTCG
151 cattGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGCTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggaA AAATATGGAT GCCAAACCCG ATAATCCCCG ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

```

g921.pep
  1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
 51 HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSADV SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPFTN
151 FLMEVMKMQP LK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

```

m921.seq
  1 ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
 51 CCACTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA

```

1325

251 A CAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 T ATGAAATCT ACCTGCGTTC GGCATAGAC AGCCAGCGGG GCGCAATCAA
 351 T ACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 A GCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 T TTTTGATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:

m921.pep

1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
 101 YEIYLRSAID SQRGAITEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng) from *N. gonorrhoeae*:

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	: : : : :					
g921	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLAPSHWADVAKISD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAITEQ					
	: : : : :					
g921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAVDSQRGEITEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	: : : : :					
g921	SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2811>:

a921.seq

1 ATGAAAAAT ACCTTATCCC TCTTTCCATT GTGGCAGTTC TTTCCGGCTG
 51 CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
 101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTCCGCGCT TGCCTCTTCG
 151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
 251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GGCATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:

a921.pep

1 MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
 101 YEIYLRSAID SQRGAITEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

m921/a921 99.4% identity in 162 aa overlap

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	: : : : :					
a921	MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNNEFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTeq					
a921	EATRLGYQVGIGKMTKVQAAQYLNNEFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTeq					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFMLEVMKMQLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFMLEVMKMQLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1  ATGGAAAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAC CGGTATCCGA CAGCGGTTT GCCGCCAATG CAAATGTCCG
201 CCGTTTTGTG GACGATGAAG TCGGGAAGG GGATTTTTC CAGGCGGAAT
251 GGCAGGATTT TTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATT
301 ATGCACCGAC CCTCCACATC GCGTCCGTGG TATGtgttcc gCacggGAAa
351 tt cGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaaAacc
401 gcgcggttat cgatgatgtg gcgCAAAaT acggcgtGCC TGCCGAGCTT
451 ATCGTGGCGA TTATCGGGAT TGAAACGAAT TACGGCAAAA ATACGGGCAG
501 TTTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551 GCGCCGGGTT TTCCAAAAA GAATGGTCG AGCTTTTAAA GCTGGCAAAA
601 GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651 GGGTATGCCG CAATTTATGC CTTGAGCTA CCGGAAATGG GCGGTGGATT
701 ATGAcgggga cggacatCGG GATATAtggg GCAACGTcgg tgatgtcgcg
751 gcatcggTTG CCAATTatAT gaagCAGCAC GGTGGCGCA CgggcggtAA
801 AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CaggcAATCA
851 TTGGCGAAAA AACCGCCCTG ACGCGGACGG TGGCGGATT GAaggCGTAc
901 ggcatcatcc ccggggaaac GCTCGCAGAT GATGAAAAGg cgTTTTTGT
951 CAAACTGGAA ACCGCACCCG GCGTGTGTTGA ATATTATTG GCGTTGAACA
1001 ATTTTTTATAC GGTATGGCAG TACAACCACA GCCGGATGTA TGTAACGgcg
1051 gt caggGACA TTGCAATTC GCTCGCGCGC CCGGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.pep

```

1  MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KESRPAFPA
51  AAVPVSDSGF AANANVRRFV DDEVKGDFS QA EWQDFDK AAYKADIVKI
101 MHRPSTSRPW YVFRGNSGR AKFHGARRFY AENRAIDDV AQKYGVPAEL
151 IVAIIGIETN YGKNTGSFRV ADALATLGFY YPRRAGFFQK ELVELLKLAK
201 EEGGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251 ASVANYMKQH GWRTGGKMLV SATLAPGADV QAIIGETAL TRTVADLKAY
301 GIIPGETLAD DEKAVLFKLE TAPGVFEYYL GLNNFYTVWQ YNHSRMVTA
351 VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1  ATGAAAAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCGTGGTA
351 TGTGTTCCCG ACGGGAAATT CCGGCAAGGC GAAATTTCCG GCGCGCGCGC
401 GGTTTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCCTG CCGAATTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CGGCAAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCCGCGC GCCGGGTTTT TCCAAAAAGA ATTGGTCGAG

```

```

601 CTTTAAAGC TGGCAAAGA AGAAGGCGC GATGTTTCG CCTTTAAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AACGTCGGCG ATGTCGCGGC ATCGGTTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGAAAA TGCTGGTGTC TGCAACATTG GCGCCGGGTG
851 CCGATGTTCA GGCAATCATT GCGGAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGTA AGGCGTACGG CATCATCCCC GCGGAAGAGC TTGCAGATGA
951 TGAAAAGCGC GTTTTGTTCA AACTGGAAAC CGCACCGGCG GTGTTTGAAT
1001 ATTATTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAACCACAGC
1051 CCGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2816; ORF 922>:

m922.pep

```

1 MKKRKILPLA ICLAALSACT AMEARPPRAN EAQAPRAVEM KKERPAFDA
51 AAVFDAAAVP VSDSGFAANA NVRRFVDEV GKGDfsraew QDFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEGG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASVA NYMKQHGWR TGGKMLVSATL APGADVQAI GEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYLLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/g922

m922.pep	10	20	30	40	50	60
	MKKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKESRPADFDAAVFDAAAVP					
g922	MEKRKILPLAICLAALSACTAMEARTPRANEAQAPRADEMKKESRPADFDA-----AVP					
	10	20	30	40	50	
m922.pep	70	80	90	100	110	120
	VSDSGFAANANVRRFVDEVGKGDfsraewQDFDKAAYKADIVKIMHRPSTSRPWYVFR					
g922	VSDSGFAANANVRRFVDEVGKGDfsraewQDFDKAAYKADIVKIMHRPSTSRPWYVFR					
	60	70	80	90	100	110
m922.pep	130	140	150	160	170	180
	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
g922	TGNSGRAKFRHGARRFYAENRAVIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
	120	130	140	150	160	170
m922.pep	190	200	210	220	230	240
	ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
g922	ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
	180	190	200	210	220	230
m922.pep	250	260	270	280	290	300
	DGDGHRDIWGNVGDVAASVANYMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
g922	DGDGHRDIWGNVGDVAASVANYMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
	240	250	260	270	280	290
m922.pep	310	320	330	340	350	360
	ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYLLGLNNFYTVWQYNHSRMYVTAVRDI					
g922	ADLKAYGIIPGETLADDEKAVLFKLETAPGVFEYLLGLNNFYTVWQYNHSRMYVTAVRDI					

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	300	310	320	330	340	350
		370				
m922.pap	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922.seq
1  ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCTGTACG GCGATGGAGG CACGCCCGCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTTCCTG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAATT CGGGCAAGGC GAAATTTTCG GCGCGCGGCC
401 GGTTTTATGC GGAACCCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCCTG CCGAATTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CCGCAAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCCG GCCGGGTTT TCCAAAAGA ATTGGTCGAG
601 CTTTAAAGC TGGCAAGA AGAAGGCGGC GATGTTTTCG CCTTAAAGG
651 CAGCTATGCG GGCGCAATGG GGATGCCGA ATTTATGCCT TCGAGCTACC
701 GGAATGGGC GGTGGATTAT GACGGGACG GACATCGGGA CATATGGGGC
751 AATGTTGGCG ATGTCGCGGC ATCGATTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GGCGGAAAA TACTGGTGTC TGCAACATTG GCGCCGGGTG
851 CCGATGTTCA GGCAATCATT GGCGAAAAA CCGCCTGAC GCGGACGGTG
901 GCGGATTGTA AGGCGTACG CATCATCCC GGCGAAGAGC TTGCCGATGA
951 TGAAGAGCG GTTTTGTTC AACTGGAAC CGCACCCGGC GTGTTGAAT
1001 ATTATTTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAATCACAGT
1051 CCGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922.pap
1  MKNRKILPLA ICLALSACT AMEARPPRAN EAQAPRADEM KESRPAFDA
51  AAVFDAAAVP VDSGFAANA NVRRFVDEV GKGFDSRAEW QDFDKAAYK
101 ADIVKIMHRP STSRPWVFR TNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEEG DVFAFKGSYA GAMGMPQFMP SSKRWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHWRT GSKILVSATL APGADVQAI GEKALTTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYVLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922.pap	MKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKESRPAFDAAVFDAAAVP					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEAQAPRADEMKKESRPAFDAAVFDAAAVP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m922.pap	VDSGFAANANVRRFVDEVGKGFDSRAEWQDFDKAAYKADIVKIMHRPSTSRPWVFR					
a922	VDSGFAANANVRRFVDEVGKGFDSRAEWQDFDKAAYKADIVKIMHRPSTSRPWVFR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m922.pap	TNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
a922	TNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
	130	140	150	160	170	180
	190	200	210	220	230	240

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```

m922.pep  ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          190      200      210      220      230      240

          250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRGTGGKMLVSATLAPGADVQAIIGEKALTRTV
          ||||||||||||||||:||||||||||||||||||||||||||||||||||
a922      DGDGHRDIWGNVGDVAASIANYMKQHGWRGTGGKILVSATLAPGADVQAIIGEKALTRTV
          250      260      270      280      290      300

          310      320      330      340      350      360
m922.pep  ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          310      320      330      340      350      360

          370
m922.pep  ANSLGGPGLX
          ||||||||
a922      ANSLGGPGLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCGTGC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCGG
201 CGGTTGGACG GCGGCATACT TGGGTAGTAG GATGTTTCAGG CATAAAACGG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTC GTTCCGCCCG AACTTTTGT
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKROAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRAVR
51  GKRRIPRHRL LLPALFGGWT GAYLGSRMFR HKTAKKRFV LFRITVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCGTGC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GCGCGTATT TCGGCAGCAT GACATTCAAA CATAAGACAG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTAA ACCAGTACGG
351 CGTTGCCCTG CCTTGCCGTA CTATTGTAC TGTCTGCGGC TTCGTGCCT
401 TGTCTCTGATT TTGTTAATC CACTATAT.T ATTTTGTCCC GCCTGAATT
451 TTCGTAAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKROAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCAR
51  GQRRIPEHRL LLPALLGGWV GAYFGSMTFK HKTAKKRFV LFRITVSGNV
101 LATLILYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HXYFVPPEF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

1330

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

	10	20	30	40	50	60
g923.pep	MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
m923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100		
g923.pep	LLPALFGGWTGAYLGSRMFRHKTAKKRFVVLFRFTVSGNVLATCILID-----					
m923	LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRFTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			110	120		
g923.pep	-----YFVPPELFFVKLGQHLX					
m923	PCRTICTVCGFVALSXFLLIHYIYFVPPEFFVKLGQNTX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923.seq

```

1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTCTCTGC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTGCACCTT TACGGCATCG ACAAACGCGG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CCTGTGTCGG
201 CGGTTGGGCG GGGCATACT TGGGCAGCAG GATATTCAGG CATAAACCGG
251 CGAAAAGCG TTTTGTGTG CTGTCCGTC TGACTGTTT GGGCAATGTC
301 CTGGCGACCC TCATCCTGAT TTATAGTGA TTAATTAA ACCAGTACGG
351 CGTTGCCCTG CCTTA.GCTC AAAGAGAACG ATTCTCTAAG GTGCTGAAGC
401 ACCAAGTGAA TCGGTTCCGT ACTATTGTA CTGTCTGCGG CTTCGTCGCC
451 TTGTCTGAT TTTGTTAAT CCACTAT.AT TATTTTGTCC CGCCTGAATT
501 TTTCGTAAAA CTCGGGCAGA ATACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923.pep

```

1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRVR
51  GKRRRIPEHRL LLPALFGGWA GAYLGSRIFR HKTAKKRFVV LFRFTVSGNV
101 LATLILIIYS LNLNQYGVAS PXAQRERFSK VLKHQVNRFR TICTVCGFVA
151 LS*FLLIHYX YFVPPEFFVK LGQNT*

```

m923/a923 84.6% identity in 175 aa overlap

	10	20	30	40	50	60
m923.pep	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
a923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m923.pep	LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRFTVSGNVLATLILIIYSGNLNLNQYGVAS					
a923	LLPALFGGWAGAYLGSRIFRHKTAKKRFVVLFRFTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			130	140	150	159
m923.pep	PC-----RTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
a923	PXAQRERFSKVLKHQVNRFTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

```
g925.seq
1  ATGAAACAAA TGCTTTTGGC cgtcggcggtg ggcGCGGTGT TGGCGGGCTG
51  CGGCAaggat gcCGGCGGtt acgaggggtTA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCTTAAT
151 AAAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

```
g925.pep
1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNLYFLN
51  KI NVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKCKGQT QAYLDARNAL PSNQTYYQRO AAIEQLKRRF
151 EAEFDELEKE IKCNKPTLL F*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

```
m925.seq (partial)
1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGCGCGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
.....
```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

```
m925.pep (partial)
1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNLYFL..
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNLYFL				
	:				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNLYFLNKINVFTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGA LSINTGIGEIPIKLSDDGKELYVERRRYVKTDAA MKDKIIAHQKCKGQT				
	60	70	80	90	100 110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

```
g925-1.seq
1  ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGCGCGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAACCGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51  KINVFTGKEE SLLSEKDG LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

m925-1.seq

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAGAGGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTAATTCCTT
151 AATAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTGTCTGA
201 AAAAGACGGG CGCCTTTTCA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAA
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

m925-1.pep..

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL
51  NKIHVVTGKE ESLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAAAMKDKI IAHQKKCGQT AQAYRDARNA LPSNQTYQQH LAAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTGKE					
g925-1	MKQMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE					
	10	20	30	40	50	

	70	80	90	100	110	120
m925-1.pep	ESLLSEKDGALSINTGIGEIPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQT					
g925-1	ESLLSEKDGALSINTGIGEIPIKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKCGQT					
	60	70	80	90	100	110

	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYQQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX					
g925-1	AQAYLDARNALPSNQTYQQHQAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

a925-1.seq

```

1  AATAAATCA ACGTGTTCAC AGGTAAGGAA GAATCTATGC TTTGTCTGA
51  AAAAGACGGG CGCCTTTTCA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAA
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

a925-1.pep

```

1  NKINVTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51  KTDAAAMKDKI IAHQKKCGQT AQAYLDARNA LPSNQTYQQH QAAIEQLKRR
101 FEAEFDELEK EIKCNGKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

		10	20	30		
a925-1.pep		NKINVTGKEESMLLSEKDGALSINTGIGE				
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTGKEESLLSEKDGALSINTGIGE					
	30	40	50	60	70	80
	40	50	60	70	80	90

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```

a925-1.pep  IPIKLSDDGKELYVERRQYVKTDAA MKDKIIAHQKCKGQTAQAYLDARNALPSNQTYQQH
|||||
m925-1      IPIKLSDDGKELYVERRQYVKTDAA MKDKIIAHQKCKGQTAQAYRDARNALPSNQTYQQH
          90      100      110      120      130      140

          100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
|||||
m925-1      LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLLX
          150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGGT
301 ACGGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GCGGGGCGCG CCTtaccGCA
401 TCCGTTTCTAGA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgCCGACAGT GGGGGGCaag tccgaacgtt gcaactGaa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYAEG
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CROWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TGAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GCGGGGCGCG CCTTACCSCA
401 TCTGTCGCGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACCC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTC ACGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCGGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYAEG
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTWVGRT
151 ADSSGQVRTL QLNNGNLNIR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

          10      20      30      40      50      60
g926.pep  MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
|||||
m926      MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
          10      20      30      40      50      60

          70      80      90      100     110     120
g926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYAEGTEDLSRQLVGFKLPIQYLHI
|||||
m926      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYAESAELSRQLVGFKLPIQYLHI
          70      80      90      100     110     120

          130     140     150     160
g926.pep  WAEGRRVAGAPYRIRSDGILEQYGTWIGQNCROWGASPNVATE

```

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m926
 ||:||||||| |||||:|:|
 WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
 130 140 150 160 170 180

a926.seq

1 ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
 51 GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
 101 GCAGTTTCAC GCGGAAGGG CCGTTGGCAG TGAAAGCGGA AGGGAAAGGT
 151 TCGTATGCAA ATTTGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
 201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
 251 ACGGCGCATT GGCAGTGGAC GGCAGAGGAA ATGTCTATCA GCGGAAAGT
 301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
 351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GCGGGGCGCG CCTTACCGCA
 401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACC
 451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
 501 GAACATCAGG CTGGTTTTCA CCGAGATTGG TATGCCGTCT GAAACCGAAA
 551 CCCAAGAACA ATGCGCGGCA CGCATACAGT AA

a926.pep

1 MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEGKG
 51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
 101 AEELSRLVVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
 151 ADSGGQVRTL QLNNGNLNR LVFTEIGMPS ETETQECCAA RIQ*

m926/a926 96.9% identity in 191 aa overlap

	10	20	30	40	50	60
m926.pep	MKHTVSASVILLTACAQLPQNNENLWQPSSEHISFSAEGRRLAVKAEGKGSYANFDWTYQ					
a926	MKHTVSASVILLTACAQLPQNNENLWQPSSEHTRSFTAEGRLAVKAEGKGSYANFDWTYQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m926.pep	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAELSRLVVGFKLPIQYLHI					
a926	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAELSRLVVGFKLPIQYLHI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
	130	140	150	160	170	180
	190					
m926.pep	ETETPERCAARTRX					
a926	ETETQECCAAARIQX					
	190					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

g927.seq

1 atgaaaacct acGCacAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
 51 CAGCCCcgca GCcgatTcaa accatCCGTC CGGAcAAaAT GCCCCGGCCA
 101 ATACCGAATC cgacGgaaAA AACATtaccC TGctcaatgc cTcgtacgat
 151 gtGACACGGT ATTTttacaa agaatacgac cacTtgtttg tcggaaCATA
 201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAA TCCCACGGCG
 251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
 301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
 351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCTACA

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401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCaa ACAGAtccgC
 451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
 501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATACGGT TACGGTCTGA
 551 AAGCCAACAA CGGcaaCGAG CAGGAAGCCC AAAAActCGT CGCATCCATC
 601 CTCAAAAACA CACCCGTTTT TGAACGGC GGACGCGC C CGCCGCCACC
 651 ACCCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
 701 agCcaactac gtCAGCAAAA AACTGA

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
 51 VTRYFYKEYD HLFVGTQYSE HPGTSVSIQ SHGGFSKQAL SVANGLQADV
 101 VTMNQSSDID LLEKKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
 151 DWNDLAKDGV NIVIAKTSN GRYAFLGAY YGLKANNGNE QEAQKLVASI
 201 LKNTPVFENG GRXPPPPSH NATSATYSSL LTKPTTSAK N*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

1 ATGAAACCT ACGACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
 51 CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGGCCA
 101 ATACCGAATC CGACGGAAA AACATTACCC TGCTCAACGC CTCATACGAT
 151 GTGGCACGGG ATTTTACAA AGAATAACA CCCTTATTTA TCAAAACATA
 201 CCAATCCGAA CACCCGGCA CATCCGTCAG CATCCAACAG TCCACGGCG
 251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
 301 GTAACCATGA ACCAATCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
 351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
 401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCAA ACAGATCCGC
 451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
 501 CAAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
 551 GTCTGAAAAA CACCAACGGC AACGAACAGG AAGCCAAAA ACTCGTCGCA
 601 TCATCCTCA AAAACACCCC CGTTTTGAA AACGGCGGAC GCKCGCCACC
 651 ACCACCTTCA CACAACGCA CATCGGCGAC GTACTCATCA CTTTGAAAA
 701 CGAAGCCAAC TACGTCAGC AAAAActGA

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
 51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQ SHGGSSKQAL SVANGLQADV
 101 VTMNQSSDID LLEKKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
 151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLV
 201 SILKNTPVFE NGGRXPPPS HNATSATYSS LLTKPTTSA KN*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
	:					
m927	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
g927.pep	HLFVGTQYSEHPGTSVSIQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	:					
m927	PLFIKTYQSEHPGTSVSIQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120
	130	140	150	160	170	
g927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGRYAFLGA					
m927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGRYAFLGA					
	130	140	150	160	170	180

```
a927.seq
1  ATGAAAACCT  ACGCACCGGC  ACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATTCAA  ACCATCCGTC  CGGACAAATC  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  ACCATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTCA  CATCCAACG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCTATTA  TCCGTAGCCA  ACAGCCCTAG  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  GCGATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCACGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTTTCCTT  GTCCGAAAAA  ACAACCCCAA  ACAGATCCCG
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAAACCTCG  GCGAACGGAC  GTACGCGCTT  CTTGGCGCGCA  TACGGTTACG
551 GTCTGAAAC  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 AACACCTTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTGGAAAA
701 CGGAGTCAAC  TACGTCAGCA  AAAAATCGA
```

a927.pep

1	<u>MKTYAPALYT</u>	<u>AALLSACSPA</u>	ADSNHPSGQN	APANTESDGK	NITLLNASYD
51	VARDFYKEYN	PLFIKTYQSE	HPGTSVSIQQ	SHGSSSKQAL	SVANGIQADV
101	VTMQSSDD	LLEKKGIVEK	GWQQALPDHA	APYTSMTMVL	NRKNNPKQIR
151	DWNDLAKDGV	NIVIANPKTS	GNGRYAFLGA	LYGYLKTTSNG	VEQEAQKLVA
201	SILKNTPEVFE	NGGRAPPPPS	HNATSATYSS	LLGKPTTSS	KN*

	10	20	30	40	50	60
m927.pep	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
a927	MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m927.pep	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLOADVVTMNQSSDIDLLEKKGLVEK					
a927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLOADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWDLAKDGVNIVIANPKTSGNGRYAFLGA					
a927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWDLAKDGVNIVIANPKTSGNGRYAFLGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m927.pep	YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA					
a927	YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA					
	190	200	210	220	230	240

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m927.pep KNX
 |||
 a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACccga CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGCGGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTTCG CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
 351 TATCGCCGTT TTTGGAAGAA AAACgctggg CATCGGTTAC AGTCTCGCTC
 401 TTTCGGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
 451 GCGGCGATTA TACATCgaT TATGcagtcg attgCcgCA GttacggctC
 501 caatCCCGCA AAAGGCACag aaggcaagat gggtaAATAT TtggcTTtgg
 551 tc aatttaTCA TTCaaTCCC atttcgtcgg ctAtggctat taCTGcaact
 601 gCCCCaaACC CTTTAATcgt caacttgatt gccGaaaaTt taggcagtag
 651 tt tccgtCTT Tcttgggggg cgTGGGcgTg ggcaaTGGCT Gttcccggcg
 701 tt atcgcctt TttcgTTATG CTTTGATTTT TATATTTTTT GTATCCGCCT
 751 GA AATTAAAG AAACGCCCAA TGCTGttcAA TTTGCCAAAG ACCGTCTGAG
 801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
 851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
 901 CA CGCTTTTA GTATCAacgc caccGCCACC GCATTATATCG GATTAAGCCT
 951 GC TTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAAA
 1001 GC GCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
 1051 TT TTTaAATA Aactcggact gattaaatGG TTCTCCGAG TGTGGCGGA
 1101 Aa gtgtcggc GGT TTTGGCG TTAGCGGCAC GGCTCGGGC GTAATCCTCG
 1151 TGCTTGctta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
 1201 ATTACCGCTA TGTTCCGCGC ATTTCTCGCT GTCGCCGTTT CACTGAATGC
 1251 CC CGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
 1301 TGACCCCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCGGCTCG
 1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGGTTTTA TCATGAGCGT
 1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTTGG TGGAAAGTTC
 1451 TGCGATATTG GTAA

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep
 1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
 51 VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
 101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELILLA PVTPSNTARG
 151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMAITAT
 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
 251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
 301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
 401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
 451 GYTTMGEWWK AGFIMSVVNF LIFSVIGSIW WKVLGYW*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGCGGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTTCG CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
 351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
 401 TTTCGGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

```

451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTCTGTCG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TT'TCCGCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCGTTATG CCTTTGATT TATATTWYT GTATCCGCCT
751 GAAATTAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTGT AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGAG TGTGGCGGA
1101 AAGTGTCCGC GGTGTTGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCGGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC G9CCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCCGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGGTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTGGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

```

1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51 AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTSPNTARG
151 GGI IHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHSNP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929.pep	MKLGFKPIPLAIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK V MPLGALSII					
m929	MKLGFKPIPLAIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK A MPLGALSII					
	10	20	30	40	50	60
g929.pep	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRG L LKTGLGMRIGYLFIAV					
m929	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRG L LKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
g929.pep	FGRKTLGIGYSLALSELLLPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
m929	FGRKTLGIGYSLALSELLLPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
g929.pep	LALVNYHSNP ISSAMAITATAPNPLIVNLI AENLGSSFRL SWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHSNP ISSAMFITATAPNPLIVNLI AENLGSSFRL SWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240

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	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADVLPALITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADVLPALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGGGLVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFAAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

a929.seq

```

1  ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTGTTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGTGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGTGC GGCATGAGC  GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTGTGT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAACT GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTGCTCGG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGCTCT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTGCTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGTT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTATATC GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGAATTGGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGCGGGA
1101 AAGTGTGCGC GGTGTTGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCGGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTGCGTTTC
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

```

a929.pep
1  MKLGFKPIPL AIAAVLCALV LALVPDGVK PQAWTLLAMF IGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTIGIGY SLALSELLLA PVTSPNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTA
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

m929/a929 99.6% identity in 487 aa overlap

m929.pep	10	20	30	40	50	60
	MKLGFKPIPLAIAAVLCALVLALVPDGVK PQAWTLLAMFVGVIAAIIGKAMPLGALSII					
a929	MKLGFKPIPLAIAAVLCALVLALVPDGVK PQAWTLLAMFIGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
m929.pep	70	80	90	100	110	120
	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
a929	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
m929.pep	130	140	150	160	170	180
	FGRKTIGIGYSLALSELLLA PVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
a929	FGRKTIGIGYSLALSELLLA PVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
m929.pep	190	200	210	220	230	240
	LALVNYHNSP ISSAMFITATAPNPLIVNLI AENLGSSFRL SWGAWAWAMAVPGVIAFFVM					
a929	LALVNYHNSP ISSAMFITATAPNPLIVNLI AENLGSSFRL SWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240
m929.pep	250	260	270	280	290	300
	PLILYXLYPPEIKETPNAVQ FAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
a929	PLILYFLYPPPEIKETPNAVQ FAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	250	260	270	280	290	300
m929.pep	310	320	330	340	350	360
	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
a929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
m929.pep	370	380	390	400	410	420
	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTAHTAMFGAFFAAAVSLNAPAM					
a929	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTAHTAMFGAFFAAAVSLNAPAM					
	370	380	390	400	410	420
m929.pep	430	440	450	460	470	480
	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
a929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
m929.pep	WKVLGYWX					

a929

WKVLGYWX

g930.seq not found yet

g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

m930.seq

```

1  ATGAACTTC CTTTATCCTA TTTGCCTAAT ATTGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAAC GAAATGGTGT TGAAGGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

m930.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNPAEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWLGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

g930-1.seq (partial)

```

1  GGCAGGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTG GAATAGTGGC AAGCTTCAAT TAACCCTGAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAAG
201 ACGTATTGCA GCATTCCAAA ACAAAATTCC CACCGGCTCG AACGATCTGT
251 TGAATCTGCG TGATTGGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351 AAGTGATGTC GTGGTGCAAT GCGGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGAAGTGTG ATATGTTCTA
501 TGTAAATTAT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601 GCCCCTTTG GTAAATGGAC ATGGGCATTC AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTCCGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701 GTTACAACAC TGATTTCGGC TTCAACCGCC TGTGTATCG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAAATGTGG ACGAGGAAA CAAAAGTTA
801 CATTGATGAT GCCGAACCTA CTGTACAACG GCGTAAACCC ACAGGTTGGT
851 TGGCAGAACT TTCCACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACGG CACCGCATG AAAGATGCTC TGCGCGCGCC
951 TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTCAAATCG GTAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAG
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GCGGCAACGA TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTATCGGG CCAAACCTA GCCGCGACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTACCG GCCGTGCATT GAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGTTATTC GTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

g930-1.pep (partial)

```

1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPDLNSG KLQLTMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKLCP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYLSVKLW TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FGEGRSRMKI WTASADVNTF FOIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLSW
401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGO IKLGGNLHYD

```

451 IFTGRALKKP EYFQTKKWT GFQVGYSF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```

1  ATGAACTTC CTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51 CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAA AACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCATTAAAC GAAAGTGGTG TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTGTA TACCGAGCTA
501 TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 AACGTATTGC AGCATTCCAG AACAAATTTC CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTGGGA ACAAGGACTG GAAAATCTCA AACGTCTCCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAAAC
701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAATAA TGGACGTTTC ATTGGCGGTA CGCCCGATGA GGAAGTTTTT
901 AACGGCCATC GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
951 AGCCCTTTTC GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA
1051 AGTTACAATA CTGATTTCCG CTTCAACCCG CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAACTGTG GATGAGGGA AAAAAAGTT
1151 ACATTGATGA TGCCGAATCG ACTGTACAAC GGCCTAAAAC TCGGGTTGG
1201 TTGGCAGAA TTTCCACAA AGAATATATC GGTGCGAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAAACGCG GCACCGGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAGC CTTTGGCGAA GGCACGTCAC GTATGAAAT TTGACGCGCA
1351 TCGGCTGATG TAAATACTCC TTTTCAAATC GGTAACAGC TATTTGCCCTA
1401 TGACACATCC GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
1451 ACAAACGGC TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTTAAA CAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTCAGGACA ATCGGCCAAA TGGTTATCGG GCCAAACTCT AGTCGGCACA
1651 GCAATTGGGA TACGCGGGCA GATAAAGCTT GCGGCAAC TGCATTACGA
1701 TATATTACC GCGCGGCAT TGA AAAAGCC CGAATTTTC CAATCAAGGA
1751 AATGGGCAAG CGGTTTCAG GTAGGCTATA CGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:

m930-1.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNP AEIRM QDIIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFQ NKFPTRSNDL
201 LNLRLDLEQL ENLKRLLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDNSGSE ATGKYQGNIT PSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGHRKEGGSN NYAVHYSAPP GKWTWAFNHN GYRYHQAVSG LSEVYDYNK
351 SYNTDFGFNR LLYRDAKRKT YLGVKLWMRE TKS YIDDAEL TVQRKRTAGW
401 LAELSHKEYI GRSTADFKLK YKRGTMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWY WRNDSLWQFK PGHQLYLGAD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*

```

m930-1/g930-1 95.4% identity in 478 aa overlap

	90	100	110	120	130	140
m930-1.pep	AINEVVLEGEHHARFQFALKRALRETGFQAGKCLHAGNINQIMSLAQNALIGRGYTTTRI					
	:					
g930-1.pep	GKCLHAGDINQIMSLAQNALIGRGYTTTRI					
		10	20	30		
	150	160	170	180	190	200
m930-1.pep	LAAPQDLNSGKLQTLTIPSYLRSIRIDRSNDDQTHAGRIAAFQNKFPTRSNDLNLRDLE					
	:					
g930-1.pep	LAAPQDLNSGKLQTLMPGYLRSIRIDRSNDDQTHAGRIAAFQNKFPTRSNDLNLRDLE					
	40	50	60	70	80	90
	210	220	230	240	250	260
m930-1.pep	QGLENLKRLLPTAEADLQIVPVEGEPNQSDVVVQWRQRLPYRVSVGMDNSGSEATGKYQG					
	:					

1343

```

g930-1.pep  QGLENLKCLPTAEADLQIVPVEREPNQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQG
              100      110      120      130      140      150
m930-1.pep  270      280      290      300      310      320
NITFSADNPLGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NITFSADNPFGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210
m930-1.pep  330      340      350      360      370      380
NHNGYRYHQAVSGLSEVYDYGKSYNTDFGNRLLYRDAKRKTYLGVKLMWRETKSYIDD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NHNGYRYHQAVSGLSEVYDYGKSYNTDFGNRLLYRDAKRKTYLSVKLWTRETKSYIDD
              220      230      240      250      260      270
m930-1.pep  390      400      410      420      430      440
AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTGMKDALARPEEAFGEGETSRMKI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  AELTVQRRKTTGWLAELSHKGYIGRSTADFKLKYKHGTGMKDALARPEEAFGEGETSRMKI
              280      290      300      310      320      330
m930-1.pep  450      460      470      480      490      500
WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLSAER
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLPAER
              340      350      360      370      380      390
m930-1.pep  510      520      530      540      550      560
GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAIGIRGQIKLGGNLHYD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLGTAIGIRGQIKLGGNLHYD
              400      410      420      430      440      450
m930-1.pep  570      580      590
IFTGRALKKPEFFQSRKWASGFQVGYTF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  IFTGRALKKPEYFQTKWVTGFQVGYSTFX
              460      470

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2857>:

```

g931.seq
1   ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCCT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAAC CGTTGCCAAT
151 TTCTGTCGCT ATGCCCGAAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301 AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCGGCC CAATTCTTTA TCAATCTGGC GGACAACGGT TCGCTCGACT
401 ACAAACACCG ACAATACGGC TACACCGTTT TCGGCAGGGT AGAAAGCGGA
451 ATGGACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTCG
551 GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCG TTTCCCAAAA
601 AACGCCGTTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

```

g931.pep
1   MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKTVAN
51  FVRYARKGFY DNTIFHRVIG GFVIQDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA OFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

1344

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2859>:

```
m931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CC TGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCTAAT
151 TT CGTGCGCT ATGCCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
201 CG TTATCGAC GGTTTTGTTA TCCAGGGCGG TGGATTGACC GAGGACTTGG
251 CA CAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AA AAACACCG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTC
351 CG CCACCAGC CAATTCTTTA TCAATCTGGC GGACCA.kCT TCGCTCGACT
401 AC AAAAACCG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 AT GAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TT ATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTGCG GTTGTGTGCG
551 GG CAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

```
m931.pep..
1  MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

g931/m931

	10	20	30	40	50	60
g931.pep	MKPKFKTVLTALLLAVSLPSMAATRVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
m931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
g931.pep	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNPVPQPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVPQPVKIRR					
	130	140	150	160	170	180
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNPVPQPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVPQPVKIRR					
	130	140	150	160	170	180
g931.pep	VVVGQX					
m931	VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

```
a931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAATACGA TTTTTCACCG
201 CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAAACACTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGT GGACAATGAT TCGCTCAACT
401 ACAAAAACCG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
```


1345

451 ATGAACACCG TTTCCAAAT CGCCGCGTC AAAACCGCCA CGCGCGGCTT
 501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep
 1 MKPKFKTVLT ALLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS OFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLTALLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
a931	MKPKFKTVLTALLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	OFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
a931	OFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
 101 TGAAAAATTA CGCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
 301 AAATACGAAT GGCTCGAGA AGAAGGAAAA ACAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep
 1 MKYIVSISLA MGLAACFSGG FKPNPWDAAS FWELKNYANP YPGSASAALD
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPYENK
 101 KYEWPREEGK TK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTG CACTCACCGC

q934.pep

```

1  MKKIIASALI  ATFALTACQD  DTQARLERQQ  KQIEALQQQL  AQQADDTVYQ
51  LT PEAVKDTI  PAQAQANGNN  GQPVTKKRRR  AVYLREPIDRK  LAAAKPDWRG
101 GR RVYRQRAG  KQIHTGGQPR  QRRRPSRACC  LPSVRTPQCA  HQQGFEHAQP
151 PC KTTGGAGA  ALPPDNRAFR  KLPSPRYARF  RQKAVNPARQ  CRLKGFQTAF
201 LY LLGALLCC  RLIFRRHFVS  KRLMSGWQF*

```

m934.seq (partial)

1	CGGCTCGAAC	AGCAGCAGAA	ACAGATTGAA	GCCCTGCAAC	AGCAGCTCGC
51	ACAGCAGGCA	GACGATACGG	TTTACCAACT	GACTCCCGAA	GCAGTCAAAG
101	ACACCATTC	TGCCGAAGCA	CAGGCAAAAC	GCAACAACgG	GCAACCCGTT
151	ACCGGTAA .A	GACGGGCAGC	AGTATATTTA	CGACCAATCG	ACAGGAAGCT
201	GGCTGCTGCA	AAGCCTGGTC	GGCGCGGCGG	CAGGCGCGTT	TATCGGCAAC
251	GCGCTGGCAA	ACAAATTAC	ACGGGCAGGC	AACCAAGACA	GTCCCGTCGC
301	CCGGCGCGCG	CGTGACAGCT	ACCATCAGCT	CGCACGCCCC	AATGCGCGCA
351	yCAGCAGGGA	TTTGAACACG	CGCAGCTTCC	GTGCAAAACA	ACAGGCGGCG
401	CAkGCGCAGC	GTTACGCCCC	GACAACGCGC	CCGsCCGsCA	ATTACGCGCG
451	CCCCGCTATG	CGCGGTTTCG	GCAGGAGGCG	GTA AACCCGG	CGCGCCAATG
501	CCGTCTGAAG	AGCTTTTACA	CGGCATTnTn	GCATTGTGTTA	GGGACATTGT
551	TATGTTGCCG	TTTGTATTTT	AGACGGCATT	TTGTTTCCAA	GCGTTTGATG
601	TCGGGATGGC	AATTCTGA			

m934.pep (partial)

```

1  ..RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51  TGXRRAAVYL RPIDRKLAAA KPGRRGRRV YRQRAGKQIH TGRQPRQSR
101 PARACSLPSV RTPQCAHQOG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151 PRYARFRQEA VNPARQCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/q934

```
m934.pep                               10      20      30  
                                     RLEQQQKQIEALQQQLAQQAADDTVYQLTPEAVKDIT  
                                     |||:|||||  
g934    MKKIIASALIATFALTACQDDTQARLERQQKQIEALQQQLAQQAADDTVYQLTPEAVKDIT  
            10      20      30      40      50      60
```



```
m934.pep          40      50      60      70      80      90  
PAAEQANGNNGQPVTGXRRRAVYLRLPIDRKLAAAAPGRRGGRRVYRQRAGKQIHTGRQPR  
||:|||||  
g934    PAQAEANGNNGQPVTGKRRAAVYLRLPIDRKLAAAAPDWRGGRRVYRQRAGKQIHTGGQPR  
           70      80      90     100     110     120
```



```
           100     110     120     130     140     150
```

```

a934.s eq
1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCC CACTCGCCGC
51 CTGCCAAGAC GACGCGCAGC CGCGGCTCGA ACAGCAGCAG AAACAGATTG
1 01 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CACAGCGATC GGGTTTACCAA
1 51 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCGAAG CACAGCAAAA
2 01 CGGCAACAAC GGGCAACCCG TTACCGG.TA AAGACGGGCA GCAGTATATT
2 51 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGG TCGGCGCGGC
3 01 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATT CACACGGGCAG
3 51 GCAACCAAGA CAGTCCCGTC GCCCGGCGCG CGCGTGCCGC CTACCATCAG
4 01 TCCGCACATA CCAATGCGCG CACCAGCAGG GATTGAACA CGCGCAGCCT
4 51 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
5 01 GCCCGCCCGC CAATTACCGC CGCCCGCCA TGC CGGTTT CCGCAGAAGG
5 51 CGGTAAATCC GCGGTGCCAA TGCCGTCTGA AGGGCTTTCA GACGGCATTT
6 01 TTGTATTTGT TAGGACATT GTTATGTTCG CGTTTGATT TTAGACGGCA
6 51 TTTTGTTC AAGAGTTTGA GTTCCGGATG GCAATTCTGA

```

a934.pap

1	<u>MKKIIASALI</u>	<u>ATFALAACQD</u>	DAQARLEQQQ	KQIEALQQOL	AQQADDTVYQ
51	LTPEAVKDTI	PAAEQANGNN	GQVPTX*RRR	AVYLRLPIDRK	LAAAKPGRRG
1 01	GRVVRQQRAG	KQIHTGRQPR	QSRPPARACR	LPSVRTSQCA	HQQGFHAQP
1 51	PCKTTGGAGA	ALPPDNAPAR	QLPPPRHARF	RQKAVNPACQ	CRLKGFQTAF
2 01	LYLLGTLLCC	RLIFRRHFVS	KLSMGWOF*		

```

m934.pep                                10          20          30
                                RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                                |||
a934      MKKIIASALIATFALAACQDDAQRLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                                10          20          30          40          50          60

                                40          50          60          70          80          90
m934.pep      PAEAQANGNNGQPVTGXRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
                                |||
a934      PAEAQANGNNGQPVTXXRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
                                70          80          90          100         110         120

                                100         110         120         130         140         150
m934.pep      QSRRPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
                                |||
a934      QSRRPARACRLPSVRTSQCAHQQGFEHAQPPCKTTGGAGAALPPDNAPARQLPPPRHARF
                                130         140         150         160         170         180

                                160         170         180         190         200
m934.pep      RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
                                |||
a934      RQKAVNPACQCRLKGFQTAFLYLLGTLCCRLIFRRHFVSKSLMSGWQFX
                                190         200         210         220         230

```

q935.seq not found yet

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGCAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GCGGGAAGAA CTGACGGCGT TGGCAGATAA TCATTATTGT
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTC AAAAAAATC
801 AGCTTATGAC GACGGGTTTC GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGGCGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCC
901 GGCAGCGACG GCTTTGATGC GAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GCGCGCGTCA ATAATGCCGC CTACGGCGCG AACGGTGGTT ATGCCGGCTG
1251 GCGCGAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTTCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCGTTG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTT GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTGTGTGCG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

```

a935.pep
1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVERYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFGSGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFEGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPIYA KRRNSEVFFV
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

	10	20	30	40	50	60
m935.pep	MLYFRYGLVWVCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVENDAPRVV					
a935	MLYFRYGLVWVCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVNDAPRVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m935.pep	DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
a935	DGDFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m935.pep	AEAVERYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAAKLDLPAPVLENVGRF					
a935	AEAVERYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAEKLDLPAPVLENVGRF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m935.pep	RKKTEGLTGWRFGSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
a935	RKKAEGLTGWRFGSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m935.pep	LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  A T G T T G T A T T   T C A G A T A C G G   C T T T T T G G T T   G T T T G G T G T G   C G G C A G G T G T
51  T T C T G C C G C C   T A T G G G G C G G   A T G C G C C C G C   G A T T T T G G A T   G A C A A G G C A T
101 T G T T G C A G G T   G C A G C G G T C G   G T G T C G G A T A   A G T G G G C G G A   A T C A G A T T G G
151 A A A G T T G A A A   A T G A T G C C C C   G C G C G T G G T T   G A C G G G G A T T   T T T T G T T G G C
201 G C A T C C G A A A   A T G T T G G A A C   A T A G T T T G C G   C G A C G C G C T C   A A C G G C A A T C
251 A G G C G G A A T T   A A T C G C T T C G   T T G G C G G A T T   T G T A T G C C A A   G C T G C C G G A T
301 T A T G A C G C G G   T T T T G T A C G G   C A G G G C G C G G   G C T T T G C T G G   C G A A A T T G G C
351 G G G A A G G C C G   G C G G A G G C G G   T G G C G C G G T A   T C G G G A A C T G   C A C G G G G A A A
401 A T G C G G C A G A   C G A G C G G A T T   T T G C T G G A T T   T G G C G G C G G C   G G A G T T T G A C
451 G A T T T C C G G C   T G A A G T C G G C   A G A A A G G C A T   T T T G C G G A G G   C G G C A A A A T T
501 G G A T T T G C C G   G C A C C G G T T T   T G G A A A A T G T   G G G G C G T T T T   C G G A A A A A A A
551 C G G A G G G G C T   G A C G G G C T G G   C G T T T T T C G G   G C G G C A T C A G   T C C G G C G G T C
601 A A T A G A A A T G   C C A A T A A T G C   C G C G C C G C A A   T A T T G C C G G C   A A A A C G G A G G
651 C C G G C A G A T A   T G C A G T G T C A   G C C G G G C G G A   G C G G G C G G C A   G G G T T G A A T T
701 A T G A A A T C G A   G G C G A A A A G   C T G A C G C C G T   T G G C A G A T A A   T C A T T A T T T G
751 T T G T T C C G T T   C C A A T A T C G G   C G G C A C G A G C   T A T T A T T T C A   G T A A A A A A T C
801 A G C T T A T G A T   G A C G G G T T C G   G C A G G G C G T A   T T T G G G T T G G   C A G T A T A A A A
851 A T G C A C G G C A   G A C G G C G G G G   A T T T T G C C G T   T T T A T C A G G T   G C A G T T G T C G
901 G G C A C G A C G   G C T T T G A T G C   G A A A C A A A A   C G G G T A A A C A   A C C G C C G C C T
951 G C C G C C G T A T   A T G C T G G C G C   A C G A G T C G G   C G T G C A G C T G   T C C C A T A C T T
1001 A C C G C C C A A A   C C C G G G A T G G   C A A T T T T C G G   T C G C G T G G A   A C A T T A C C G C
1051 C A A C G C T A C C   G C G A A C A G G A   T A G G G C G G A A   T A C A A T A A C G   G C A G G C A G G A
1101 C G G G T T T T A T   G T T C G T C G G   C A A A A C G T T T   G G G C G A A T C G   G C A A C T G T G T
1151 T C G G C G G C T G   G C A G T T T G T G   C G G T T T G T G C   G G A A A C G C G A   A A C G G T G G G C
1201 G G C G C G G T C A   A T A A T G C C G C   C T A C C G G C G C   A A C G G T G T T T   A T G C C G G T T G
1251 G G C G C A G G A G   T G G C G G C A G T   T G G G C G G T T T   G A A C A G T C G G   G T T T C C G C G T
1301 C T T A T G C C C G   C C G C A A C T A T   A A G G G C A T T G   C G G C T T T C T C   G A C A G A G G C G
1351 C A A C G C A A C C   G C G A A T G G A A   T G T C T C G C T G   G C T T T G A G C C   A C G A C A A G T T
1401 G T C G T A C A A A   G G T A T C G T G C   C G G C G T T G A A   T T A T C G T T T C   G G C A G G A C G G
1451 A A A G T A A T G T   G C C G T A T G C G   A A A C G C C G C A   A C A G C G A G G T   G T T T G T G T C G
1501 G C G G A T T G G C   G G T T T T G A

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1  M L Y F R Y G F L V   V W C A A G V S A A   Y G A D A P A I L D   D K A L L Q V Q R S   V S D K W A E S D W
51  K V E N D A P R V V   D G D F L L A H P K   M L E H S L R D A L   N G N Q A D L I A S   L A D L Y A K L P D
101 Y D A V L Y G R A R   A L L A K L A G R P   A E A V A R Y R E L   H G E N A A D E R I   L L D L A A A E F D
151 D F R L K S A E R H   F A B A A K L D L P   A P V L E N V G R F   R K K T E G L T G W   R F S G G I S P A V
201 N R N A N N A A P Q   Y C R O N G G R Q I   C S V S R A E R A A   G L N Y E I E A E K   L T P L A D N H Y L
251 L F R S N I G G T S   Y Y F S K K S A Y D   D G F G R A Y L G W   Q Y K N A R Q T A G   I L P F Y Q V Q L S
301 G S D G F D A K T K   R V N N R R L P P Y   M L A H G V G V Q L   S H T Y R P N P G W   Q F S V A L E H Y R
351 Q R Y R E Q D R A E   Y N N G R Q D G F Y   V S S A K R L G E S   A T V F G G W Q F V   R F V P K R E T V G
401 G A V N N A A Y R R   N G V Y A G W A Q E   W R Q L G G L N S R   V S A S Y A R R N Y   K G I A A F S T E A
451 Q R N R E W N V S L   A L S H D K L S Y K   G I V P A L N Y R F   G R T E S N V P Y A   K R R N S E V F V S
501 A D W R F *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  A T G T T G T A T T   T C A G A T A C G G   T T T T T T G G T T   G T T T G G T G T G   C G G C A G G T G T
51  T T C T G C C G C C   T A T G G G G C G G   A T G C G C C C G C   G A T T T T G G A T   G A C A A G G C A T
101 T G T T G C A G G T   G C A G C G G T C G   G T G T C G G A T A   A G T G G G C G G A   A T C G G A T T G G
151 A A A G T T G A C A   A T G A T G C C C C   G C G C G T G G T T   G A C G G G G A T T   T T T T G T T G G C
201 G C A T C C G A A A   A T G T T G G A A C   A T A G T T T G C G   C G A C G T G C T C   A A C G G C A A T C
251 A G G C G G A T T T   G A T C G C T T C G   T T G G C G G A T T   T G T A T G C C A A   G C T G C C G G A T
301 T A T G A C G C G G   T T T T G T A C G G   C A G G G C G C G G   G C T T T G C T G G   C G A A A T T G G C
351 G G G A A G G C C G   G C G G A G G C G G   T G G C G C G G T A   T C G G G A A C T G   C A C G G G G A A A
401 A T G C G G C A G A   C G A G C G G A T T   T T G C T G G A T T   T G G C G G C G G C   G G A G T T T G A C
451 G A T T T C C G G C   T G A A G T C G G C   A G A A A G G C A T   T T T G C C G A G G   C G G A A A A A T T
501 G G A T T T G C C G   G C G C C G G T T T   T G G A A A A T G T   G G G G C G T T T T   C G G A A A A A A G
551 C G G A G G G G C T   G A C G G G C T G G   C G T T T T T C G G   G C G G C A T C A G   T C C G G C G G T C

```

1350

	310	320	330	340	350	360
m935.pep	GSDGFDATKRVNNRRLPPYMLAHGVQVLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFDATKRVNNRRLPPYMLAHGVQVLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVSASYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVSASYARRNYKGVAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNVFYAKRRNSEVFVSADWRF					
a935	GRTESNVFYAKRRNSEVFVSADWRF					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGcgcgAACCA CCGcgcgcga AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCaccgT CGGCGTACAA AAAGTCATTA CCCTTACCA AAACCTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRONNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRONNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVNYIT VASLPRTA...

```

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

This corresponds to the amino acid sequence <SEQ ID 2880; ORF 936.a>:

m936/a936 95.3% identity in 128 aa overlap

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRTTGAQTTDDNVMALRIETT					
		:: :	:			
a936	MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAVGAKSAVDRTTGAQTTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLRONNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVNYIT					
a936	ARSYLRONNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVNYIT					
	70	80	90	100	110	120
m936.pep	VASLPRTA					

1352

|||||||
a936 VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
130 140 150 160 170 180

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

g936-1.seq

```

1  ATGAAACCCA AACACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGccgAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC STCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACAC TTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

g936-1.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVTILYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

m936-1.seq

```

1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51 CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 AACTTTGGAA CACATCCAAA GTCCGCGCCA CGCTGTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

m936-1.pep

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIV YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVTILYQNYV
201 QR*

```

m936-1/g936-1 95.5% identity in 202 aa overlap

	10	20	30	40	50	60
m936-1.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
	: : : : : : : : : :					
g936-1	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAKSVIDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936-1.pep	ARSYLRQNNQTKGYTPQISVVGYNRHLHLLGQVATEGEKQFVGQIARSEQAAAEGVYNYIT					
	: : : : : : : : :					
g936-1	ARSYLRQNNQTKGYTPQISVVGYNRHLHLLGQVATEGEKQFVGQIARSEQAAAEGVYNYIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m936-1.pep	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT					
	: : : : : : : : :					

1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180
              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following g partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGCGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTCTG
101 GCGCGAAATC CGCGCTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAAAACCACC ACCAAGGCT ACACGCCCCA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCCGCGAAG GCGTGTACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAACCGT CGGCGTACAA AAAGTCATCA CCCTTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTAAVLSLAL GGCVS AVVGG AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHL LLL GQVATEGEKQ
101 FVGQIARSEQ AEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

a936-1/m936-1 97.0% identity in 202 aa overlap

m936-1.pep      10      20      30      40      50      60
MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAASVDRRTTGAQTDDNVMALEIET
|||||
a936-1          10      20      30      40      50      60
MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAGVGAASVDRRTTGAQTDDNVMALEIET

m936-1.pep      70      80      90      100     110     120
ARSYLRQNNQTKGYTPQISVVGYNRHL LLL GQVATEGEKQFVGQIARSEQAAEGVYNYIT
|||||
a936-1          70      80      90      100     110     120
ARSYLRQNNQTKGYTPQISVVGYNRHL LLL GQVATEGEKQFVGQIARSEQAAEGVYNYIT

m936-1.pep      130     140     150     160     170     180
VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
|||||
a936-1          130     140     150     160     170     180
VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT

m936-1.pep      190     200
QKVSTTVGVQKVITLYQNYVQRX
|||||
a936-1          190     200
QKVSTTVGVQKVITLYQNYVQRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTTAgT ATTGTTAGC TTTGTGCCAT TATGTGTCCG
51 CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAT
101 GGAAactGGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
151 GCACTTGCCT CACCGGTTTA CATTCAGACC GGCTCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGACTGaccg GCAataccgA CATTTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAATCGgacg GCAACGGCAA

```

g937.pap

1 MKNILLVFVS FVPLCVRTDL PLNIEDIMTD KGKWKLETSL TYLNSENSRA
51 ALASPVYIQT GSASFIPVPT EIQENGSTND MLAGTLGLRY GLTGNTDIYG
101 SG SYLWHEER KLDGNGKTRN KRMSDISAGI SHTFLKDGKN PALIAFLEST
151 VYEKSNRKAS SGKSWLIGAT TYKAIDPIVL SLTAAAYRNG SKTSLDDVKY
201 KAGYWNMLNP NISFAANDRI SLTGGIQWLQ KQPDRIHGKK ESARNTSTYA
251 HF¹GAGFGFTK TAALNASARF NVSGQSSSEL KLGVOHTF*

m937.seq

seq	ATGAAGCGCA	TCTTTTGGCC	CGCCTTGCCC	GCCATCCTGC	CTTTATCCAC
51	TTATGCCGAC	CTGCCCTTGA	CGATTGAAGA	CATAATGACC	GACAAGGGAA
101	AA.TGGAAACT	GGAAACTTCC	CTTACCTACC	TGAACAGCGA	AAACAACCGC
151	GC.CGAACTTG	CCGCACCGGT	TTACATTCAA	ACCGGCGCAA	CCTCGTTTAT
201	CC.CCATTCCG	ACCGAAATCC	AAGAAAAACG	CAGCAATAAC	GATATGCTCG
251	TCGGCAGCGT	CGGTTTGGCG	TACggAATGA	CCGGGAATAC	CGACATTTTAC
301	GGCAGCGGCA	GCTATCTGTG	GCACGAAGAA	CGCAAACTCG	ACGGCAACAG
351	CA.AAACCCGC	AACAAACGGA	TGTCCGACGT	ATCCCTCGGC	ATCAGCCACA
401	CT.TTCCTTAA	AGACGACAAA	AACCCCGCCC	TAATCAGCTT	TCTTGAAGAG
451	ACGGTTTACG	AAAAATCGCG	CAACAAAGCA	TCGTCGGGAA	AATCCTGGGT
501	CA.TCGGCGCC	ACCACCTACA	AAGCCATAGC	TCCGATTGTC	CTTTCCTCTA
551	CCCGCGCCTA	CCGCATCAAC	GAGCAGAAAA	CCCTTTTCAGA	CGGCATCCGC
601	TACAAATCGG	GCAACTACCT	GCTGCTCAAC	CCCAACATCT	CATTTGCTGC
651	CAACGACAGA	ATCAGCCTGA	CCGGAGGCAT	CCAATGGCTG	GGCAGGCAGC
701	CCGACCGGAC	GGACGGCAAA	CGGGAATCCT	CCAGAAACAC	ATCCACCTAC
751	GCCCATTTTC	GCGCAGGTTT	CGGTTTCACC	AAAACCACGG	CTTTAAACGC
801	ATCCGCAAGT	TTCACAGTTT	CAGGGCAAAG	CAGTTCGGAA	CTGAAATTTC
851	CGGTACAGCA	TACATTTTAA			

m937.pap..

1 MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
51 AELAAPVYIQ TGATSFPIPI TEIQENGSTNT DMLVGTGLRL YGLTGNTDIY
101 GSGSYLWHEE RKLDSGSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLSDGIR
201 YKSGNYLLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGYGFET KTTALNASAR FNVSGQSSSE LKFPVQHTF*

Homology with a predicted ORF from *N. gonorrhoeae*

g937/m937

	10	20	30	40	50	59
g937.pep	MKNILL-VFVSFVPLCVRTDLPLNIEDIMTDKGKWKLETSLTYLNSENSRAALASPVIYIQ					
m937	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVIYIQ					
	10	20	30	40	50	60
	60	70	80	90	100	110
q937.pep	TGSASFIPVPTEIQENGSNNTDMLAGTLGLRYGLTGNTDIYGSGSYLWHEERKLGDGNGKTR					

m937	120	130	140	150	160	170	179
g937.pep	NKRMSDISAGISHTFLKDGKNPALIAFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV						
m937	130	140	150	160	170	180	
g937.pep	180	190	200	210	220	230	239
m937	190	200	210	220	230	240	
g937.pep	240	250	260	270	280	289	
m937	250	260	270	280			

```

a937.seq
1 ATGAAGCGCA TCTTTTGGCC CGCTTGCCC GCCATCTGCG CTTTATCCGC
51 TTATGCCGCA CTGCCCTTGA CGATTGAAGA CATATAGACC GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACGCGA AAACAACCGC
151 GCCGAACTTG CCGCAGCGGT TTACATCCAA ACCGCGCGAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCAGCGT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACGG
351 CAAAACCGGA AACAAACGGA TGTCCGAGT ATCCTCTGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCTGCCC TTATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCGTCGTC CTCTCATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCCAATATAT CTTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GCGAAGCAGC
701 CGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTCG CGCGAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGACGCT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTGG
851 GCGTACAGCA TACGTTTTAA

```

a937.pep

1	MKRIFLPALP	AILPLSAYAD	LPLTIEDIMT	DKGKWKLETS	ITYLNSENNRR
51	AELAAPVYIQ	TGATSFIPIP	TEIQENGST	DMLVGTGLRL	YGLTGNTDIY
101	SGSGYLWHEE	RKLDGNGKTR	NKRMSDVSIG	ISHTFLKDDK	NPALISFLES
151	TVYEKSRNKA	SSGKSWLIGA	TTYKAIDPVV	LSLTAAYRIN	GSKTLLSNTK
201	YKAGNYWMLN	PNISFAANDR	ISLTGGIQWL	GKQPDRLDGK	KESARNTSTY
251	AHEGAGFGFT	KTTALNASAR	FNVSGQSSSE	LKFGVQHTF*	

```

      10      20      30      40      50      60
m937.pep  MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
          |||||:|||||
a937      MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
          10      20      30      40      50      60

      70      80      90      100     110     120
m937.pep  TGATSFIPPIPTIEQENGSNNTDMLVGTGLGRLYGLTGNTDIYGGSYLWHEERKLDGNSKTR
          |||||:|||||
a937      TGATSFIPPIPTIEQENGSNNTDMLVGTGLGRLYGLTGNTDIYGGSYLWHEERKLDGNGKTR
          70      80      90      100     110     120

```

1356

	130	140	150	160	170	180
m937.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a937	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTTALNASAREFNVSGQSSSELKFGVQHTFX					
a937	KESARNTSTYAHFGAGFGFTKTTALNASAREFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCCTCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATCCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

1  MKRLTLIAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATCCGG
201 CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCCG
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CGGGTATGCC GGGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTCAGCATC AGGCATATAT
501 TGTGAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGGAAGATAT TGCAAACCGT ATGTCTGAAG AAGATTTGAA AGCGGTCGCC
601 AACTTTATCC AAGGTTTGCG TTAA
```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

1  MKRLTLIAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTGSAAV MKPVVMNLS QDILNVSAFY
101 AKQPKSGEA NPKNPELGA KIYRGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAIVEQ MNAYKSGQRK NTIMEDIANR MSEEDLKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLIAFVLAAGAVSASP	KADVEKGKQVAATVCAACHA	ADGNSGIAMY	PRLAAQHTAY		
a939	MKRLTLIAFVLAAGAVSASP	KADVEKGKQVAATVCAACHA	ADGNSGIAMY	PRLAAQHTAY		

1357

```

              10      20      30      40      50      60
              70
m939.p<ep    IYHQTIGIRDVNAP
              |||||
a939         IYHQTIGIRDGKRTHGSAAVMKPVVMNLSDDILNVSIFYAKQPKSGEANPKENPELGA
              70      80      90     100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1  ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGC CGCCGGC GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTC AAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCG TGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAA AGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAA AAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAA GGCAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.pep
1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVOKSAQG SCGASKSAEG
51 SCGAASKAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGC CGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTC ATAAATC CGCCCATGCG TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCG TGCGGCG CGGCTGTTT TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAA ATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSANG SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

```

              10      20      30      40      50
m950.pep    MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSANGSCGASKSAEGSCGA-----
              |||||
g950         MNKNIAAALAGALSLSLAAGAVAANKPASNATGVOKSAQSGCGASKSAEGSCGASKSAEG
              10      20      30      40      50      60

              60      70      80      90     100
m950.pep    -----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              |||||
g950         SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90     100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGCG TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGTTT TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

1358

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKS AHG SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

```

              10      20      30      40      50      60
a950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKS AHG SCGASKSAEGSCGAAGSKAG
              |||||
m950           MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKS AHG SCGASKSAEGSCGAAGSKAG
              10      20      30      40      50      60

              70      80      90      100
a950.pep      EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
              |||||
m950           EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              70      80      90      100
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
1  ATGATTATGT TACCCGCCCG TTCACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGACAGGCGT ATGCTGCCCG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201 CAGGGTGTTT ACGCTGTTGG GCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTTGGAACG CACAAAATCC
301 CCCGAAGTCG CCGAACGCGC CTTGGAAATG GCCGTGTGCG TGAACGCGTT
351 TGAACAGGCG GAAATGATTT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG GCGGGGTGGC TCGGGAACGT ATTGAGGGAA
451 GGGGGAATC AGCATCTGGA CGGGTGGAA GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCGAGG TATTTTGCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GTGGCTCAA AAAGCATCGA AAGCGGTTCG CCGTGGCGCG
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CGGTGTTCCG
651 CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAATA TTGCCCCCA CTTTAATGAC GTTGCGTCTG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAC CTTTCGGCCG TCTGGCAGGA AATGGAATT ATGAATCTGG
851 TTTCCTCGC TAAGCCGGAT GATGCCATG CGCGTTTGAA CGTGCTGTTG
901 GAACACAACC CGAATGCAAA CCGTATATAT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAA GAAGGTGCGT CCGTTATCGA CCGGTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGTTGAA
1101 AAAAGTGTC GCGCCGGAAT ACCTGTTTCA CAAAGGCGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCGGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGCGGA AACTTCCCGA ACAGCAGGGG CCGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACCTTC GCGGCGGGA
1351 AGCACGGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTACGA
1401 ACAGTTCCGC AAACGGGGAA AATGATTGC CGACCTGAA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAAATC AACC CGGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCCCGAAGTT GCCGCCATT TGGGCGAAGT
1701 GTTGTGGGCA TTGGGCGAAC GCGATCAGGC GGTGACGTA TGGACGACGG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GCGGGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
1  MIMLPARFTI LSVLAAALLA GOAYAAGAAD VELPKEVGKV LRKHRRYSEE
```

```

51  EIKNERARLA AVGERVNRVF TLLGGETALO KQOAGTALAT YMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMIYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNQOHLDDLE EVLAQSDDDVQ KRRIFLLLVQ AAVQGGVVAQ KASKAVRRRA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL ORLAKLDEI LPPTLMTLRL
251 TARKYPEILD GFFEQTDTQN LSAVWOEMEI MNLVSLRKPD DAYARLNVLL
301 EHNENANLYI QAAILAANRK EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLKKVS APEYLFDKGV LAAAAAELD GGRAALRQIG
401 RVRKLPQQG RYFTADNLSK IQMLALSCLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA RSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQYAYOI NPDDTAVNDS IGWAYYLLKGD AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

m951.seq

```

1  ATGATTATGT TACCTAACCG TTTCAAAATG TTAAGTGTGT TGACGGCAAC
51  CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCGGTGCG GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTCA GAAAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTTGCGGCAG TGGGCGAGCG
201 GGTTAATCAG ATATTACGT TGCTGGGAGG GAAACCCGCC TTGCAAAGG
251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCCGA ACGCGCCTTG GAAATGGCCG TGTCGCTGAA
351 CGCGTTTGAA CAGGCGGAAA TGATTATCA GAAATGGCCG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AAACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAAGAG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
501 GCGCGGACGAA GGACAGAACC GCAGGCTGTT TTTATTGTTG GCACAGCCG
551 CCGTGCAACA GACGGGTTG GCGCAAAAAG CATCGAAAGC GGTTCGCCGC
601 CCGGCGTTGA AATATGAACA TCTGCCGAA GCGGCGGTTG CCGATGTGGT
651 GTTCAGCGTA CAGGACGCG AAAAGGAAA GGCATCGGA GCTTTGCAGC
701 GTTTGGCGAA GCTCGATACG GAAATATTGC CCCCACCTT AATGACGTTG
751 CGTCTGACTG CACGCAATA TCCCGAATA CTCGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTTT CGGCCGCTG GCAGGAATG GAAATTATGA
851 ATCTGGTTTC CCTGCACAGG CTGGATGATG CCTATGCCG TTTGAACGTG
901 CTGTTGGAAC GCAATCCGAA TGCAGACCTG TATATTCAGG CAGCGATATT
951 GGCGGCAAAC CGAAAAGAAG GTGCTCCGT TATCGACGGC TACGCCGAAA
1001 AGGCATACGG CAGGGGGACG GAGGAACAGC GGAGCAGGGC GCGGCTAACG
1051 GCGGCGATGA TGTATGCCGA CCGCAGGGAT TACGCCAAGG TCAGGCAGTG
1101 GCTGAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CGGCTGCGGC GGCTGTCGAG TTGGACGGCG GCAGGGCGGC TTTGCGGCAG
1201 ATCGGCAGGG TGCGGAAACT TCCCGAACAG CAGGGGCGGT ATTTTACGGC
1251 AGACAATTG TCCAAAATAC AGATGCTCGC CCTGTCGAAG CTGCCCGATA
1301 AACGGGAGGC TTTGAGGGG TTGGACAAGA TTATCGAAAA ACCGCTGCCC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGTACAGC GGTCAAGTGT
1401 TTACGATCGG CTGGCAAGC GGAATAAAT GATTTCAGAT CTTGAAAGGG
1451 CGTTACGGCT TGCACCCGAT AACGCTCAGA TTATGAATA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCCAA ACGTTTGAC GAAGGTTTCG CCCTGCTTCA
1551 GACGGCATAC CAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGGCGTA TTACCTGAAA GGCGACGCGG AAAGCGCGCT GCCGTATCTG
1651 CCGTATTCGT TTGAAAACGA CCCCAGAGCC GAAGTTGCCG CCCATTGCGG
1701 CGAAGTGTG TGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 CGCAGGCGGC ACACCTTACG GGAGACAAGA AAATATGGCG GGAACGCTC
1801 AAACGTCACG GCATCGCATT GCCCAACCT TCCGAAAAC CTCGGAAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

m951.pep

```

1  MIMLPNRFKM LTVLTATLIA GQVSAAGGGA GDMKQPEVG KVFRKQORYS
51  EEEIKNERAR LAAVGERVNQ IFTLLGETA LQKQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIYQKWR QIEPIPGKAQ KRAGWLRNVL
151 RERGNQHLDG LEEVLAQADE GQNRVFLLL AQAAVQDGL AQKASKAVRR
201 AALKYEHLPE AAVADVFSV QGREKEKAIG ALQRLAKLDT EILPPTLMTL
251 RLTAARKYPEI LDGFFEQTDT QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAILAAN RKEGASVIDG YAEKAYGRGT EEQSRRAALT
351 AAMMYADRRD YAKVRQWLKK VSAPEYLFDK GVLAATAAVE LDGGRALRQ
401 IGRVRKLPQO QGRYFTADNL SKIQMLALS LDPKREALRG LDKIIEKPPA
451 GSNTELQAEA LVQRSVYDR LGKRKMMISD LERAFRLAPD NAQIMNNLGY
501 SLLTDSKRLD EGFALLQYAY QINPDDTAVN DSIWAYYLLK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDQAV DVWTQAAHLT GDKKIWRETL
601 KRHGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

1360

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

	10	20	30	40	50	60
m951.pep	MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVGVFRKQORYSEEEIKNERAR					
g951	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGVKLRKHRRYSEEEIKNERAR					
	10	20	30	40	50	
	70	80	90	100	110	120
m951.pep	LAAVGERVNIQFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
g951	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
	60	70	80	90	100	110
	130	140	150	160	170	180
m951.pep	QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLGLEEVLAQADEGQNRVFLLL					
g951	QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLGLEEVLAQSDDVQKRIFLL					
	120	130	140	150	160	170
	190	200	210	220	230	240
m951.pep	AQAAVQQDGLAQKASKAVRRAALKYEHLPAAVADVFSVQGREKEKAIGALQRLAKLDT					
g951	VQAAVQQGGVAQKASKAVRRAALKYEHLPAAVADVFGVQGREKEKAIEALQRLAKLDT					
	180	190	200	210	220	230
	250	260	270	280	290	300
m951.pep	EILPPTLMTLRLTARKYPEILDGFEQTDTONLSAVWQEMEIMNLVSLHRLDDAYARLNV					
g951	EILPPTLMTLRLTARKYPEILDGFEQTDTONLSAVWQEMEIMNLVSLRKPDDAYARLNV					
	240	250	260	270	280	290
	310	320	330	340	350	360
m951.pep	LLERNPNADLYIQAILAANRKEGASVIDGYAEKAYGRGTEEQRSRAALTAAMMYADRRD					
g951	LLEHNPANLYIQAILAANRKEGASVIDGYAEKAYGRGTGEQGRAMTAAMIYADRRD					
	300	310	320	330	340	350
	370	380	390	400	410	420
m951.pep	YAKVRQWLKKVSAPEYLFDKGVLAATAAELDGGRAALRQIGRVKRLPEQQGRYFTADNL					
g951	YAKVRQWLKKVSAPEYLFDKGVLAATAAELDGGRAALRQIGRVKRLPEQQGRYFTADNL					
	360	370	380	390	400	410
	430	440	450	460	470	480
m951.pep	SKIQMLALSCLPKDREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD					
g951	SKIQMLALSCLPKDREALIGLNIIAKLSAAGSTEPLAEALAQRSIIYEQFGKRKMIAD					
	420	430	440	450	460	470
	490	500	510	520	530	540
m951.pep	LERAFRLAPDNAQIMNNGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	LETALKLTPDNAQIMNNGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
	480	490	500	510	520	530
	550	560	570	580	590	600
m951.pep	GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL					
g951	GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWTQAAHLRGDKKIWRETL					
	540	550	560	570	580	590
	610					
m951.pep	KRHGIALPQPSRKPRK					
g951	KRYGIALPEPSRKPRKX					
	600	610				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:

```
a951.seq
1  ATGTTACCCG CCGTTTCAC CATTATCT GTGCTCGCGG CAGCCCTGCT
51  TGC CGGGCAG GCGTATGCCG CCGCGCGCGC GGATGCGAAG CCGCCGAAGG
101 AAG TCGGAAA GGTTTTCAGA AAGCAGCAGC GTTACAGCGA GGAAGAAATC
151 AAA AACGAAC GCGCAGCGCT TCGGCGAGTG GCGGAGCGGG TTAATCAGAT
201 ATT TACGTTG CTGGGAGGGG AAACCGCCTT GCAAAAGGGG CAGGCGGGAA
251 CGG CTCTGGC AACCTATATG CTGATGTTGG AACGCACAAA ATCCCCCGAA
301 GTC GCCGAAC GCGCCTTGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
351 GGC GGAATG ATTTATCAGA AATGGCGGCA GATTGAGCCT ATACCGGGTA
401 AGG CGCAAAA ACGGGCGGGG TGGCTGCGGA ACGTGCTGAG GGAAGAGGA
451 AAT CAGCATC TAGACGACT GGAAGAAGTG CTGGCTCAGG CGGACGAAGG
501 ACA GAACCGC AGGGTGT TATTGTTGGC ACAAGCCGCC GTGCAACAGG
551 ACG GGTGGC GCAAAAAGCA TCGAAAGCGG TTCGCCGCGC GGCCTTGAGA
601 TAT GAACATC TGCCCGAAGC GCGGTTGTC GATGTGGTGT TCAGCGTACA
651 GGG ACGCGAA AAGGAAAAGG CAATCGGAGC TTGCGAGCGT TTGGCGAAGC
701 TCG ATACGGA AATATTGCCC CCCACTTTAA TGACGTTGCG TCTGACTGCA
751 CGC AATATC CCGAAATCT CGACGGCTT TCGAGCAGA CAGACACCCA
801 AAA CCTTTCG GCGCTCTGGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
851 TGC ACAGGCT GGATGATGCC TATGCGCGT TGAACGTGCT GTTGGAAACG
901 AAT CCGAATG CAGACCTGTA TATTCAGGCA GCGATATTGG CGGCAAAACG
951 AAA AGAAGGT GCTTCCGTTA TCGACGGCTA CGCCGAAAAG GCATACGGCA
1001 GGG GGCAGCG GGAACAGCGG GCGAGGCGG CAATGACGGC GCGCATGATA
1051 TAT GCCGACC GAAGGGATTA CACCAAAGTC AGGCAGTGGT TGAAAAAAGT
1101 GTC CGCGCCG GAATACCTGT TCGACAAAGG TGTGCTGGCG GCTGCGCGCG
1151 CTG TCGAGTT GGACGCGCGC AGGGCGGCTT TCGGCGAGAT CGGCAGGGTG
1201 CGG AACTTC CCGAACAGCA GGGCGGTAT TTTACGGCAG ACAATTGTG
1251 CAA AATACAG ATGTTGCGCC TGTCGAAGCT GCCCGACAAA CGGAGGCTT
1301 TGA GGGGTT GGACAAGATT ATCGAAAAAC CGCTGCCCG CAGTAATACA
1351 GAG TTACAG CAGAGGCATT GGTACAGCGG TCAGTTGTTT ACGATCGGCT
1401 TGG CAAGCGG AAAAAATGA TTTCAGATCT TGAAAGGGCG TTCAGGCTTG
1451 CAC CCGATAA CGCTCAGAT ATGAATAATC TGGGCTACAG CTGCTTTCC
1501 GAT TCCAAAC GTTTGGACGA AGGCTTCGCC CTGCTTCAGA CGGCATACCA
1551 AAT CAACCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
1601 ACC TGAAGG CGACGCGGAA AGCGCGTGC CGTATCTCG GTATTGTTT
1651 GAA AACGACC CCGAGCCCGA AGTTGCCGCC CATTGGGCG AAGTGTGTG
1701 GGC ATTGGGC GAACGCGATC AGGCGGTTGA CGTATGGACG CAGGCGGCAC
1751 ACC TTACGGG AGACAAGAAA ATATGGCGGG AAACGCTCAA ACGTCACGGC
1801 ATCGCATTGC CCCAACCTTC CCGAAACCT CCGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

```
a951.pep
1  MLPARFTILS VLAAALLAGQ AYAAGAADAK PPKEVGKVFR KQORYSEEEI
51  KNERARLAHV GERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSPE
101 VAERALEMAV SLNAFEQAEM IYOKWROIEP IPGKAQKRAK WLRNVLRERG
151 NQHL DGLLEV LAQADEGQNR RVFLLAQAA VQDGLAQKA SKAVRRAALR
201 YEHLPEAAVA DVVFSVQGRE KEKAIGALQR LAKLDTEILP PTLMLRLTA
251 RKYPEILDGF FEQTDTONLS AVWQEMEIMN LVSLHRLDDA YARLNVLLER
301 NPNADLYIQ AILANRKEG ASVIDGYAEK AYGRGTGEQR GRAAMTAAMI
351 YADRRDYTKV RQWLKKSAP EYLFDKGVLA AAAVELDGG RAALRQIGRV
401 RKLPEQGRY FTADNLSKI MFALSKLPDK REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYSLLS
501 DSKRLDEGFA LLQYAYQINP DDTAVNDSIG WAYYLGDAE SALPYLRYSF
551 ENDPEPEVAA HLGEVLWALG ERDQAVDVT QAAHLTGDKK IWRETLKRHG
600 IALPQPSRKP RK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```
a951.pep      10      20      30      40      50
               MLPARFTILSVLAAALLAGQAYAG--AADAKPPKEVGKVFRKQORYSEEEIKNERAR
               ||| || :|:|:|:|:|:|:| ||| :| | | | | | | | | | | | | | | | | |
m951          10      20      30      40      50      60
               MIMLPNRFKMLTTLTATLIAGQVSAAGGGAGDMKQPKVEGKVFRKQORYSEEEIKNERAR
               ||| || :|:|:|:|:|:|:| ||| :| | | | | | | | | | | | | | | | | |
a951.pep      60      70      80      90     100     110
               LAAVGERVNQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
```

q952.seq (partial)

1	TTGTCTTATC	GTTTGAATGC	TGCACCGATG	TTTAACGATA	ATCCTGTTGT
51	TTACGGAAAA	ATCAAATTGC	AGAGTTGGAA	AGCGCGGCGG	GATTTCARAT
101	TTGTAAGACA	GGATTTGGAT	TTTTCTCTCG	GGGCGGCTTC	GGTGGCGACG
151	CTTTTGAACA	ATTTTTCACG	GCAAAAGCTG	ACGGAAGAAG	AAGTGTGGGA
201	AAAAC TG GGT	AAGGAACAGA	TGCGCGCGTC	GTTTGAGGAT	ATGCGGCGCA
251	TTATGCCCGA	TTTGGGTTTT	GAGCGGAAAG	GCTATGCCCT	GTC TTTCGAA
301	CAGCTCGCGC	AGTTGAAAAA	CCCCGTCATC	GTGTATCTGA	AATACCGCGA
351	AGACGACCAT	TTTTTCGGAT	TCCGCGGAGT	GGATGGCAAT	ACGGTTTTCG
401	TTGCCGACCC	GTGCGCGGGT	CATGTTTCGA	TGAGCAGGGC	GCAGTTTTTG
451	GAGGCTTGGC	AAACCCGTGA	GGGAAATTTG	GCAGGCAAAA	TTTTGGCGCT
501	CTGCGCCGAA	AAAGCGGAGG	CGATTTCAAA	TAAATTTGTT	TTACACATCT
551	ATCCCAAGCG	GCAGACGGAG	TTTTGCAGTC	GACAGGTA	ATGTGCGCGT

601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)

```

1  ..LSYRLNAAPM FNDNPVYVGK IKLQSWKARR DFNIVKQDLD FSCGAASVAT
51  LNNFYGQKL TEEVLEKLG KEQMRASFED MRRIMPD LGF EAKGYALSFE
101 QLAQLKIPVI VYLKVRKDDH FSVLRGVDGN TVLLADPSPG HVSMSRAQFL
151 EAWQTREGNL AGKILAVVPK KAEAISNKL FTHHPKQTE FAVGQVKWWR
201 AY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq

```

1  ATGATGAAGT TCAAATATGT TTTCTGTTG GCGTGTGTTG TCGTTTCTTT
51  ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTGTGTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG CGCGCGCGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATTT TTCCTGTGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT CGCGCGCATT
301 ATGCTGTGAT TGGGTTTGA GCGCAAGGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCGCAG TTGAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGGCA TGTTC AATG AGCAGGGCGC AGTTTTTGA
501 TCGTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCTGTCA
551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
601 CCAAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep

```

1  MMKFKYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKARRDFNI
51  VKQDLDFSCG AASVATLLNN FYGQTLTEE VLKLDKEQM RASFEDMRRI
101 MPDLGF EAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTOH
201 PKRQTEFTVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952: 92.5% identity in 201 aa overlap

```

                                10      20      30      40
g952.pep                      LSYRLNAAPMFNDNPVVYVGKIKLQSWKARRDFNIVKQDLD FSCG
                                |||
m952                          MMKFKYVFLACVVVLSYRLNAAPMFNDNPVVYVGKIKVQSWKARRDFNIVKQDLD FSCG
                                10      20      30      40      50      60

                                50      60      70      80      90      100
g952.pep                      AASVATLLNNFYGQKL TEEVLEKLGKEQMRASFEDMRRIMPD LGFEAKGYALSFEQLAQ
                                |||
m952                          AASVATLLNNFYGQTL TEEVLEKLDKEQMRASFEDMRRIMPD LGFEAKGYALSFEQLAQ
                                70      80      90      100      110      120

                                110     120     130     140     150     160
g952.pep                      LKIPVIVYLKVRKDDHFSVLRGVDGNTVLLADPSPGHVSM SRAQFLEAWQTREGNLAGKI
                                |||
m952                          LKIPVIVYLKVRKDDHFSVLRGIDGNTVLLADPSLGHVSM SRAQFLDAWQTREGNLAGKI
                                130     140     150     160     170     180

                                170     180     190     200
g952.pep                      LAVVPKKA E AISNKLFFTHHPKQTEFAVGQVKWWRAYX
                                |||
m952                          LAVIPKKAETISNKLFFTOHPKQTEFTVGQIRQARAE
                                190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq

```

1  ATGATGAAGT TCAAATATGT TTTCTGTTG GCGTGTGTTG TCGTTTCTTT

```

a952.pep

1	MMKFYKYVFL	ACVVVLSLSYR	LNAAPMFNDN	PVYVGKIKVQ	SWKERRDFNI
51	VKQDLDLDFSCG	AASVATLLNN	FYGQTLTEEE	VLKKLDKEQM	RASFEDMRRI
101	MPDLGFEAKG	YALSFEQLAQ	LKIPVIVYLK	YRKDDHFSVL	RGIDGNTVLL
151	ADPSLGHVMS	SRAQFXDAWQ	TREGNLAGIK	LAVVPKKAET	ISNKLFFTHH
201	PKRQTEFVAG	QTRQARAE*			

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

```

a952/m952      97.7% identity in 218 aa overlap

              10           20           30           40           50           60
a952.pep      MMKFKYVPELLACVVVSLSYRLNAAPMFNDNPVVYGKIKVQSWKERRDFNIVKQDLDFSCG
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m952           MMKFKYVPELLACVVVSLSYRLNAAPMFNDNPVVYGKIKVQSWKARRDFNIVKQDLDFSCG
              10           20           30           40           50           60

              70           80           90          100          110          120
a952.pep      AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m952           AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ
              70           80           90          100          110          120

              130          140          150          160          170          180
a952.pep      LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVMSRAQFXDAWQTREGNLAGKI
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m952           LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVMSRAQFLDAWQTREGNLAGKI
              130          140          150          160          170          180

              190          200          210          219
a952.pep      LAVVPKKAETISNKLFFTHHPKQTEFVAGQIRQARAEX
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m952           LAVIPKKAETISNKLFFTQHPKQTEFTVAGQIRQARAE
              190          200          210

```

g953.seq

1	ATGAAAAAAA	TCATCTTCGC	CGCGCTCGCA	GCGGCAGCGC	TCGGCACTGC
51	CTCCGCCACC	TACAAAGTGG	ACGAATATCA	CGCCAACCTG	CGTTTCGCCA
101	TCGCACCACT	CAACACCATT	ACCAACGTGC	GCGGTTTTTA	CGGTCGTACC
151	GGTTCCGTCG	AGTTTCATCA	AGCAAAACGC	GACGGCAAAA	TCGACATCAC
201	CATTCCCCTC	GCCAACTTGC	AAAGCGGTTT	GCAACCCCTC	ACCGCCACCC
251	TGAAATCCCG	GCACATCTTC	GATGCCGCTC	AATATCCGGA	CATCGCTGCA
301	GTTTCCACA	CAATCAACTT	CACACGCAAA	AAACTGTGTT	CCGTGTACGG
351	CAACCTGACC	ATGCGCGGCA	AAACCGCCCC	CGTCAAACCT	AAAGCCGAAA
401	AATTCAACTG	CTACCAAAGC	CCGATGGCGG	AAACCGAAGT	TTGCGGCGGC
451	GACTTCAGCA	CCACCATCGA	CCGCACCAAA	TGGGGCGTGG	ACTACCTCGT
501	TACGCGCGGT	ATGACCAAAA	ACGTCCGCAT	CGACATCCAA	ATCGAAGCTG
551	CAAAACAATA	A			

1	MKKT	IFAAAL	AAAVGTASAT	YKVDEYHANV	RFAIDHFNST	TNVGGFFYGLT
51	GSVE	FDQAKR	DKGIDITIPV	ANLQSGSQPF	TGHLKXSADIF	DAAQYDPDIRF
101	VSTK	FNFNKG	DLGVSDGNLT	MRGKTAPVKL	KAEFKNCYQS	PMAETEVCGG
151	FDST	TIDRTK	WGVLDLVNAG	MTKNVRIDIQ	IEAAKQ*	

1	ATGA	AAAAA	TCATCTTCGC	CGCACTCGCA	GCCGCCGCCA	TCAGTACTGC
51	CTCC	CGCCCC	ACCTACAAAG	TGGACGAATA	TCACGCCAAC	GCCCGTTTCG
101	CCAT	CGACCA	TTTCAACACC	AGCACCACG	TCGGCGGTTT	TTACCGTCTG
151	ACC	GTTCCG	TCGAGTTCGA	CCAAGCAACA	GCCGACGGTA	AAATCGCATC
201	CACC	ATCCCC	ATTGCCAACC	TGCAAAGCGG	TTCGCAACAC	TTTACCGACC
251	ACCT	GAAATC	AGCCGACATC	TTCGATGCCG	CCCAATATCC	GGACATCTCGC
301	TTTG	TTTCCA	CCAAATTCAA	CTTCAACGGC	AGAAATCTGG	TTTCCGTTGA
351	CGG	AACCTG	ACCATGCACG	GCAAAACCGA	CCCCGTCAA	CTCAAAGCCG
401	AAAA	ATTCAA	CTGCTACCAA	AGCCCGATGG	AGAAAACCGA	AGTTTGTGGC
451	GCGC	ACTTCA	GACCAACCAT	CGACCGCACC	AAATGGGGCA	TGACTACCT
501	CGTT	AACGTT	GGTAGACCA	AAAGCGTCCG	CATCGACATC	CAAATCGAGG
551	CAGC	CAACA	ATAA			

1	MKKI IFAALA	AAAISTASAA	TYKVDEYHAN	ARFAIDHFNT	STNVGGFYGL
51	TGSV EDFQAK	RDGKIDITIP	IANLQSSQSH	FTDHLKSADI	FDDAAQYPPDIR
101	FVST KFNFG	KKLVSDVGNL	TMHGKTAAPVK	LKAEKFNICYQ	SPMEKTEVCG
151	GDFS TTIDRT	KWGMVDYLVN	GMTKSVRIDP	QIEAAKQ*	

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

```

10      20      30      40      50      60
m953.pep  MKKIIIFAAALAAAISTASAAITYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK
          | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g953      MKKIIIFAAALAAAVGTASA-TYKVDEYHANVRFADHFNTSTNVGGFYGLTGSVEFDQAK
          10      20      30      40      50

          70      80      90      100      110      120
m953.pep  RDGKIDITTIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNKKLVSDGNL
          | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g953      RDGKIDITIPVANLQSGSQPFTGHLKSADIFDAAQYPDIRFVSTKFNFNKKLVSDGNL
          60      70      80      90      100      110

          130      140      150      160      170      180
m953.pep  TMHGKTAPVKLKAKEFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVMGTMKSVRID
          | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g953      TMRGKTAPVKLKAKEFNCYQSPMAETEVCGGDFSTTIDRTKWGVDYLVNAGMTKNVRIDI
          120      130      140      150      160      170

m953.pep  QIEAAKQX
          | | | | |
g953      QIEAAKQX
          180

```

1	ATGAAAAAAA	TCATCATCGC	CGCGCTCGCA	GCAGCCGCCA	TCGGCACTGC
51	CTCCGCGGCC	ACCTTACAAAG	TGGACGAATA	TCACGCGCAAC	GCCCGTTTCT
101	CTATCGACCA	TTTCAACACC	AGCAACCAAC	TCGGCGGTTT	TTACGGTCTG
151	ACCGGTTCCG	TTGAGTTCGA	CCAAGCAAAA	CGCGACGGTA	AAATCGCATC
201	CACCATCCCC	GTTGCCAAC	TGCAAGACGG	TCGCAACAC	TTTACCGACC
251	ACCTGAAATC	AGCGGCATC	TTTCATGCCG	CCCAATATCC	GGACATCCGC
301	TTTGTTTCCA	CCAAATTCAA	CTTCAACGGC	AAAAAATCGG	TTTTCCGTGA

1366

```

351 CCGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGCGGC
451 GGC GACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGT TAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
1 MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
51 TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYDIR
101 FVSTKFNENG KKLVSVDGNL TMHGKTAPVK LKAKEFNCYQ SPMLKTEVCG
151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

```

a953/m953      97.3% identity in 187 aa overlap

a953.pep      10      20      30      40      50      60
MKKIIIAALAAAIGTASAAATYKVDEYHANAREFSIDHFNTSTNVGGFYGLTGSVEFDQAK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953          10      20      30      40      50      60
MKKIIIFAALAAAISTASAAATYKVDEYHANAREFAIDHFNTSTNVGGFYGLTGSVEFDQAK

a953.pep      70      80      90      100     110     120
RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYDIRFVSTKFNENGKKLVSDGNL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953          70      80      90      100     110     120
RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYDIRFVSTKFNENGKKLVSDGNL

a953.pep      130     140     150     160     170     180
TMHGKTAPVKLKAKEFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953          130     140     150     160     170     180
TMHGKTAPVKLKAKEFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI

a953.pep      QIEAAKQX
|||||
m953          QIEAAKQX

```

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
1 ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
51 GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTGCCAATA
101 AATATCAATT TGCAGATGAG AACAGGCTT TTTATTTTGA ACGCGCCGCC
151 CGTTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT
201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
251 TTAICTCAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
301 TACCGCGTCT GCAAACAGGC TCGCAAGAT GCAGAAATCC TGATGAAGAG
351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTTAGAT AAGGAAAGTT
401 ATCAAAATTA CCGAAAATCA ATGCAAGAAT GCCGTAAAC AATAACGGAA
451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
1 MKKFYFVLLA LGLAACGQEQ SQKADAEQYF FANKYQFADE KQAFYFERAA
51 RFRVLQQGLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDP
101 YRVCKQAAQD AEILMKSMVT SGGGGTTDLN KESYQNYRKS MQECKRTITE
151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

g957.seq (partial)

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTC CGTTGCA GTCGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCCAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTT CGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CCGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG AGGGATGAAG GCGAACAGTC TTGTGGTCCG
801 cta t gatgcg gacggtctgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaa aaaaacc ccaaagtgtc gaattattatt tgaaaaacgg aaatcttttt
901 att gccaat cttcgacggt aaccttgaaa acggtatggcg taacggcgga
951 tat gcaaacc tatcatgcgc aacaacggt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

g957.pep (partial)

```

1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLEQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MREILMPRGMK ANSLVVG YDA DGLPQKVYWS VDNGKKPQSV EYLLKNGNLF
301 IAQSSTVTILK TDGVTADMQT YHAQQTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

m957.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCTT TGCCGGAAGT GTGGATGACG
251 TCCGTTTGA GTCGGAAGA GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCCAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTT CGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CCGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG AGGGATGAAG GCGAACAGTC TTGTGGTCCG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACC CAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAAGAC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAATAAT TGGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGCGCAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTCTCTA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

m957.pep

```

1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLEQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
```

1368

251 MREIMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYILKNGNLF
 301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
 351 LENLEKEVRR YAEAAARRSG GRRDLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

	10	20	30	40	50	60
g957.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNFVAKLARLFRNA					
m957	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKPNFVAKLARLFRNA					
	10	20	30	40	50	60
g957.pep	70	80	90	100	110	120
m957	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
g957.pep	130	140	150	160	170	180
m957	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLNRDRPFSVNVYGGTAVHGENYETTGEYRVV					
	130	140	150	160	170	180
g957.pep	190	200	210	220	230	240
m957	WQPDGVSFDAAGRKGIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVDFFREESNRIAS					
	190	200	210	220	230	240
g957.pep	250	260	270	280	290	300
m957	DSRDYVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSVDNGKKRQSF EYILKNGNLF					
	250	260	270	280	290	300
g957.pep	310	320	330			
m957	IAQSSTVTLKTDGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
m957	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

1	ATGTTTAAAA	AATTCAAACC	GGTACTGTTG	TCATTTTTTG	CACTTGTATT
51	TGCCCTTTGG	CTGGGAACGG	GTATTGCCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAAATCCGA	ATGCTTTTGT	GGCGAAACTT
151	GCCCAGCCTGT	TCCGAAATGC	CGACAGGGCG	GTTGTCATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TTGCCGGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCGGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAAACG	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTTGATGC	GTCGGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCTCGGGT	GTTATCAGAT	GGCCAGGTA	TATTTGGCGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGAATCGGCG	GATTCTGTGT	TTTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAAACAGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAAT	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC

951 CTA TCATGCG CAACAGACGT GGTATTAGA TGGCGGCGG ATTGTCCGCG
 1001 AAG AGAAACA GGGGACAGA CTGCCTGATT TTCCTTGAA CTTGGAAGAT
 1051 TTG GAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGCGA GACGTTCCGG
 1101 CGG CAGGCGC GACCTTTCTC ACTGA

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

a957.pep
 1 MFKKFKPVL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
 51 ARL FRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDY LALAVRLSRLK
 101 EKA KWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLRYN
 151 DRP FSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
 201 CLG CYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
 251 LMP RGMKANS LVVGYDADGL POKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
 301 SST VALKADG VTADMOTYHA QOTWYLDGGR IVREKQGDR LPDFPLNLED
 351 LEKEVSRYAE AAARRSGRR DLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

a957.pep	10 20 30 40 50	MFKKFKPVL SFFALVFAFW LGTGIAYEIN PRWFLSDTATE---NPNAFVAKL ARLFRNA
m957	10 20 30 40 50 60	MFKKFKPVL SFFALVFAFW LGTGIAYEIN PRWFLSDTATEV PKNPNAFVAKL ARLFRNA
a957.pep	60 70 80 90 100 110	DRAVVIVKESMRT EESLAGAVDD GPLQSEKDY LALAVRLSRLKEKAKWFHVTE QEHGEEV
m957	70 80 90 100 110 120	DRAVVIVKESIRTEENLAGTVDD GPLQSEKDY LALAIRLSRLKEKAKWFHVTE QEHGKEV
a957.pep	120 130 140 150 160 170	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLRYNDRPFSVNVYGGTVHGENYETTGEYRVV
m957	130 140 150 160 170 180	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLRYNDRPFSVNVYGGTVHGENYETTGEYRVV
a957.pep	180 190 200 210 220 230	WQPDGVSVDASGRGKIGEDVYEHCLG CYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS
m957	190 200 210 220 230 240	WQPDGVSVDASGRGKIGEDVYEHCLG CYQMAQVYLAKYRDVANDEQKVWDFRKNRIAS
a957.pep	240 250 260 270 280 290	DSRDSVFYQNMRELMPRGMKANS LVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF
m957	250 260 270 280 290 300	DSRNSVFYQNMRELMPRGMKANS LVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF
a957.pep	300 310 320 330 340 350	IAQSSTVALKADGVTADMOTYHAQOTWYLDGGRIVREKQGDRLPDFPLNLEDLEKEVSR
m957	310 320 330 340 350 360	IAQSSTVALKADGVTADMOTYHAQOTWYLDGGRIVREKQGDRLPDFPLNLENLEKEVRR
a957.pep	360 370	YAEAAARRSGRRDL SHX
m957		YAEAAARRSGRRDL SHX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

g958.seq
 1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
 51 TTTCCGCACG CATTGCGCCG CCGATACCGT TCGCGCGGAA GAGGCGGACG

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101 GCGGTGTCGC AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAGCT
151 TCCGATTGTA CCCTCGGTTT GACCTGCCTG TTTTGCACTA ACGAAAAGCGG
201 CAGC CCGGAG AGAACCGAAG CCGCCGTCCA AGGCAGCGGC GAAGCATCCG
251 TCCC CGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TGCAGCGGGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGT AGGCGA CCGGTTGCGC CTCCAACAGG ACGGTACGCT GATTCGGGGC
451 GAAA CCCTGA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACGT
501 CCGT ATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAAAG GTCAGCCGCA
551 CCGC CGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCTATTC
601 AACA CCTGTT CCGCCGAGGA TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
651 CGAA CCGGAT CGGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCCTTCG
701 TGTT CCGCGG CGTTCCTCTT TTCTATACGC CTTGGGCGGA CTTCCCGCTT
751 GACG GCAACG GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCGCGTTC
801 GGAC GCGGTT TCCCTTTCCG TCCCTTATTA TTTCAACCTT GCCCCCAACT
851 TCGA TGCCAC TTTCGCCCCC GGCATTATCG GCGAACGCGG CGCGACGTTT
901 GACG GACAAA TCCGTTACCT GCGTCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCAGGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAA ATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GGCGGGTGTC
1051 GATT TCAACC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAA GAAATC GCCGGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
1151 ATGG CCGCAG GCGGGCGGGA GGCAGCCTGA ATGCGGCGCT TTCGGTTCAG
1201 AAAT ACCAGA CGCTGGCAAA CCAAGAGCGG TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAAT CGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCCGCCAA
1351 GACG GAGGCC GACTGGTCTG GTATCCCGGT ATCAAATGGG ATTTACAGCA
1401 CAGC TGGGGC TACGTCCGCC CCAAACCTCG GCTGCACGCC ACTTATTACA
1451 GCCT CGACAG TTTCCGGCGC AAAGCATCCC GCAGCGTCGG GCGCGTTTGT
1501 CCGG TTGTCA ATATCGACGG CCGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTC GCGCGC GGAGTCGTGC AAACCATCGA GCCGCGCCTG TTCTACAAC
1601 ATAT TCCTCG CAAATCTCAA AACGACCTGC CCAATTTTCA TTCGTCGGAA
1651 AGCA GCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGAC CGCATC AACGCCGCCA ACAGCCTTTC CACCGCCCTG CAGAGCCGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTGAG
1801 AAAT TCTATT TCAAGGATGA TCGGTGATG CTTGACGGCA GCGTCGGCAA
1851 AAAT CCGCGC AGCGGTTCCG ACTGGGTGGC ATTCGCTCC GCGGGCATAG
1901 CGGG GCGTTT CACCTCGAC AGCAGCATCC ACTACAACCA AACGACAAA
1951 GCGGCCGAAG ATTACGCGGT CCGCGCAGGG TACCGCCCGC CCGCCGGA
2001 AGTGTGTAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGGC GAGCGG TTCCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCCGTCGTCC GCTACAAC
2151 CCGT TTTGAA GCCAAAAAAC CGATAGAAAT GCTTGCCCGT GCAGAATACA
2201 AAAG CAGTTG CCGCTGCTGG GCGCGGGGCG GTACGCCCA ACCTACGTT
2251 ACCGGCGAAA ACACCTACAA AAACGCCGTC TTTTTCAC TTCAATTGAA
2301 AGAC CTCAGC AGCGTCGGCA GAAACCCCGC AGCGAGGATG GATGTCGCGG
2351 TTCC CGGCTA CATCCCCGCC CACTCTCTTT CCGCCGAGC CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

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g958.pep
1 LARLFSLKPL VLALGFCEFT HCAADTVAAE EADGRVAEGG AOGASESAQA
51 SDLT LGSTCL FCSNESGSPE RTEAAVQSG EASVPEDYTR IVADRMESQS
101 KVKVRAEGSV IIERDGAVLN TDWADYDQSG DTVTVGDRFA LQDGTLLRG
151 ETLTYNLDQO TGEAHNVME TEQGGRLQO VSRTEMLGE GRYKLTETQF
201 NTCASAGDAGW YVKAASVEAD RGKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLPRD YSGQDITLWL PHDKKSGRNN RYQAKWQHRH DISOTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLRNV WLDYGGRAAG GSNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSHDGRQ
451 DGSRLVVYPG IKWDFNSWG YVRPKLGLHA TYYSLDSFGG KASRSVGRVL
501 PVVNIDGGTT FERNTLFGG GVVQTIERPL FYNYPKASQ NDLPNFDSSSE
551 SSFGYQGLFR ENLYYGNDR I NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSGVGNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLOADGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIENLAG AEYKSSCGCW GAGVYAQRV
751 TGENTYKNAV FFSLQLKDLN SVGRNPAGRM DVAVPGYIPA HSLSAGRNKR
801 P*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

```

m958.aeq
1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCCTCTG
51 CTTCCGACAG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGTCCGA ACCCATAACG

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTGTCA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCA TCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTGCTCG AACGCAACCG
351 GACGACCCCTC AATACCGATT GGGCGGATTA CGACCAGTCG GGCGACACCG
401 TTA CCGCAGG CGACCGGTC GCCCTCCAAC AGGACGGTAC GCTGATTCTG
451 GGC GAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGT CCGCATG GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCA CCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAAACCCAA
601 TTC AACACCT GTTCCGCCG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGT CGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCT
701 TCG TGTTCCG CGGCGTTCCC ATTTTCTACA CCCCTTGGCG GGAATCTCCG
751 CTT GACGGCA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCCGCCG
801 TTC GGACGGC GTTTCCTTT CCGTTCCTTA TTATTTCAAC CTGCCCCCA
851 ATC TCGATGC CAGTTCGCG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTT GACGGGC AGGTACGCTA CTTGCGGCGG GATTATGCCG GCCAGTCCGA
951 CCT GACCTGG CTGCCGCAGC ACAAGAAAAG CCGCAGGAAT AACCGCTATC
1001 AGG CGAAATG GCAGCATCGG CACGACATT CCGACACGCT TCAGCGGGGT
1051 GTC GATTTCG ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAA CAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATT ATGGCGG CAGGCGCGCG GCGGCGAGCC TGAATGCCGG CTTTCGGTT
1201 CTG AATACC AGACGCTGGC AAACCAAGC GGCTACAAAG ACAAACCGTA
1251 TGC CCTCATG CCGCGCCTTT CGGTGAGTG GCGTAAAAAC ACCGCGAGGG
1301 CGC AATCGG CGTGTCCGCA CAATTTACCC GATTACGCCA CGACAGCCGC
1351 CAA GACGGCA GCCGCCTGGT CGTCTATCCC GACATCAAAAT GGGATTTCAG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAT CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTG CCCATTG TCAACATCGA CAGCGCGCGA ACTTTTGAGC GGAATACGCG
1551 GAT GTTCGGC GGAGAAGTCC TGCAAACCT CGAGCCGCGC CTGTCTACA
1601 ACT ATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTCTGTC
1651 GAA AGCAGCT TCGGTACGG GCAGCTCTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAGGCC
1751 GTATTTTGGG CGGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGT
1801 CAG AATCTT ATTCAAGGA TGATGCGGTG ATGCTTGAGC GCAGCGTCCG
1851 CAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTTGCC TCCGCGAGCA
1901 TCGGCAGCGC CTTTCATCTC GACAGCAGCA TCCACTACAA CAAAACGAC
1951 AAACGCGCGC AGAAGTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTCTG AACGCCCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCC TCCGTTACAA
2151 CTACGGTTTT GAAGCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGTGTACGC CCAACGCTAC
2251 GTT ACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTG GCAGAAACCC CGCAGACAGG ATGGATGTG
2351 CCGTTCGCCG CTATATCACC GCCACTCTC TTTCCGCCG ACGCAACAAA
2401 CGACCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

m958.pep

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1 LARLFSLKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51 PTSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMERGQ
101 SQVQVRAEGN VVVERNRTTL NTDWADYDQS GDTVTAGDRF ALQDGTLLR
151 GETLTYNLEQ QTGEAHNVRM EIEQGRRRLQ SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFVFGVGP IFYTPWADFP
251 LDGNNRKSGLL VPSLSAGSDG VLSVPYYFN LAPNLDATFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSINAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRN TGRAQIGVSA QFTRFSDHRS
451 QDGSRLVYYP DIKWDFNSW GYVRPKLGLH ATYYSNRFQ SQEARRVSRT
501 LPIVNIDSGA TFERNTRMFG GEVLQTLPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYQQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGSVGKKP RNRSDWVAF SSGISRFIL DSSIHNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GA EYKSSCGC WGAGVYAORY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNK
801 RP*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

1372

m958/g958 89.3% identity in 802 aa overlap

```

      10      20      30      40      50      60
m958.pep LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC
          |||||:|||||:|:|||||:|:|:|||||:|:|:|||||
g958     LARLFSLKPLVLALGFCFGTHCAA-DTVAAEEADGRVAEGGAQGASESAQASDLTLGSTC
          10      20      30      40      50

      70      80      90     100     110     120
m958.pep LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGSQVQVRAEGNVVVERNRTTL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g958     LFCSNESGSPERTEAAVQGSGEASVPEDYTRIVADRMEGQSKVKVRAEGSVIERDGAVL
        60      70      80      90     100     110

      130     140     150     160     170     180
m958.pep NTDWADYDQSGDVTVTAGDRFALQQDGTILIRGETLTYNLEQQTGEAHNVMEIEQGGRRRLQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g958     NTDWADYDQSGDVTVTGDRFALQQDGTILIRGETLTYNLDQQTGEAHNVRMETEQGGRRRLQ
        120     130     140     150     160     170

      190     200     210     220     230     240
m958.pep SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAFFVGGVVP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g958     SVSRTAEMLGEGRYKLTETQFNTCSAGDAGWYVKAASVEADRGKGIGVAKHAAFFVGGVVP
        180     190     200     210     220     230

      250     260     270     280     290     300
m958.pep IFYTPWADFPDGNRKSGLLVPSLSAGSDGVSLVPYYFNLPNLDATFAPSVIGERGAV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g958     LFYTPWADFPDGNRKSGLLVPSVSAGSDGVSLVPYYFNLPNFDATFAPGIIGERGAT
        240     250     260     270     280     290

      310     320     330     340     350     360
m958.pep FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g958     FDGQIRYLRPDYSGQTDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG
        300     310     320     330     340     350

      370     380     390     400     410     420
m958.pep YYRDFYGNKEIAGNVNLRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g958     YYRDFYGGEEIAGNVNLRVWLDYGGRAAGGSLNAGLSVQKYQTLANQSGYKDEPYAIM
        360     370     380     390     400     410

      430     440     450     460     470     480
m958.pep PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g958     PRLSADWHKNAGRAQIGVSAQFTRFSHDSRQDGSRLVVYPGIKWDFSNSWGYVRPKLGLH
        420     430     440     450     460     470

      490     500     510     520     530     540
m958.pep ATYYSLNRFSGQEARRVSRITLPIVNIDSGATFERNTRMFGEVLQTLERLFFNYIPAKS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g958     ATYYSLDSFGGKASRSVGRVLPVVNIDGGTTFERNTRLFGGGVVQTIERLFFNYIPAKS
        480     490     500     510     520     530

      550     560     570     580     590     600
m958.pep QNDLPNFDSSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g958     QNDLPNFDSSSESSFGYGQLFRENLYYGNDRINAANSLSAVQSRILDGATGEERFRAGIG
        540     550     560     570     580     590

      610     620     630     640     650     660
m958.pep QKFYFKDDAVMLDGSVGKKPRNSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g958     QKFYFKDDAVMLDGSVGKNPRSRDWVAFASGGIGGRFTLDSSIHYNQNDKRAEHYAVGA
        600     610     620     630     640     650

      670     680     690     700     710     720
m958.pep SYRPAQGVNLRARYKYGRNEKIYLSKSDGSYFYDKLSQLDLAQWPLTRNLSAVVRYNYGF
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g958     GYRPAQGVNLRARYKYGRNEKIYLAQDGSYFYDKLSQLDLAQWPLTRNLSAVVRYNYGF
        660     670     680     690     700     710
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          730      740      750      760      770      780
m958.pep  EAKKPIEVLGAAYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR
          |||||
g958      EAKKPIEVLGAAYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPAGR
          72 O      730      740      750      760      770

          790      800
m958.pep  MDVAVPGYITAHSLSAGRNRKP
          |||||
g958      MDVAVPGYIPAHSLSAGRNRKPX
          78 O      790      800

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

```

a958.seq
1  TTG GCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTT CGGCACG CATTGCGCCG CGCCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACA ATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCCGA ACCCATACAG
151 CCT ACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGG CAGCCCG GAGAGAACC AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCA TCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCG CAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAATCG
351 GAC GACCCCTC AATGCCGATT GGGCGGATTA CGACCAGTCG GCGGACACCG
401 TTA CCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGC GAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGT CCGTATG GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCA CCGCCGA AATGTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTC AACACCT GTTCCGCCG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGT CGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCG TGTTCGG CGGCGTTCCT ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTT GACGGCA ACCGCAAAAG CGGCCTGCTC GTTCCCTCAC TGTCCGCCGG
801 TTC GAGCGCG GTTTCCTTT CCGTTCCTTA TTATTTCAAC CTTGCCCCCA
851 ATC TCGATGC CACGTTTCGCG CCCGGCGTGA TCGGCGAACG CGGCGCGGTC
901 TTT GACGGGC AGGTACGCTA CTTGCCGCCG GATTATGCCG GCCAGTCCGA
951 CCT GACCTGG CTGCGGCACG ACAAGAAAAG CGGCAGGAAT AACCCTATC
1001 AGG CGAATG GCAGCACCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTC GATTTC AACAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAA CAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATT ATGGCGG CAGGCGGCGG GCGGCGAGCC TGAATGCCGG CCTTTCGGTT
1201 CTG AAATACC AGACGCTGGC AAACCAAGC GGCTACAAAG ACAACCCGTA
1251 TGC CCTGATG CCGCGCCTTT CCGCCGATTG GCGCAAAAC ACCGCGAGGG
1301 CGC AAATCGG CGTGTCCGCC CAATTTACCC GTTCAGCCA CGACAGCCGC
1351 CAA GACGGCA GCCGCTCGT CGTCTATCCC GACATCAAAT GGGATTTACG
1401 CAACAGCTGG GGTACGTCC GTCCCAAAC CCGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACCGC
1551 GAT GTTCGGG GCGGAGTCC TGCAAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACT ATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTGTCG
1651 GAA AGCAGCT TCGGCTACGG GCAGCTTTT CGTGAAGAAC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCGGCC GTGCAAAGCC
1751 GTATTTTGA CCGCGCGACG GGGGAAGAGC GTTTCGCGC CGGCATCGGG
1801 CAGAAATCT ACTTCAAAAA CGACGCAATC ATGCTTGACG GCAGTGTCCG
1851 CAAAAAACC CGCAGCCGTT CCGACTGGGT GGCATTGCGC TCCAGCGGCA
1901 TCGGCAGCCG CTTTATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAACTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAAAATACG GCGCAACGAA AAAATCTACC
2051 TGA AGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GCGCGCTGAC GCGCAACCTG TCGGCGCTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAAGCAG TTGCGGCTGC TGGGGCGCGG CCGTGTACGC CCAACGCTAC
2251 GTTACCGGGG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTCC
2351 CCGTTCCCGG CTATATCCCC GCCCACTCTC TTTCCGCGG ACGCAACAAA
2401 CGGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

```

a958.pep
1  LARLFSLKPL VLALGFCEGT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PLSLSLGSST LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEOGQ
101 SQVQVRAEGN VVVERNRTTL NADWADYDQS GDTVTAGDRF ALQQDGLTIR
151 GETLTYNLEQ QTGEAHNVRM ETEHGGRRLO SVSRTAEMLG EGHYKLTETOQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAVFVGGVP IFYTPWADFP

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251 LDGNRRSGLL VPSLSAGSDG VLSVPYYFN LAPNLDTFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QFTRFSHDSR
451 QDGSRVLVVP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPI VNIDSGM TFERNTRMFG GGVLTQLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDV MLDGSVGGKP RSRSDWVFA SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVRYNYGF EAKKPIEVL GAEEKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

	10	20	30	40	50	60
a958.pep	LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC					
m958	LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC					
	10	20	30	40	50	60
	70	80	90	100	110	120
a958.pep	LFCSNESGSPERTEAAVQSGEASIPEDYTRIVADRMEGQSQQVRAEGNVVVERNRTL					
m958	LFCSNESGSPERTEAAVQSGEASIPEDYTRIVADRMEGQSQQVRAEGNVVVERNRTL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a958.pep	NADWADYDQSGDVTAGDRFALQQDGTIRGETLTYNLEQQTGEAHNVRMETEHGGRRLQ					
m958	NTDWADYDQSGDVTAGDRFALQQDGTIRGETLTYNLEQQTGEAHNVMEIEQGGRRRLQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
a958.pep	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKIGVAKHAAFFVGGVP					
m958	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKIGVAKHAAFFVGGVP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a958.pep	IFYTPWADFPLDGNRRSGLLVPSLSAGSDGVLSVPYYFNAPNLDTFAPGVIGERGAV					
m958	IFYTPWADFPLDGNRRSGLLVPSLSAGSDGVLSVPYYFNAPNLDTFAPSVIGERGAV					
	250	260	270	280	290	300
	310	320	330	340	350	360
a958.pep	FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
m958	FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
	310	320	330	340	350	360
	370	380	390	400	410	420
a958.pep	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
m958	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
	370	380	390	400	410	420
	430	440	450	460	470	480
a958.pep	PRLSADWRKNTGTRAQIGVSAQFTRFSHDSRQDGSRLVVPDIKWDFSNSWGYVRPKLGLH					
m958	PRLSVEWRKNTGTRAQIGVSAQFTRFSHDSRQDGSRLVVPDIKWDFSNSWGYVRPKLGLH					
	430	440	450	460	470	480
	490	500	510	520	530	540
a958.pep	ATYYSLNRFQSGEARRVSRTLPIVNIDSGMTFERNTRMFGGGVLTQLEPRLFYNYIPAKS					
m958	ATYYSLNRFQSGEARRVSRTLPIVNIDSGMTFERNTRMFGGEVLTQLEPRLFYNYIPAKS					

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	490	500	510	520	530	540
a958.pep	550	560	570	580	590	600
	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRINTANSLSAVQSRILDGATGEERFRAGIG					
m958	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRINTANSLSAVQSRILDGATGEERFRAGIG					
	550	560	570	580	590	600
a958.pep	610	620	630	640	650	660
	QKFYFKNDVAVMLDGSVGGKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
m958	QKFYFKNDVAVMLDGSVGGKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
	610	620	630	640	650	660
a958.pep	670	680	690	700	710	720
	SYRPAQGGKVLNARYKYGRNEKIYKSDGSYFYDKLSQDLDSAQWPLTRNLSAVVRYNYGF					
m958	SYRPAQGGKVLNARYKYGRNEKIYKSDGSYFYDKLSQDLDSAQWPLTRNLSAVVRYNYGF					
	670	680	690	700	710	720
a958.pep	730	740	750	760	770	780
	EAKKPIEVLAGAIEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
m958	EAKKPIEVLAGAIEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
	730	740	750	760	770	780
a958.pep	790	800				
	MDVAVPGYIPAHSLSAGRNRKP					
m958	MDVAVPGYIPAHSLSAGRNRKP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTGGG
51  CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

g959.pep

```

1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEEKAAR VGGKITDIDL EHDGRPHYD VEIVKNGQEQ KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

m959.pep

```

1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEEKAALR VGGKITDIDL EHDNGRPHYD VEIVKNGQEQ KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

m959/g959 95.4% identity in 108 aa overlap

	10	20	30	40	50	60
m959.pep	MN IKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR					
	: : : : : :					
g959	MN IKHLLLTAAATALLGISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR					
	10	20	30	40	50	60
	70	80	90	100	109	
m959.pep	VG GKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX					
	: : : : : :					
g959	VG GKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

1	ATGAACTTCA	AACGCCTTCT	CTTGACCGCC	GCCGCAACCG	CACTGATGGG
51	CATTTCGCGC	CCCGCACTCG	CCCACCACGA	CGGACACGGC	GATGACGACC
101	ACGGACACGC	CGCACACCAA	CACAGCAAAC	AAGACAAAT	CATCAGCCGC
151	GCCCAAGCCG	AAAAAGCAGC	GTTGGCGCGT	GTCGGCGGCA	AAATCACCGA
201	CATCGATCTC	GAACACGACA	ACGGCCGTCC	GCACTATGAT	GTCGAAATCG
251	TCAAAAACGG	ACAGGAATAC	AAAGTCGTTG	TCGATGCCCG	TACCGGCCGC
301	GTGATTTCCT	CCCGCCGCGA	CGACTGA		

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

a959.pep

1	MNFKRLLTLTA	AATALMGISA	PALAHHDGHG	DDDHGHAHQ	HSKQDKIISR
51	AQAEEKAALAR	VG GKITDIDL	EHNDNGRPHYD	VEIVKNGQEY	KVVVDARTGR
101	VISSRRDD*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a959.pep	MNFKRLLLTAAATALMGISAPALAHHDGHGDDDHGHAHQHNSKQDKIISRAQAEKAALAR					
	: : : : : : :					
m959	MN IKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR					
	10	20	30	40	50	60
	70	80	90	100	109	
a959.pep	VG GKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX					
	: : : : : :					
m959	VG GKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX					
	70	80	90	100		

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

1	ATGCAAGTAA	ATATTCAGAT	TCCCTGTATG	CTGTACAGAC	GCGGGAGTGT
51	TAAGCCCCC	TTGTTTGAAG	CTCCGCGGCT	CCTGCCGAGC	TTCACCGACC
101	CCGTGTGTC	CAAGCTCTCT	GCTCCCGGCG	GCTACATTGT	CGACATCCCC
151	AAAGGCAATC	TGAAAACCGA	AATCGAAAAG	CTGGCCAAAC	AGCCCCAGTA
201	TGCCATCTG	AAACAGCTCC	AAGTAGCGAA	AAACGTCAAC	TGGAACCAGG
251	TGCAACTGGC	TTACGATAAA	TGGGACTATA	AGCAGGAAGG	CTTAACCAGA
301	GCCGGTGCG	CGATTATCGC	GCTGGCTGTT	ACCGTGGTTA	CTGCGGGCGC
351	GGGAGTCGGA	GCCGCACTAG	GCTTAAACGG	CGCAGCCGCA	GCAGCGGCCG
401	ATGCCGCCTT	TGCCTCACTC	GCTTCTCAGG	CTTCCGTATC	GCTCATCAAC
451	AATAAAGGGC	ATGTCGGCAA	AACCTGAAG	GAACCTGGCA	GAAGCCGCAC
501	GGTAAAAAAT	CTGGTTGTAG	CGGCGGCAAC	GGCAGGCGTA	TCCAACAAAC


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551 TCGGTGCCCTC TTCCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAAACAAC
601 CTC AACGTTA ACCTGGCCAA TGC GGGCAGT GCCGCGCTGA TCAACACCGC
651 TGT TAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAT ATCCTGGCGG
701 CAT TGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GAT CAGCACT ATGTGCGCCA CAAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG CGGAATAAGG GCAAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTGCGG GAGGCTTGG TTAATAATAC CGATTTTAGC
901 GAT ATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCCTA
951 TGC CAAACTT CGCGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATA CTGCTGC ACAAACCGCA CAAAACGCGG TAGAAAAATA TCGGTTAAAA
1051 GCT GTTGTA GCTGTGCAAA AGTGTTTAT AAGGTAGCCA GAAAGGATT
1101 AAAA AACGGG AAAATCAACG TTAGAGATT AAAACAGACG TTGAAAGACG
1151 AAG GTTATA TTTAGCCGAC AACCTGACCA CCTTATTGTA CGAAACATTG
1201 GAT TGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTG GAACAGAGCT
1251 GAA TCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTATG
1301 AAA AAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACA TACATGA AAAATAATCC TTTTGAAAA CAGCTGGCTC AAATTCAGA
1401 AAA GACAACG CTTCCGACGC AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAA ACCAAGG GTTATTAATA ACCGGTGATA GGTTTTATTT AGATGGCCAA
1501 CAT AAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAAT TTAAGTTTGT
1551 TCT AAATATG GATGGTTCGC TTAACCAAAT GAAACTGGG GCAGCAAAAG
1601 GTC GTAAATT AAACCTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

```

m960.pep
1  MQVNIQIPCM LYRRGSVKPP LFEAPRLPLS FTDVVPKLS APGGYIVDIP
51  KGNLKTEIEK LAKQPEYAYL KQLQVAKNVN WNQVQLAYDK WDYKQEGLTR
101 AGA AIALAV TVVTAGAVG AALGLNGAAA AAADAFAASL ASQASVSLIN
151 NKGDVGGTLK ELGRSRTVKN LVVAAATAGV SNKLGASSLA TWSETPWVNN
201 LNVNLANAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GEASKIKGL
251 DQH YVAHKIA HAVAGCAAAA ANKGRQDGA IGAAVGEIVG EALVKNTDFS
301 DMT PEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVV TAAKVYV KVARGLKNG KINVRDLKQT LKDEGVNLAD NLTLFDETL
401 DWN DAKAVID IVVGTELNRA NKGEAAQKVK EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPFKG QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TGDRFYLDGO
501 HKN HLEVFDK NGNFKFVLNM DGSINQMRGT AAKGRKLNK *

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a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

```

m961.seq
1  ATGAGCATGA AACACTTTCC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51  CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AAT TACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTTA
251 AAGGTCTGGG TCTGAAAAA GTCGTGACTA ACCTGACCAA AACCCTCAAT
301 GAAAACAAAC AAAACGTCGA TGCCAAAGTA AAAGCTGACG AATCTGAAAT
351 AGAAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTGCTGA AGAGACTAAG ACAATATCG TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CCGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAAAACA
651 AAA CGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAGGCCG
701 AAGCTGCCGC TGGCACAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCAGACG CTTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAAG CGCGCTCTCC
901 GGCCTGTTCC AACCTTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCAGT
951 CGGCGGTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGT TCTCCG CAGCCTACCA TGTCGGCGTC AATTACGAGT GGTA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

```

m961.pep
1  MSMKHFFPAKV LTTAILATFC SGALAATSDD DVKKAATVAI VAAYNNGQEI

```

```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEA FN DIADS LDETNTKADE
201 AVKTFANEAKQ TAEETKQNV D AKVKAETA A GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPYNVGR FNVTAAGGY KSESAVAIGT GFRFTENFAA KAGVAVGTSS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet
a961.pep not found yet

g972.seq not found yet
g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

```

m972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTTCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GAAGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTGTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCAGGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGCGG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAAAT CTCGTTTGTG TCGTGTATAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACCTTGATG AATTGGGGGT TATGTCTTTT AAAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

```

m972.pep
1  LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGLLEIP QRRGKQDGVF
51  VDWFISFTFHE DTLLKVSGCP LPSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFQXQNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICKRKF NMPVPERFDQ RKKKLNLTFF
301 HKLHYAKNAV GKLNVFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKQYEYLS KVVHQNVDYD YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

```

a972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTCG GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTATTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTGTAG AAAATTAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATG GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAATCTG
1151 ACAAATTCGA TAGGGAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

a972.pep

```

1  LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGK GKLEIP QRRGKQDGVF
51  VDWSITFHE DTLLKVS GCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFGGQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLAL DFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFPICRKF NMPVPERFDQ RKKTNLNLTFE
301 HKLHYAKNAV GKLNVFMIEM GFDNSEIVES LKADSGFPGK LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKQYEYLS KVIHQNVDDYD YF*

```

m972/a972 99.3% identity in 422 aa overlap

	10	20	30	40	50	60
m972.pep	LTNRGGAKLKTXSKSSERMSEVEYFSHFISDGK GKLEIPQRRGKQDGVFVDWSITFHE					
a972	LTNRGGAKLKTNKSSERMSEVEYFSHFISDGK GKLEIPQRRGKQDGVFVDWSITFHE					
	10	20	30	40	50	60
m972.pep	DTLLKVS GCP LFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE					
a972	DTLLKVS GCP LFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE					
	70	80	90	100	110	120
m972.pep	VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALDFDGEYTPDQ					
a972	VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALDFDGEYTPDQ					
	130	140	150	160	170	180
m972.pep	VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALDFDGEYTPDQ					
a972	VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALDFDGEYTPDQ					
	190	200	210	220	230	240
m972.pep	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKNSRFVRVY EKGRQLGDKE					
a972	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKNSRFVRVY EKGRQLGDKE					
	250	260	270	280	290	300
m972.pep	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFPICRKF NMPVPERFDQRKKNLNLTFE					
a972	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFPICRKF NMPVPERFDQRKKNLNLTFE					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m972.pep	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPGGLEPEKYALEMLRDGLKHGFI					
a972	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPGGLEPEKYALEMLRDGLKHGFI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVVDYD					
a972	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVVDYD					
	370	380	390	400	410	420
m972.pep	YFX					
a972	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

```

g973.seq
1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCCG
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATCGGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTGCGCGT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTGCGC CTGCCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCAAC TTTGAAGACA TCATCGAGCa aatcgtcggt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCAATC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTTCGGTACG GAatacggca gcgaagaagc cgacaccatc ggcggctTGG
701 TCATTCAAGG ATTGGGACAC CTGCCCCGTC GCGGCGAAAA AGTCCTTatc
751 ggcgGTTTGC agttcacggt CGCCCCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgcggttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

```

g973.pep
1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLLE
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQFHLKSVLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFPGT EYGSEEADTI GGLVIQELGH LPVRGEKVL I
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

```

m973.seq
1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCCG
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTTCGGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTGCGCGT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTCATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCAAC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTCm
601 GaACGcTGGC GCATCCATGC AGTACCGAA ATCGAAGACA TCAACACCTT

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651 CTTCGGCACG GAATACAGCA kCGAAGAAGC CGACACCATT GGCGGCCTGG
 701 TCATTCAAGA GTTGGGACAT CTGCCCCGTGC GCGGCGAAAA AGTCCTTATC
 751 GCGGGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973 . pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLRLE
 51 KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG EIEDEFDEDD SADNIHAVSS
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIOELGH LPVRGEKVL
 251 GGLQFTVARA DNRRLHTLMA TRVK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

m973 . pep	10	20	30	40	50	60
	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLRLEKVLDFSDLEV					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLRLEKVLDFAELEV					
	10	20	30	40	50	60
m973 . pep	70	80	90	100	110	120
	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
g973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
m973 . pep	130	140	150	160	170	180
	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFFEDIIEQIVG					
g973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFFEDIIEQIVG					
	130	140	150	160	170	180
m973 . pep	190	200	210	220	230	240
	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIOELGH					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAFPGTEYGESEADTIGGLVIOELGH					
	190	200	210	220	230	240
m973 . pep	250	260	270			
	LPVRGEKVLIGGLQFTVARADNRRLHTLMA TRVKX					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMA TRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973 . seq

1 ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
 51 ACTGCCCGCG GAACCCGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA
 151 AAAGTCCTCG ATTTTCTGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
 201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAA CGCATCACCG
 251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGTGAAGAC
 301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAATATAT
 351 GTTCAACCCC GAGCAGTTCC ACCTCAAATC GATATTGCGC CCTGCCGTCT
 401 TCGTCCCGCA AGGCAAATCG CTGACCGCCC TTTTAAAGA GTTCCGCGAA
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG
 551 ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTCCGCC

1382

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601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCGGCAGC GAATACAGCA GCGAAGAAGC CGACACCATC GGCGGCCTGG
701 TCATTCAGGA ATTGGGACAC CTGCCCCTGC GCGGCGAAAA AGTCCTTATC
751 GCGCGTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
  1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLRLLE
 51 KVLDFSDLEV RDMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
201 ERWRIHAATE IEDINAFPGT EYSSEADTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
a973	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973.pep	RDMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
a973	RDMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFPGTEYSSEADTIGGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
a973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
 51 TGCCTGCGGC GGTGAGGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGCAATT TAAAATCGA ATTCAAACAC CAGCGTGGG
251 ACAGCCTTTT CCCCGCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTCTTCCGA AGATTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
451 CACACGGGCG ATTTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTCGAAAACG TCCCCCTGAT TATCAAAGAA CTGGAACACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTCATCGC CAATTATGTG
601 AAAACAAC CCGCCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATCTACG CCAATATTT TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A

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1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

```

g981.pep
1  MKKKWIAAALA CSALALSACG GQKDAAPA ANPGKVYRVA SNAEFAPPES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK MNKVGVTG
151 HTGDFS SVKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SD SAVIAN YV
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE GQAAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

```

m981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TC GCGCTGTC
51  TGCCGTGCGG GGT CAGGGCA AAGATACGCG CGCGCTGCC GCCAACCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCGG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTA AACAAACGCG ATGCGGACGT TGTGATGTCG
301 GCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCAGG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTCTCTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTCATCGC CAATTATGTG
601 AAAAACAATC CGGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATTTACG CCAATATTT TGCAAAGAA GACGACAGG CCGCAAATA
801 A

```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

```

m981.pep
1  MKKKWIAAALA CSALALSACG GQKDTAAPA ANPKVYRVA SNAEFAPPES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK MNKVGVTG
151 YTGDFS SVKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SD SAVIAN YV
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE DGQAAK*

```

m981/g981 98.1% identity in 266 aa overlap

```

10      20      30      40      50      60
981.pep  MKKKWIAAALACSALALSACGGQKDTAAPAANPKVYRVASNAEFAPPESLDSKGNVEGF
          |||
g981     MKKKWIAAALACSALALSACGGQKDAAPAANPGKVYRVASNAEFAPPESLDSKGNVEGF
          |||

10      20      30      40      50      60

70      80      90      100     110     120
981.pep  DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE
          |||
g981     DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE
          |||

70      80      90      100     110     120

130     140     150     160     170     180
981.pep  ITQVVLVPGKGVSSSEDLKMNKVGVTGTYTGDFS SVSKLLGNDNPKIARFENVPLIIKE
          |||
g981     ITQVVLVPGKGVSSSEDLKMNKVGVTGTYTGDFS SVSKLLGNDNPKIARFENVPLIIKE
          |||

130     140     150     160     170     180

190     200     210     220     230     240
981.pep  LENGGLDSVVSDSAVIAN YVKNKPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
          |||
g981     LENGGLDSVVSDSAVIAN YVKNKPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
          |||

190     200     210     220     230     240

250     260
981.pep  EKVRESGEYDKIYAKYFAKEDGQAAKX
          |||
g981     EKVRESGEYDKIYAKYFAKEGGQAAKX
          |||

250     260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAAGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCC AGTTTGCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTT GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCAAG TCGTCCTCGT TCCGAAAGGC AAAAAATAT
401 CTTCTTCCGA AGATTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TCCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAAAACAATC CGACCAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAAATATTT TGCAAAGAA GACGACAGG CCGCAAATA
801  A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
1  MKKWIAAALA CSALALSACG GQKDAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVM
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPGK KISSSEDLK NMNKVGVTG
151 YTGDFSVSKL LGNDNPFIAR FENVPLIIKE LENGGLDSV SDSAVIANV
201 KNNPTKGMDF VTLPDFTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEYD
251 KIIYAKYFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAALAC SALALSACGGQKDTAAPANPDKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALAC SALALSACGGQKDAAPANPDKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMGVTITDDRQKSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMGVTITDDRQKSMDFSDPYFE					
	70	80	90	100	110	120
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMGVTITDDRQKSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMGVTITDDRQKSMDFSDPYFE					
	130	140	150	160	170	180
m981.pep	ITQVVLVPGKGVSSSEDLKNMNKVGVTGYTGDFSVSKLLGNDNPFIARFENVPLIIKE					
a981	ITQVVLVPGKGVSSSEDLKNMNKVGVTGYTGDFSVSKLLGNDNPFIARFENVPLIIKE					
	130	140	150	160	170	180
m981.pep	LENGGLDSVVS DSAVIANVKNP KGMDFVTLPDFTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVVS DSAVIANVKNP KGMDFVTLPDFTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
m981.pep	LENGGLDSVVS DSAVIANVKNP KGMDFVTLPDFTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVVS DSAVIANVKNP KGMDFVTLPDFTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
m981.pep	EKVRESGEYDKIIYAKYFAKEDGQAAKX					
a981	:					
	250	260				
m981.pep	EKVRESGEYDKIIYAKYFAKEDGQAAKX					
a981	KKVRESGEYDKIIYAKYFAKEDGQAAKX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982. seq
1   atcgcatcgc aaaaccttcg attcgacaat cgattcctcc aaaaaatggt
51  caacggcgTg aatattttgc cggccgcGga ttgggtagcC ttgGGcgcCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCG GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAAGTAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAGT CGCGTCCAAA ACCAacgaCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAaggcA TGAAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGccg ttgCCGCTTt ggTTgAAGAg cTGAAAAACA
401 TCGCCAAACC TTGCGATACT TCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCGG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCTTACT TTATCAACGA CGCGGAAAAA CAAATCGCGG GTCTGGACAA
651 TCCGTTTGTG TTGCTGTTG CAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCCGTGTT GGAACAAGTG GCGAAAGCCA GCCGCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGCGC ACTTTGGTCG TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
851 CCGCGCAAAG GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATTtccGAAG Aagtccgcct GTCTTTGGAA AAAGcgactT TgGacgaCTT
951 Gggtcaaac aaACGcatCG AAATCGGtga agaaaacact ACCGTCATcg
1 001 acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTGTC CGAAATCCGC
1 051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1 101 CGCGCTTGCC AAATGGCAG GAGGCGTGGC AGTGATCAAA GTCGGCGCGG
1 151 CGACCGAAGT CGAAATGAAA GAGAAAAAG ACCGCGTGGA AGACGCGCTG
1 201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1 251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGCAATG
1 301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TGCGCGCCGT TGAGTCTCCG
1 351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1 401 CAAAGTGTG GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGGCG
1 451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCTGC CAAAGTAACC
1 501 CGTTCCGCGC TGCAACACGC CGCGTCTAtC GCCGGTCTGA TGCTGACGAC
1 551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
1 601 TGGGGGGAAT GGGCGGTATG GCGGCGATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982. pep
1   IASQNLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAAALVEE LKNIAKPCDT SKEIAQVSI
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLLENLDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LLFDKKISNI RDLLPVLEQV AKASRPLLI
251 AEDVEGEALA TLVVNNIRGI LKTVAVKAPG FGDRRKAMLO DIALITGGVV
301 ISEEVGLSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALNLH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYNV GSGEYGDMIG MGVLDPKVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGGM GGM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982. seq
1   ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCG GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAAGTAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAGAAGT TGCGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCGG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCTTACT TCATCAACGA TCGGAAAAA CAAATCGCTG CTTTGGACAA

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1386

```

651 TCCGTTTGTGTA TTGTTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCTGTTTTT GGAACAAGTG GCAAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGAGGCATC CTGAAAACCG TTGCCGTCAA AGCCCCTGCG TTCGGCGACC
851 GCCGCAAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CGGCGTGGTG
901 ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTTGG CGACGCAGCC CAAATCGAAG CGCGTGTGTC CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTGGCT AAATTGGCAG GCGGCGTGGC AGTCATCAA GTCCGTGCCG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGG AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TGC GCGCGCTGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCTGCGC TGCAACACGC CGCATCTATC GCCGCGTTGA TGCTGACCAC
1551 TGATTGCATG ATCGCTGAAA TCCCCGAAGA CAAACCGGCT GTGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCGATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2964; ORF 982>:

```

m982.seq
1 ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51 AAACGGCGTG AACATTCTGG CAAACGCGCT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCG GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT TGGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGCACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCTG CTTTGACAA
651 TCCGTTTGTGTA TTGTTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCTGTTTTT GGAACAAGTG GCAAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGAGGCATC CTGAAAACCG TTGCCGTCAA AGCCCCTGCG TTCGGCGACC
851 GCCGCAAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CGGCGTGGTG
901 ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTTGG CGACGCAGCC CAAATCGAAG CGCGTGTGTC CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTGGCT AAATTGGCAG GCGGCGTGGC AGTCATCAA GTCCGTGCCG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGG AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TGC GCGCGCTGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCTGCGC TGCAACACGC CGCATCTATC GCCGCGTTGA TGCTGACCAC
1551 TGATTGCATG ATCGCTGAAA TCCCCGAAGA CAAACCGGCT GTGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCGATGA TGTA

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m982/g982 95.8% identity in 544 aa overlap

```

m982.pep      10      20      30      40      50      60
MAAKDVQFGNEVRQKMNNGVNI LANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
: : : : : | : | : : : : | : : : : : : : : : : : : : : : : : : : : : :

```

1387

g982	IASQNLRFDNRFLOKMNNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
m982.pep	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRGI
	70 80 90 100 110 120
g982	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRGI
	70 80 90 100 110 120
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
g982	DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
m982.pep	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
g982	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV
	250 260 270 280 290 300
g982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV
	250 260 270 280 290 300
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
g982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
g982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
m982.pep	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKNGYGYNA
	430 440 450 460 470 480
g982	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKNGYGYNA
	430 440 450 460 470 480
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGMLTTDCMIAEIPEDKPAVPDMGGMGM
	490 500 510 520 530 540
g982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGMLTTDCMIAEIPEDKPAVPDMGGMGM
	490 500 510 520 530 540
m982.pep	GGMMX
g982	GGMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

```

a982.seq
1  ATGGCAGCAA AAGACGTACA ATTCGGCAAT GAAGTCCGCC AAAAAATGGT
51 AAACGGCGTG AACATTTTGG CAAACGCCGT GCGCGTAACC TTGGGTCCCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT CGCGTCCAAA ACCAACGACG
251 TGGCGGGCGA CGGTACGACT ACCGCCACCG TATTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATACGT TACCGCCGGT ATGAACCCGA CCGACCTGAA
351 ACGCGGTATC GACAAAGCCG TCGCCGCTTT GGTGAAGAG CTGAAAAACA

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1388

```

401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCCG GCTTGGACAA
651 TCCGTTTGTA TTGCTGTTTCG ACAAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1 001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTGC CGAAATCCGC
1 051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1 101 GCGCGTTGCC AAAGTGGCAG GCGGCGTGGC AGTAATCAAA GTCGGTGCCG
1 151 CGACCGAAGT GGAATGAAA GAGAAAAAAG ACCGCGTGGG AGACGCGCTG
1 201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGTTGTCAG GCGGCGCGCT
1 251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGCAATG
1 301 CAGACCAAGA CGCAGCGCTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1 351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1 401 CAAAGTGTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGCGG
1 451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1 501 CGTTCGCGC TGCAACACGC CGCGTCTATC GCCGGCCTGA TGCTGACCAC
1 551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1 601 TGGGCGGCAT GGGTGGTATG GCGGCGATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

```

a982.pep
1  MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSI
101 AEGMKYVTAG MNPTDLKRG I DKAVAALVEE LKNIAPCDT SKEIAQVGS
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGY
201 SPYFINDAEK QIAGLDNPFV LLDKKISNI RDLLPVLEQV AKASRPILLI
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGTV
301 ISEEVLGSLE KATLDDLQGA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENH TGNADQDAGV QIVLRAVES
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSGEYDMIE MGVLDPARV
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGM GGM*

```

m982/a982 99.3% identity in 544 aa overlap

```

          10      20      30      40      50      60
m982.pep  MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHITKDGVTVAKEI
          |||
a982      MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHITKDGVTVAKEI
          10      20      30      40      50      60

          70      80      90     100     110     120
m982.pep  ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG I
          |||
a982      ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG I
          70      80      90     100     110     120

          130     140     150     160     170     180
m982.pep  DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
          |||
a982      DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
          130     140     150     160     170     180

          190     200     210     220     230     240
m982.pep  KLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
          |||
a982      KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
          190     200     210     220     230     240

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1389

	250	260	270	280	290	300
m982 . pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m982 . pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQOIETATSDY					
a982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQOIETATSDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m982 . pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m982 . pep	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKNGYGYNA					
a982	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKNGYGYNA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m982 . pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM					
a982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM					
	490	500	510	520	530	540
m982 . pep	GGMXX					
a982	GGMXX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986 . seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCCTT
51	GCTGGCAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCCGACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAGGCAG	CCCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCCTTCTAC
301	GAATTTTTC	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCACGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTC
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCGT	CAAAATCGGC	AATCCCAAAA	ATTGAAACC	GGGCGAATGG
601	GTCGCTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAACAGCG	TGACCGCCGG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCCT
701	TCATCCAAAC	CGACGTTGCC	ATCAATCCGG	GCAATTCCGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgTCGGCATC	AATTGCGAAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTCGC	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTTCAGGA	AGTATCCTAC	GGTTTGGCAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGCGCTG	CAGGCGGGCG	ACATCGTCTT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TCGGCGCCAT
1101	TACGCCGGGA	AAAGAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAAACAA	AGCCAAGCTG	GGCAACGCCg	ccgagcATAC	CGGCgcatCA
1201	TCCAAACAG	ATGAAGcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtcgtacgg	gtttccgacg	cggcagaacg	cGCAGGCTTA

1390

1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
 1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAC GTCCCCCTGC
 1451 TGGTCAtgcy ccgTGGCAAC ACGTGTTC TCGCATTAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

g986. pep

1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
 101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILTN THVVAGMGSI
 151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
 301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
 401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

m986. seq

1 GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
 51 GCTGGCAGGC TGCACAAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
 101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
 151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCCGCG
 201 AGTCGTCAAT ATTCAGGCAG CCCCAGCCCC CCGCACCCAA AACGGCAGCG
 251 GCAATGCCGA AACGATTCC GACCCGATTG CCGACAACGA CCCGTTCTAC
 301 GAATTTTCA AACGCCTCGT CCCGAATATG CCCGAAATCC CCCAAGAAGA
 351 AGCAGATGAC GGCAGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
 401 ACGGCTACAT CCTGACCAAT ACCCAGCTCG TTACCGGCAT GGGCAGTATC
 451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTT
 501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
 551 TGCCCGTCGT CAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
 601 GTCGCCGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCCG
 651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCTT
 701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
 751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
 801 CAGCGGCGGA TTCATGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
 851 TGAATGTCGC CGAACAGCTG AAAACACCG GCAAAGTCCA ACGCGGACAA
 901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTCGCAC AATCGTTCCG
 951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
 1001 CCGCAGAACG TGCCGGCCTG CAGGCGGGCG ACATCGTCCT CAGCCTCGAC
 1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
 1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GCGGAAGAAA
 1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
 1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
 1251 GGTGCAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
 1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
 1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
 1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAC GTCCCCCTGC
 1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

m986. pep..

1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
 101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILTN THVVTGMGSI
 151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
 301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

Computer analysis of this amino acid sequence gave the following results:

1391

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

	10	20	30	40	50	60
m986 . pep	VFKKYQYLALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	: : : : : : : : : :					
g986	VFKKYQYFALAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986 . pep	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD					
	: : : : : : : : :					
g986	VQSEGPVVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPNMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986 . pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	: : : : : : : : :					
g986	GGLNFGSGFIISKNGYILTNTHVVGMSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986 . pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFSDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	: : : : : : : : :					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFSDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986 . pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	: : : : : : : : :					
g986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

	310	320	330	340	350	360
m986. pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	:					
g986	LGVIIQEVSYGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986. pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	:					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986. pep	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRGDEILAVGQVPVND EAGFRKAMD KAGKN					
g986	AGITLQTHTDSSGKHLVVVRVSDAAERAGLRGDEILAVGQVPVND EAGFRKAMD KAGKN					
	430	440	450	460	470	480
	490	500				
m986. pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

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a986.seq
1      GTGTTCAAAG  AATACCAATA  CCTCGCTTGT  GCAGCACTGT  GTGCCGCCCTC
51     ACTGGCAGGG  TGCACAAAG  CCGGCAGCTT  TTTCCGTTGC  GACAAAAAAG
101    AGCATCCTT    TGTAGAACGC  ATCAAACACA  CCAAGAGACA  CGGCAGCGTC
151    AGTATGCTGC  TGCCCGACTT  TGTCCAACTG  GTTCAAAGCG  AAGGCCCGGC
201    AGTCGTCAAT  ATTCAAGGAC  CCCC CGCCCC  GCGCACCCAA  AACGGCAGCA
251    GCAATGCCGA  AACC GATTCC  GACCCGCTTG  CCGCAGAGCA  CCCGTTCTAC
301    GAATTTTTCA  AACGCCTCGT  CCGGAACATG  CCGGAATCCG  CCGAAGAAGA
351    AGCAGATGAC  GNGG GATTGA  ACTTCGGTTC  GGGCTTCATC  ATCAGCAAAG
401    ACGGCTATAT  TCTGACCAAT  ACGCACGTGG  TTACCGGCAT  GGGCAGTATC
451    AAAGTCCTGC  TCAACGACAA  GCGCGAATAT  ACCGCAAAAT  TCATCGGTTT
501    GGATGTCTCG  TCCGATGTCG  CCCTTCTGAA  AATCGACGCA  ACGGAAGAGC
551    TGCCCGTCGT  CAAAATCGGC  AATCCCAAG  ATTTGAAACC  GGGCGAATGG
601    GTCGCGGCCA  TCGGCGCGCC  CTTGCGCTTC  GACAACAGCG  TGACCGCCGG
651    CNTCGTGTC  GCCAAAGGCA  GAAGCCTGCC  CAACGAAAGC  TACACACCTT
701    TCATCCAAAC  CGACGTTGCC  ATCAATCCGG  GCAACTCCGG  CGGCCCGCTG
751    TTCAACTTAA  AAGGACAGGT  CGTCGGCATC  AACTCGCAAA  TATACAGCCG
801    CAGCGCGGGA  TTCATGGGCA  TTTCCTTCGC  CATCCCGATT  GACGTTGCCA
851    TGAATGTCGC  CGAACAGCTG  AAAAACACCG  GCAAAGTCCA  ACGCGGACAA
901    CTGGGCGTGA  TTATTCAAGA  AGTATCCTAC  GGTTTGGCAC  AATCGTTCGG
951    TTTGGACAAA  GCGCGCGGCG  CACTGATTGC  CAAATCTCTG  CCGGCGACCC
1001   CCGCAGAAAG  TGC GCGGCTG  CGGGCGGGCG  ACATCGTCCT  GACGCTCGAC
1051   GGCGGAGAAA  TACGTTCTTC  CGGCGACCTT  CCCGTTATGG  TCGGCGCCAT
1101   TACGCGGGGA  AAAGAAGTCA  GCCTCGGCGT  ATGGCGCAAA  GGCGAAGAAA
1151   TCACAATCAA  AGTCAAGCTG  GGCAACGCGG  CCGAGCATAT  CGGCGCATCA
1201   TCCAAAACAG  ATGAAGCCCC  CTCACCGGAA  GAGCAATCCG  GTACGTTCTC
1251   GGTCCAATCC  GCAGGCATTA  CCCTTCAGAC  ACATACCGAC  AGCAGCGGCG
1301   GACACCTCGT  CGTCGTACGG  GTTTCGACG  CGGCAAGAAG  CGCAGGCTTG
1351   AGGCGCGGCG  ACGAAATTCT  TGCGGTAGGG  CAAGTCCCCG  TCAATGACCA
1401   AGCCGGTTTC  CGGAAGACTA  TGGACAAGGG  AGGCAAAAAC  GTCCCTCTGC
1451   TGATCATGCG  CGCTGGCAAC  ACGCTGTTTA  TCGCATATAA  CTTGCAATAA

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a986.pap

1	VFKKYQYLAL	AALCAASLAG	CDKAGSFFGA	DKKEASFVER	IKHTKDDGSV
51	SMLLPDFVQL	VQSEGPVVN	IQAPAPRTQ	NGSSNAETDS	DPLADSDFFY
101	EFFKRLVPNM	PEIQEEADD	GGINFGSGFI	ISKDGYLTN	THVVTMGMSI
151	KVLLNDKREY	TAKLIGSDVQ	SDVALLKIDA	TEELPVQTK	NPKDKLPGEW
201	VAAIGAPFGF	DNSVTAGDVQ	AKGRSLPNES	YTPFIQTVDA	INPFGNSGGPL
251	FNLLKGOVVG	NSQIYSRSGG	FMGISFAIPI	DVAMNVAEQL	KNTGKVGORG

1393

301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQHTD SSGGHLVVVR VSDAERAGL
 451 RRGDEILAVG QVPVND EAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

m986/a986 98.2% identity in 499 aa overlap

m986 . pep	10	20	30	40	50	60
	VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
a986	10	20	30	40	50	60
	VFKKYQYLALAALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL					
m986 . pep	70	80	90	100	110	120
	VQSEGPVAVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD					
a986	70	80	90	100	110	120
	VQSEGPVAVNIQAAPAPRTQNGSSNAETDSPLADSDPFYEFFKRLVPNMPEIPQEEADD					
m986 . pep	130	140	150	160	170	180
	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	130	140	150	160	170	180
	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
m986 . pep	190	200	210	220	230	240
	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGIVSAKGRSLPNESYTPFIQTDA					
a986	190	200	210	220	230	240
	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGXVSAKGRSLPNESYTPFIQTDA					
m986 . pep	250	260	270	280	290	300
	INPGNSGGFLFNKQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	250	260	270	280	290	300
	INPGNSGGFLFNKQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
m986 . pep	310	320	330	340	350	360
	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	310	320	330	340	350	360
	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
m986 . pep	370	380	390	400	410	420
	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	370	380	390	400	410	420
	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
m986 . pep	430	440	450	460	470	480
	AGITLQHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVND EAGFRKAMDKAGKN					
a986	430	440	450	460	470	480
	AGITLQHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVND EAGFRKAMDKAGKN					
m986 . pep	490	500				
	VPLLIMRRGNTLFIALNLQX					
a986	490	500				
	VPLLIMRRGNTLFIALNLQX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

g987. seq

1 ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCTCCTTC TCTGTTCATG

1394

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51  TTCTTCATGG TTGCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTGG CGCAACGaCA TTTCCGGCAG GCTGCTGTTC
301 AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTt
351 ggacgacaAC AACAcgcgcg gcttgacga tctcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCTGTTCa ACCCCTtCGT CTAACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAGGCCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGacg gCAAACGCAT
1251 CTTTCATCGG TCATTCAACC TCGACCCCGG TTCCGCACGG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 AccctCGCCG AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAACGCA TCGCGCAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG

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This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

```

g987.pep
1  MKTRSLISLL CLLCSCSSW LPPLEERTES RHFNTSKPVL LDNILQIRHT
51  PHNNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAERG VVRVLLDDN NTRGLDOLL ALDSHPNI*V RLENPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPIIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRESAR LNTEMGVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHPATRK TYPNEPEAKL WKRIAAILK
501 LLPIEGLL*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

```

m987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTGTAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GGCATCCCAA TATCGAAGTG CGCTGTTCa ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTTCGCC
601 GATTGAGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC

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1395

901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCCG
 951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTTCCCACA AAATCCGGCA
 1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
 1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
 1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
 1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
 1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
 1251 CTTTCATCGT TCGTTCAACC TCGACCCCG TTCCGCGCGT CTAACACCG
 1301 AAATGGGCGT TGTTATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
 1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
 1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
 1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAA AATCCTATCC
 1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

m987.pep

1 MKTRSLISLL CLLLCSCSSW LPFLEERTES RHFNSTSKPVR LDNILQIRHT
 51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
 101 NLVYLAAERG VRVRLLLDDN NTRGLDDLLL ALDSHPNIEV RLFNPFVLRK
 151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
 201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGDIG KGLQALGYND
 251 ETSRHALLRY RETVEQSPLY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
 301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
 351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPARSAR LNTEMGVVIE SPKIAEQMER
 451 TLADTTPAYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIAAILSL
 501 LLPIEGLL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

m987.pep	10	20	30	40	50	60
	MKTRSLISLLCLLLCSCSSWLPFLEERTESRHFNSTSKPVRLDNILQIRHTPHTNGLSDIY					
g987	MKTRSLISLLCLLLCSCSSWLPFLEERTESRHFNSTSKPVLLDILQIRHTPHNGLSDIY					
	10	20	30	40	50	60
m987.pep	70	80	90	100	110	120
	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNVLVYLAAERGVRVRLLLDDN					
g987	LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNMYLAAERGVRVRLLLDDN					
	70	80	90	100	110	120
m987.pep	130	140	150	160	170	180
	NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
g987	NTRGLDDLLLALDSHPNIXVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
m987.pep	190	200	210	220	230	240
	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
g987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
m987.pep	250	260	270	280	290	300
	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR					
g987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDSPAKGLDRDR					
	250	260	270	280	290	300
m987.pep	310	320	330	340	350	360
	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNLSLQATDVA					

1396

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|||||
g987      RKPPFIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNLSLQATDVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987. pep AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS LHAKTFIVDGKRIFIG
          |||||
g987      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS LHAKTFIVDGKRIFIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987. pep SFNLDPRSARLNTMGVIVIESPKIAEQMERTLADTTPAYAYRVTLDRHNRLQWHPATRK
          |||||
g987      SFNLDPRSARLNTMGVIVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHPATRK
          430      440      450      460      470      480

          490      500      509
m987. pep TYPNEPEAKLWKRIA AKILSLLPIEGLLX
          |||||
g987      TYPNEPEAKLWKRIA AKILSLLPIEGLLX
          490      500

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

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a987. seq
1  ATGAAACAC GCAGCCTAAT TTCCCTTTTA TGCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCAC TGAAGAAGC GACGGAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTCCCGGCGG ACTGCTGTTT
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCGCGCTCA ACCGCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCAGCA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCGCGCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCGCG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCT GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGG TCATTCAACC TCGACCCCGG TTCCGCACGG CTCATACTG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

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This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987. pep
1  MKTRSLISLL CLLLCSCSSW LPPLERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VRVRLLEDN NTRGLDDLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTD FRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPPFIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL

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1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPARSAR LNTEMGVVIE SPKIAEQMER
 451 TLADTSPEYA YRVTLDRHNR LQWHDPAIRK TYPNEPEAKL WKRIAAILLS
 501 LLPIESLL*

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987. pep	MKTRSLISLLCLLLSCSSWLPPEERTESRHFNTPSKPVRLDNILQIRHTPHTNGLSDIY					
a987	MKTRSLISLLCLLLSCSSWLPPEERTESRHFNTPSKPVRLDNILQIRHTPHTNGLSDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m987. pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
a987	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m987. pep	NTRGLDDLLALDSHPNIEVRLNPFVLRKWRALGYLTDFPRLNRRMHNKSFADNRATI					
a987	NTRGLDDLLALDSHPNIEVRLNPFVLRKWRALGYLTDFPRLNRRMHNKSFADNRATI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m987. pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVEVSHDFDRYWASHSAHNATRIIRSGDIG					
a987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVEVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m987. pep	KGLQALGYNDTSRHALLRVETVEQSPLYQKIQTGCIDWQSVTRTLISDDPAKGLDRDR					
a987	KGLQALGYNDTSRHALLRVETVEQSPLYQKIQTGRIDWQSVQTRTLISDDPAKGLDRDR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m987. pep	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA					
a987	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m987. pep	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLSHAKTFIVDGKRIFIG					
a987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLSHAKTFIVDGKRIFIG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m987. pep	SFNLDPARSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNRLLQWHDPAIRK					
a987	SFNLDPARSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDRHNRLLQWHDPAIRK					
	430	440	450	460	470	480
	490	500	509			
m987. pep	TYPNEPEAKLWKRIAAILLSLLPIESLLX					
a987	TYPNEPEAKLWKRIAAILLSLLPIESLLX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq

1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

1398

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTCGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTTAATCAAC CGCCgaggcg
251 CagttTGCGc gGCGgacaag ctgGATTTGG TCAAATGccg Cgtcgaggcg
301 catAAgGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTCTGT TTATACGAAC GCCAgatgcg tggTGtcatG CAcggcgaca
401 ccggttACCGT CCGTCCTGcG ggtatggaCC GCAGGGGccg ccgcGAAGgg
451 acgtttcttGG ATATTGTCTGA ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGGCGTGG CGATTTTGGG GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTGGGAA CCGGACGGCG TGGCGCGTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAAt cgAAATTGCC GTGCGCAAGC ATCATTGCCC GCaccgaATC
751 AGTGAagcgt gtGcCAAATC CGcgaAAAAA Attcccgacc ATGTACGCCAA
801 AAGCGATTTG AAAGGCCGCG TCGATTTGTG CGACCTTCCT TTGGTAACGA
851 TAGACGCGCA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
901 GTCGGACGCA ATTACCGCCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCCGCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 GCGTGTATTT CCCGCGCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGAAA
1201 TGGCTTTTCA ACGGCATCGG GAATCCGCAC AAAGCCCAAA TCGACACGCT
1251 TTACAAGCTG TTTAAATTTT TGCAGAAAAA ACGTCTGGCG CGCGGGGCGG
1301 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAAA TTGTCCCGCT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGGCGA ATGTTTGGCG GCGGATTTT CTGTTGAAAA
1451 ACAACATAC GGCTTTGTTT CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGGCGACAAC CCGTCGCGGA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGGCGG TTTACGAACC GCATTGCGAA GGGCATTTCG GTTTGGCTTA
1701 TGAAGCATAC GCCCACTTTA CCTCGCCCAT CCGCGCTAT CCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGGAAGAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTTT GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGAAAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTGCGGTGA ATATTTGAAG GcaaaatCtc ccgggggtgtg
1951 gcaaaTtttg gaATATTTGT CACTTTGGAC GATATccata tcgacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGGCGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTTGCCG TCCGGGTCGC GCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCCGGAG AAAGCGGCAG GCGGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGGCGGCGG GGAAAGGGA ATCGAAAAAC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGGCGT
2301 GCCTGCCGTT GCCGAATCGG GAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1  MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFGFVAV LMPMDEGDFV LYERQMRGVM HGDTVTVRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSVILE PDGVARFKPE
201 SQQVIVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHLPHRF
251 SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMIFFDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQLGL LGLQLGGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSWQALGVH TSFCERRADD AGRDVENWLK TYMRDKVGE IFEGKISRGV
651 ANFGIFVTLT DIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPAV AESGKKAKKP VPIKVKRKG KS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```
m988. seq (partial)
1 ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51 CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAAGC TGCGAAAAAA ATTCCCGTCC ATGTACGCAA
351 AAGCGATTG AAAGGCCGCG TCGATTGCG CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
451 GTCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
501 TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATT TCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
651 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGAAA
751 TGGATTTCAG ACGGCATCGA CCATCGGTAC AAAGCCCAA TCGACACCCT
801 TTACAACTC TTCAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTC CTGTTGAAAA
1 001 ACAAGCATAC GGCTTTGTTT CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1 051 CTCGCCACCC TCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1 101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1 151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1 201 CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCTTA
1 251 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1 301 CCGTACACCG CGCCATCAA GCGGTGTTGA ATCAGCAAAC CTACACGCCA
1 351 AAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1 401 TGCCGACGAC GCCAGCCGCG ACGTGAAAAA CTGGCTGAAA ACCTATTATA
1 451 TGCGCGATAA GGTGCGCGAA GTATTGCAAG GTAAAATCTC CGGCATGACC
1 501 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1 551 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
1 601 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCACAT GGGGGACAGG
1 651 GTTGCCGTCC GGGTCGCCC TGCCGATTG GATGACGGAA AAATCGATT
1 701 TGTCTGATT GCCGGGGGGA GCGGCAGGG GCGGAAAGTT AAATCATCCG
1 751 CGTCTGCCAA ACCGGCAGG ACGGCGGGGA AAGGAAGCC GAAAACCGCC
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1400

1801 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
 1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGTT CCGATTAAGG
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
 51 SGQVIVGEIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHQF
 101 SEACAKAAK IPVHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPDAE LLQVMMLRSM
 401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQOQTYTP
 451 KKSQWALGVH TSFCERRADD ASRDVENWLK TYMRDKVGE VFEGKISGMT
 501 SFGIFVTLTG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
 551 VAVRVARADL DDGKIDFVLI AGSGRGRKV KSSASAKPAG TAGKGKPKTA
 601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKKRKKG S*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGMHGD	TVTVRPAGMDRRGRREGTFLDIVERAQSKVVGRFYMDRGVAILEPED				
	130	140	150	160	170	180
m988.pep	40	50	60	70	80	90
	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA					
g988	KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA					
	190	200	210	220	230	240
m988.pep	100	110	120	130	140	150
	VRKHHLPHQFSEACAKAAKIPVHVRKSDLKGRVDLRDLP LVTIDGETARDFDDAVFAEK					
g988	VRKHHLPHRFSEACAKSAKIPDHVRKSDLKGRVDLCDLP LVTIDGETARDFDDAVFAEK					
	250	260	270	280	290	300
m988.pep	160	170	180	190	200	210
	VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVIPMLPENLSNGICSLNPDV					
g988	VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFPRRMIPMLPENLSNGICSLNPDV					
	310	320	330	340	350	360
m988.pep	220	230	240	250	260	270
	ERLCMVCDMVVTYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL					
g988	ERLCMVCDMVVTYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSDGIGNPHKAQIDTLYKL					
	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
g988	FKILQKKRLARGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE					
g988	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALAEQFKGRPDAE					

	490	500	510	520	530	540
m988. pep	400	410	420	430	440	450
	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYTP					
g988						
	LLQVMMLRSMQQAVYEPHCEGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNRRKTYTP					
	550	560	570	580	590	600
m988. pep	460	470	480	490	500	509
	KKSWQALGVHTSFCERRADDASRDVENWLKTYMYMRDKVGEVFEGKIS-GMTSFGIFVTLT					
g988	:	:	:	:	:	:
	NKSWQALGVHTSFCERRADDAGRDEVWLKTYMYMRDKVGEIFEGKISRGVANFGIFVTLT					
	610	620	630	640	650	660
m988. pep	510	520	530	540	550	569
	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
g988						
	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
m988. pep	570	580	590	600	610	629
	IAGGSGRGRKVKSSASAKPAGTAGKGPKPTAAEKKTARGGKVRGRGASAAAESRKAKKP					
g988						
	IAGESGRRRKVKLSASAKPAGAAGKGKSKTTAEKKTARCGKVRGRGVPAAVESGKKAKKP					
	730	740	750	760	770	780
m988. pep	630	640				
	VPIKVKRKGKXS					
g988						
	VPIKVKRKGKXS					
	790					

a988.seq	1	ATGAATAAAA	ATATTAATC	TTTAAATTTA	CGGGAAAAAG	ACCCGTTTTT
51	AAGTCGTGAA	AAACAGCGTT	ATGAACATCC	TTTGCCAGT	CGGGAATGGA	
101	TAATCGAGCT	GCTTGAACGT	AAAGGCGTAC	CATCCAAGAT	TGAAGCTTTG	
151	GTACGCGAAT	TGTCGATTAA	GGAGAAGAG	TACGAATTTT	TCGAACGTCG	
201	TCTGAAGGCG	ATGGCGCGGG	ACGGTCAGGT	TTTAAATCAAC	CGTCGGGGCG	
251	CGGTTTGC	GGCGGACAAA	TTGGATTG	TCAAATGCCG	TGTCAGGCG	
301	CACAAAGACC	GCTTCGGTTT	CGCGTGCCG	CTCAGCCCG	CCAAAGACGG	
351	TGATTTTG	TTGTACGAAC	GCCAGATGCG	CGGCATTATG	CACGGCGATA	
401	TTGTCACTGT	TCGTCTGCC	GGCATGGACG	GTAGGGGCCG	CCCGGAAGGG	
451	ACGGTTCTG	ATATTGTGCA	ACGCGCGCAA	AGCAAAGTGG	TCCGCGCTTT	
501	CTANATGGAT	AGGGGCGTGG	CGATTTTGA	GCCGGAAGAC	AAGCGTCTGA	
551	ACCAAAGCAT	CGTATTGGAA	CGGACGGCG	TGGCGGTTT	CAAACCTGAA	
601	TCCGGTCAGG	TCATCGTCGG	CGAAATTGAG	GTTTATCCTG	AGCAAAACCG	
651	GCCGGCAGT	GCAAAAATCA	TGGAAGTTT	GGCGGATTAT	GCCGACAGCG	
701	GCATGGAGAT	TGAATTGCC	TCGCGCAAGC	ATCATTTGCC	GCACCAATTC	
751	AGTGAAGCGT	GTGCCAAAGC	CGCGAAAAAA	ATTCCCGACC	ATGTACGCAA	
801	AAGCGATTG	AAAGGCCGCG	TGATTTGCG	CGACCTGCCT	TTGGTAACGA	
851	TAGACGGCGA	AACGGCTCGA	GATTTTGACG	ATCGCGTGT	TGCCGAGAAA	
901	ATCGGACGCA	ATTACCGTCT	GGTCGTGGCG	ATTGCCGATG	TCAGCCATTA	
951	TGTCGCGCCC	GATGACGCTA	TCGACACGGA	CGTCCAGGA	CGCAGCACCA	
1001	GTGTTTACTT	CCCGCGCCGC	GTGATTCCCA	TGTTCCGGGA	AAACCTGTCC	
1051	AACGGCATCT	GCTCGCTCAA	TCCTCATGTC	GAGCGTTTGT	GTGTGGTGTG	
1101	CGATATGGTT	ATCACTTACG	CGGGCAATAT	CAAAGAATAC	CGCTTCTACC	
1151	CGCCCGTGAT	GCGCTCTCAT	GCCCGCCCTGA	CCTACAACCA	AGTTTGGAAA	
1201	TGCGTTTCAG	GCGGCATCGA	GCACTCCGTT	AAAACCCAAA	TCGACACGCT	
1251	TTACAAATC	TTCAAAATCC	TTCAGAAAAA	GC GTTTCGAA	CGCGGGGCGG	
1301	TGGAGTTTGA	CAGCATCGAA	ACCCAAATGC	TTTTCGACGA	CAACGGTAAA	
1351	ATTGAAAAAA	TCGTCCCCGT	TGTCCGCAAC	GATGCCACAC	AGCTGATTGA	
1401	AGAATGTATG	TTGGCGGCGA	ACGTTTGC	AGCGGATTTT	CTGTTGAAAA	
1451	ACAAGCATAC	CGCATGTTC	GCAACCAT	TGGGGCCAC	GCCCCGAAAA	
1501	CTCGCGCCT	TGCGCGAGCA	GCTCGTCTG	TTGGGGCTTC	AACTTGGCGG	
1551	CGGCGACAAC	CCGTCGCCGA	AAGACTATGC	CGCGCTTGCC	GGACAGTTCC	

1 601	AAGGCAGGCC	GGATGCCGAA	TTGCTGCAAG	TCATGATGTT	GCGCTCCATG
1 651	CAACAGGCGG	TTTACGAACC	GCATTGCGAC	GGACACTTTG	GTCTTGCCTA
1 701	CGAAGCATAC	GCCCACCTCA	CCTCGCCCAT	CCGCGCCTAT	CCCAGACTGA
1 751	CCGTACACCG	CGCCATCAAA	GCCGCTGTTA	ATCAGCAAAC	CTACACGCCA
1 801	AAAAAAGACT	GCCAGGCTTT	GGGGCTGCAT	ACCTCGTTCT	GTGAGCGCCG
1 851	TGCCGACGAC	GCCAGCGCGC	ACGTGGA AAA	CTGGCTGAAA	ACCTATTATA
1 901	TGCGCGATAA	GGTCGGCGAA	GTATTGGAAG	GTA AAATCTC	CGGCATGACC
1 951	AGTTTTGGTA	TCTTTGTAA C	ACTGGACGGC	ATCCACATTG	ACGGCTTG GT
2 001	GCATATCAG	GATTTGGGCG	AAGACTATTT	CAACTTCCCG	CCCCAAATCA
2 051	TGGCAATCGA	AGGCGAACGC	AGCGGCATCC	GTTTCAACAT	GATGGACAGG
2 101	TGTGCCGTCC	GGGTCGCGCG	TGCCGATTTG	GATGACGGAA	AAATCGATT T
2 151	TGTCCTGATT	GCCGGGGGGA	GCGGCAGGGG	GCGGAAAGTT	AAATCATCCG
2 201	CGTCTGCCAA	ACCGGCAGGG	ACGCGGGGGA	AAGGGAAGCC	GAAAACCGCC
2 251	GCCGAGAAAA	AAACAGCGCG	AGGCGGCAAA	GTAAGGGGAA	GGGGCGCGCT
2 301	TGCCGCCGCA	GAATCGAGGA	AAAGGGCAAA	GAAACCGGTT	CCGATTAAAG
2 351	TAAAAAAAACG	GAAAGGCAAAA	TCATAA		

This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

a988.pcp

1	MNKNIKSLNL	REKDPFLSRE	KQRYEHPLPS	REWIIELLER	KGVPSKIEAL
51	VRELSIKEEE	YEFFERRLKA	MARDGQVLIN	RRGAVCAADK	LDLVKCRVKA
101	HKDRFGFAVP	LTPAKDGDFV	LYERQMGRIM	HGDIVTVRPA	GMDGRRGRREG
151	TVLDIRVERAQ	SKVVGFRFXMD	RGVAILEPED	KRLNSQSVLPE	PDGVARFKPKE
201	SEQVIVGEIE	YVPEQNRPAV	AKIIEVLGDY	ADSGMEIEIA	VRKHHLPHQF
251	SEACAKAAKK	IPDHVRKSDL	KGRVDLRDL	LVTIDGETAR	DFDDAVFAEK
301	IGRNYRLVVA	IADVSHYVRP	DDAIDTDAQE	RSTSVYFPRR	VIPMLPENLS
351	NGICSLNPHV	ERLCVVCDMV	ITYAGNIKEY	RFYPAPVMRSH	ARLTYNQVWK
401	WLSGGVIEHPF	KTQIDTLTKL	FLKIQKKRFE	RGAVEFDSIS	TQMLFDDNGK
451	IEKIVPEVVR	DAHKLIEECM	LAANVCAADF	LLKNKHTALF	RNHLDPTPEK
501	LAALREQLGL	LGLQLGGGDN	PSPKDYAALA	GQFKGRPDAE	LLQVMMLRSM
551	QQAVYEPHCD	GHFGLAYEAY	AHFTSPIRRY	PDLTVHRAIK	AVLNQQTYYT
601	KKSQWALGVH	TSFCERRADD	ASRDVENWLK	TYMYRDKVGE	VFEGKISGMT
651	SFGIFVTLDG	IHIDGLVHIS	LDGEDYFNFR	PEIMAEGER	SGIRFNMGDR
701	VAVRVARADD	DDGKIDFVLI	AGSGSGRKRV	KSSASAKPAG	TAGKGKPKTA
751	AEKKTARGGL	VRGRGASAAA	ESRKKAKKPV	PIKVKKRKGK	S*

m988/a988 97.0% identity in 641 aa overlap

		10	20	30
m988.pep		TVLDIVERAQSKVVGRFYMDRGVAILEPED		
a988	LYERQMRGIMHGDI VTVRPAGMDGRGRREGTVLDIVERAQSKVVGRFXMDRGVAILEPED			
	130 140 150 160 170 180			
		40 50 60 70 80 90		
m988.pep	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA			
a988	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA			
	190 200 210 220 230 240			
		100 110 120 130 140 150		
m988.pep	VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK			
a988	VRKHHLPHQFSEACAKAAKKIPDHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK			
	250 260 270 280 290 300			
		160 170 180 190 200 210		
m988.pep	VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFRRVIPMLPENLSNGICSLNPDV			
	: : : : : :			
a988	IGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFRRVIPMLPENLSNGICSLNPHV			
	310 320 330 340 350 360			
		220 230 240 250 260 270		
m988.pep	ERLCMVCDMVVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGI DHPYKAQIDTLTKL			
	: : : : :			
a988	ERLCVVCDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSGGIEHPFKTQIDTLTKL			

1403

	370	380	390	400	410	420
m988. pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQ	MI	FDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF			
a988	FKILQKKRFERGAVEFDSIETQ	ML	FDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF			
	430	440	450	460	470	480
m988. pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSFKDYAALVEQFKGRPDAE					
a988	LLKNKHTALFRNHLGPTPEKLAALREQLGLLGLQLGGGDNPSFKDYAALAGQFKGRPDAE					
	490	500	510	520	530	540
m988. pep	400	410	420	430	440	450
	LLQVMMLRSMQQAVYEPHCDGHFLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
a988	LLQVMMLRSMQQAVYEPHCDGHFLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
	550	560	570	580	590	600
m988. pep	460	470	480	490	500	510
	KKSWQALGVHTSFCERRADDASRDVENWLKTYIMRDKVGEVFEGKISGMTSFGIFVTLDG					
a988	KKSWQALGVHTSFCERRADDASRDVENWLKTYIMRDKVGEVFEGKISGMTSFGIFVTLDG					
	610	620	630	640	650	660
m988. pep	520	530	540	550	560	570
	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
	670	680	690	700	710	720
m988. pep	580	590	600	610	620	630
	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKAKKPV					
a988	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKAKKPV					
	730	740	750	760	770	780
m988. pep	640					
	PIKVKKRKGKXS					
a988	PIKVKKRKGKXS					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989. seq

1	ATGACCCCTT	TCACACTGAA	AAAAACCGTC	CTGCTGCTCG	GCACTGCCTT
51	TGCCGCCGCA	TCTGTCCACG	CATCCGGCTA	CCACTTCGGC	ACACAGTCGG
101	TCAACGCGCA	AAGCACGGCA	AATGCCGCCG	ACGCGTCGAC	CATCTTCTAC
151	AATCCC GCCG	GCCTGACCAA	ACTCGACAGC	AGCCAGATT	CCGTCAACGC
201	CAACATCGTG	CTGCCCAGCA	TTCATTATGA	AGCAGATTCC	GCCACCGACT
251	TTACCGGGCT	TCCCGTCCAA	GGTTCTAAAA	ACGGCAAAAT	CACCAAAACC
301	ACGGTCGCAC	CCCACATTTA	CGGCGCATAC	AAAGTCAACG	ACAATCTGAC
351	CGTGGGCTTG	GGCGGTGACG	TCCCCTTCGG	CTCTGCCACC	GAATACGAAA
401	AAGATTCCGT	GTTGCGCCAC	AACATCAACA	AACTCGGTCT	GACCAGCATC
451	GCCGTCGAAC	CTGTCGCCGC	GTGGAAATC	AACGAACGCC	ATTCCTTCGG
501	CGCAGGCATC	ATCGCCCAAC	ATAATTCCGC	CGAACTGCCG	AAATATGCCG
551	ACTGAGGAAT	CCCCAAAAAA	GCGCAAATGC	TGCAAGCAAC	ACCTTCTAAT
601	CCTACTGCCG	CTGCTCAAAT	CAAGGCCGAC	GGACACGCCG	ATGTCAAAGG
651	CAGCGATTGG	GGCGTCGGCT	ACCAACTGGC	GTGGATGTGG	GACATCAACG
701	ACCGCGCGCG	CGTGGGCGTG	AACTACCGTT	CCAAAGTTTC	ACACACGCTC
751	AAAGGCGATG	CCGAATGGGC	GGCAGACGGC	GCGGCGGCGA	AACAACAGTG
801	GAATGACAAT	ATGCTCACAC	CGCTCGGTTA	CACGGCGAAT	GAAAAAGCCA
851	GTGTCAAAAT	CGTAACGCCT	GAGTCTTTGT	CCGTACACGG	CATGTACAAA

1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAACCTGGA CGCGCCACAG
951 CCGCTTCAAT AAGCGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAACTG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCCGCAAC GCCGACTacc
1151 GCATGAACAG CCTGCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TCGGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

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This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```

g989. pep
1  MTFPTLKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51  NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNDNLTVGL GVVVPFGSAT EYKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAAQIKAD GHADVKGSDW GVGYQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAQKQWQNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMKY
301 VSDKADLFGD VTWRHSRFN KAELFFEKEK NIANGKKS DR TTITPNWRNT
351 YKVLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSAGM
401 KYHIGKNHVV DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQYTYKFK *

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

```

m989. seq
1  ATGACCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51  TGCCGCGGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCAGCGCA AATGCCCGCG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA
201 GATTTCGGTC AACGCCAACA TCGTGTCTGC CAGCATTCTAT TATGAGGCGG
251 ATTCGGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTT GAAAAGCGGC
301 AAAATCACCA AAACCAACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCGGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAACCGC CCAAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTGAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAACATC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACGGCGAA TGAAAAGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCGGCGA
951 CGTAACCTGG ACGCGCCACA GCCGCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAAGAAAA AACCGTCGTC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCG
1151 TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTTCTCCG CCGGTATGAA ATACCATATC GGTA AAAACC ACGTCGTGCA
1251 TGCCGCCCTAC ACCCATATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACCACG CCGACATCAT CGGTCTGCAA TACACCTACA AATTCAAATA
1401 A

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This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```

m989. pep
1  MTPSALKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKPPKPNQVA EAAKIQADGH ADVKGS DWGF GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAEWADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGMKYKVD KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

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1405

351 PNWRNTYKVG FGGSYQISEP LQIRAGIAFD KSPVRNADYR MNSLPDGNRI
 401 WFSAGMKYHI GKNHVVDAAI THIHINDTSY RTAKASGNDV DSKGASSARF
 451 KNHADIIGLQ YTYKFK*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

	10	20	30	40	50
g989. pep	MTPFTLKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL				
m989	MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL				
	10	20	30	40	50
	60	70	80	90	100
g989. pep	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNKGKITKTTVAPHIYGAYKVNDN				
m989	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN				
	70	80	90	100	110
	120	130	140	150	160
g989. pep	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHN				
m989	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT				
	130	140	150	160	170
	180	190	200	210	220
g989. pep	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI				
m989	SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFYQLAWMWDI				
	190	200	210	220	230
	240	250	260	270	280
g989. pep	NDRARVGVNYSKVSHTLKGDAEWAADGAAKQWQNDNMLTPLGYTANEKASVKIIVTPES				
m989	NDRARVGVNYSKVSHTLKGDAEWAADGAAKAMWS-TMLAANGYTANEKARVKIIVTPES				
	250	260	270	280	290
	300	310	320	330	340
g989. pep	LSVHGMKYVSDKADLFGDVTWTRHSRFNKAELFFEKEKNIANGKKSDDRTTITPNWRNTYK				
m989	LSVHGMKYVSDKADLFGDVTWTRHSRFDKAEVFEKEKTVVKGK-SDRTTITPNWRNTYK				
	300	310	320	330	340
	360	370	380	390	400
g989. pep	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
m989	VGFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
	360	370	380	390	410
	420	430	440	450	460
g989. pep	AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX				
m989	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX				
	420	430	440	450	460

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989. seq

1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTACTGCTCG GCACTGCCTT
 51 TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCACTTCGGC ACACAGTCGG
 101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA
 151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA
 201 GATTTCCGTC AACGCCAACA TCGTGTGCC CAGCATTCAT TATGAGGCGG
 251 ATTCCGCCAC CGACTTTACC GGGCTTCCG TCCAAGGTC GAAAAGCGGC

1406

```
301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTTCGT
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCGGAGC
551 TGCGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAACTA CCGTTCACAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GCGGAAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTCG GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1 001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCCAAC
1 051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTTCTTATC AAATCAGCGA
1 101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCCGCA
1 151 ACGCCGACTA CCGCATGAAC AGCCTGCCCG ACGGCAACCG CATCTGGTTC
1 201 TCCGCCGCGA TGAATATCCA TATCGGCAAA AACCACGTCG TCGATGCCGC
1 251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCACG GCGAAGGCAA
1 301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTTCGCGCAG TTTCAAAAAC
1 351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

```
a989.pep
1  MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEAADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGS DWFGYQ LAWMWDINDR ARVGVNYSRK
251 VSHTLKGDAE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMVKVSDKA DLFGDVTWTR HSRFDKAEIV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIGK NHVVDAAATH IHINDTSYRT AKASGNDVDS KGASSAREFKN
451 HADIIGLQYT YKFK*
```

m989/a989 93.1% identity in 467 aa overlap

```

      10      20      30      40      50      60
m989.pep MTPSALKKTVLLLTAFAAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
|||||
a989     MTPSALKKTVLLLTAFAAAASQASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
      10      20      30      40      50      60

      70      80      90     100     110     120
m989.pep TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVDN
|||||
a989     TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVDN
      70      80      90     100     110     120

      130     140     150     160     170     180
m989.pep LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSGAGIIAQHT
|||||
a989     LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSGAGIIAQHT
      130     140     150     160     170     180

      190     200     210     220     230     240
m989.pep SAELRKYADWGIKSAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWFGYQLAWMWDI
|||||
a989     SAELRKYADWGIMEKAKALKETPPNPT---KAAQIKADGHADVKGSDWFGYQLAWMWDI
      190     200     210     220     230

      250     260     270     280     290     299
m989.pep NDRARVGVNYSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTAN EKARVKIVTPES
|||||
a989     NDRARVGVNYSKVSHTLKGDAEWAADDAMAKQLWDANKLALLGYTPSEKARVKIVTPES
```

1407

	240	250	260	270	280	290
m989. pep	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEIVFEKEKTVVKGKSDRTTITPNWRNTYKV					
a989	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEIVFEKEKTVVKGKSDRTTITPNWRNTYKV					
	300	310	320	330	340	350
m989. pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
	360	370	380	390	400	410
m989. pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
	420	430	440	450	460	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990. seq
1   ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGGC GGTAAAAAGT CAATTACAGG ATTTATACAA AACAAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTTAGTA CGCTCAAACA GACGATGCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCCAC GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCCGATA ATGCCGCAT CCGCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTCTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGCCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CAAAACGGC GGATTCCGGT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGACGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGGC
1001 TCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CCGCGTGATG
1201 GGCGGCAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGTATGTTT ATGGCGGGGG TGTTTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCCTGCGG AACGCTACAA
1401 AACCAGAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTCGGAAAA GGCAATAATG TGCGGTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GGCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
1601 GCATTGCGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCGGTAT TGAAGCCGGT TGAAGAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990. pep

1408

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLQKQMP DLINKLVEDS VLTSPHNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLKQOC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIIRGGA AADGWRKGVQ IGGEVFRVQN EGSRLAIGVM
401 GGRAGQHASV NGKGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTGK WTASVEGGYN ALVAEGIVGK GNNVRFYLQP
501 QAQFTYLGVN GGFTDSEGT VGLLGSQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

```

a 990 . seq
1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAACATAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTTATACAA AACAAGACCC
301 GAAGCTTGGG AAGAAAATAA AAAACGACT GAGGAGGCGT ATATAGAACA
351 GCTTGACCA AAATTTAGTA TACTCAAACA GAAAAACCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCAC GTCCGCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTCTCTGTTT GGCTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGGCCG GAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCCT
851 TTAACAAAA TTACCGCAGG GGACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGCGGAT TTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAATAACT TTGTTCCGGC
1001 TGCGTGCCGC CGACAGGGG GACGACGTGT ATGCCGCGA TCCGTCCTCGT
1051 CAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GCGGCGCAA AGCGTGCAA ATCGGCGGCG
1151 AGGTGTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CGGCTGATG
1201 GCGGCGAGG CTGGCCAGCA CGCATCAGT AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGTT ATGGCGGGG TGTATTGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTGAAGG CGGCTACAAC GCGTTTGTGG
1451 CGGAAGGCGT TGTCGGAAAA GGCAATAATG TGCGGTTTTA CCTGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGACGCGG TCAGTGCAA AGCCGCGCCG
1601 GCATTCCGGC AAAAACCCTT TTTGCTTTC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTTGCACAGG TCAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCCGCAT TGAAGCCGTT TGGAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGACGG CGACAAAGAA GCCGATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

```

a 990 . pep
1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITDY GDNLKDAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DLINKLVEDS VLTSPHNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEDKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLKQOC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIIRGGA AADGRRKGVQ IGGEVFRVQN EGSRLAIGVM

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1409

401 GGRAGQHASV NGKGAAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY
 451 QRFKHRINDE NRAERYKTG WTASVEGGYN ALVAEGVVGK GNNVRFYLQP
 501 QAQFTYLGVN GGFTDSEGTA VGLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
 551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHSARIG
 601 YGKRTDGDKE AALSLKWL*F

m990/a990 96.0% identity in 619 aa overlap

m990 - pep	10	20	30	40	50	60
	MFRAQLGSNTRSTKIGDDADFSFSKPKPGTSHYFSSGKTDQNSSEYGYDEINIQQKNYN					
a990	10	20	30	40	50	60
	MFRAQLGSNTRSTKIGDDADFSFSKPKPGTSHYFSSGKTDQNSSEYGYDEINIQQKNYN					
m990 - pep	70	80	90	100	110	120
	SGILAVDNMPVVKKYITEKYGADLKQAVKSQLQDLYKTRPEAWAENKKRTEEAYIAQFGT					
a990	70	80	90	100	110	120
	SGILAVDNMPVVKKYITDYGDNLDKAVKKQLQDLYKTRPEAWAENKKRTEEAYIEQLGP					
m990 - pep	130	140	150	160	170	180
	KFSTLKQTMPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
a990	130	140	150	160	170	180
	KFSILKQKNPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
m990 - pep	190	200	210	220	230	240
	MTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP					
a990	190	200	210	220	230	240
	MTLKDSLWEPRRHSDIHMLETSDNARIRLNTKDEKLTVHKAYQGGADFLFGYDVRESDEP					
m990 - pep	250	260	270	280	290	300
	ALTFEKQVSGQSGVVLERRPENLKTLDGRKLIAAKTADSGSFAFKQNYRQGLYELLKQC					
a990	250	260	270	280	290	300
	ALTFEKQVSGQSGVVLERRPENLKTLDGRKLIAAEKADSNSFAFKQNYRQGLYELLKQC					
m990 - pep	310	320	330	340	350	360
	EGGFCLGVQRLAIPAEAVLYAQAYAAANTLFGRLAADRGDDVYAADPSRQKLWLRFIGG					
a990	310	320	330	340	350	360
	EGGFCLGVQRLAIPAEAVLYAQAYAAANTLFGRLAADRGDDVYAADPSRQKLWLRFIGG					
m990 - pep	370	380	390	400	410	420
	RSHQNIIRGGAAADGWRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSD					
a990	370	380	390	400	410	420
	RSHQNIIRGGAAADGRRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSY					
m990 - pep	430	440	450	460	470	480
	LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY QRFKHRINDENRAERYKTGWTASVEGGYN					
a990	430	440	450	460	470	480
	LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY QRFKHRINDENRAERYKTGWTASVEGGYN					
m990 - pep	490	500	510	520	530	540
	ALVAEGIVGKGNVRFYLQPPAQFTYLGVNGGFTDSEGTA VGLLGSGQWQSRAGIRAKTR					
a990	490	500	510	520	530	540
	ALVAEGVVGKGNVRFYLQPPAQFTYLGVNGGFTDSEGTA VGLLGSGQWQSRAGIRAKTR					
m990 - pep	550	560	570	580	590	600
	FALRNGVNLQPPFAAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHSARIG					
a990	FALRNGVNLQPPFAAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHSARIG					

1410

	550	560	570	580	590	600
	610	620				
m990 . pep	YGKRTDGDKEAALSLKWLFX					
a990	YGKRTDGDKEAALSLKWLFX					
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

```

g992 . seq
1  ATGTTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCCC TGTCGCTTTT GGGCGCGTTG GGTATACGG
101 GATATGACAG TGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GGCACCTGCAG GGGACGTGGG TTTGACGCGC CCCGTTCCGC GACGGGCATC
201 GCGGAAATCC GGGCAGAGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGATACCCCT TCACGTCATC GACGGCGACG GCGCGAAACA TAAAATTCGG
301 ATGGCGTATA TCGACGCACC GGAGATGAAA CAGGCTTACG GTACACGTTT
351 GCGCGACAAC CTGCGCGCGG CGGCGGAGG TAGGAAAGTC AGTGACGTG
401 TGTGTGAAAC CGACCGCTAT CAGCGCGAAG TGGCGCAGGT ATCCGCGGCG
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGCGG CGTGGCATT
501 TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GCGCGATTTT GCCGACTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAATCCGC AAGCGCCGTG GCGGTACCGC CGGCGAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATCCGTGGG CGAATGGTTG GGCATTGCTT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

```

g992 . pep
1  MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGVDSEAV RTAVAVLDVL
51  GTAGDVGFDA PVRRRASAKS GHSYTGTVSK VYDGDTHLVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDLNLQVQ DGAAWHYKSY AKEQDKADF ADYADAQIQ ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWMDSVGEWL GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

```

m992 . seq
1  ATGTTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCCC TGTCGCTTTT GGGTCCGTTG GGTATACGG
101 GGTACGGCAG CGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GCGCGGCGCAG GGGACGCGGG TTTGACGCGC CCCGCTCCGC GCCGAGCATC
201 GCGGAAATCC GGGCAGGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGACACCCCT TCACGTTATC GACGGCGACG GCGCGAAACA CAAAATCCGG
301 ATGGCGTATA TCGACGCGCC GGAGATGAAA CAGGCTTACG GCACGCGTTC
351 GCGCGACAAC CTGCGCGCGG CGGCGGAAG CAGGAAAGTC AGCGTGCGCG
401 TGTTGATAC CGACCGCTAC CAGCGCGAAG TGGCGCAGGT TTCTGTCGGC
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGCGG CGTGGCATT
501 TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GCGCGATTTT GCCGATTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAATCCGC AAGCGCCGTG GCGGTACCGC CGAGCAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTGCTT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

```

m992 . pep
1  MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTYGSEAV RTAVAVLDVL
51  GAAGDAGSDA PARRRASAKS GHRYTGTVSK VYDGDTHLVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDLNLQVQ DGAAWHYKSY AKEQDKADF ADYADAQIQ ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWMDAVGEWL GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

1411

	10	20	30	40	50	60
m992.pep	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
g992	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
g992	PVRRRASAKSGHSYTGTVSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVSVRVFD TDRYQREVAQVSVGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF					
g992	LRAAAEGRKVSVRVFETDRYQREVAQV SAGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF					
	130	140	150	160	170	180
	190	200	210	220	230	
m992.pep	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIX					
g992	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDSVGEWLGIX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

a992.seq

1	A	T	G	T	T	C	A	G	A	C	G	G	C	A	T	T	G	A	A	A	A	A	T	A	T	C	A	T	
51	G	A	A	T	G	G	C	T	T	C	C	G	T	C	G	C	T	T	T	G	G	T	G	C	G	T	T	G	T
101	G	G	T	A	C	G	C	G	A	G	G	C	G	T	G	C	G	G	T	T	G	C	C	G	T	A	C	T	C
151	G	G	C	G	C	G	C	A	G	G	C	G	G	T	T	C	C	A	C	G	C	G	C	C	C	C	C	C	C
201	G	G	C	G	A	A	T	C	C	G	T	A	C	A	C	A	G	G	C	A	C	G	G	T	T	C	A	A	A
251	G	C	G	A	C	C	C	T	T	C	A	C	G	T	T	A	T	C	A	C	G	T	T	A	T	C	A	C	C
301	A	T	G	G	C	G	T	A	T	C	A	C	G	C	G	C	C	G	A	G	A	T	G	A	A	C	A	G	A
351	G	C	G	C	A	A	C	T	G	C	G	C	G	C	G	G	A	A	G	C	A	G	A	A	G	T	C	A	G
401	T	G	T	T	C	G	A	C	A	C	A	C	T	A	C	A	G	A	G	A	G	A	G	T	C	T	A	T	C
451	A	A	A	C	C	G	A	T	T	G	A	A	C	T	G	A	T	G	C	A	G	G	T	G	C	A	G	A	T
501	T	A	A	A	G	T	T	A	G	A	A	C	A	G	A	A	C	A	G	A	A	C	A	G	A	A	C	A	T
551	C	C	G	A	C	G	T	C	A	A	T	C	A	G	G	C	G	A	A	A	G	G	A	A	C	A	A	A	G
601	A	A	A	A	T	C	C	G	A	A	G	C	C	G	T	G	A	A	A	A	G	A	A	C	A	A	A	A	G
651	G	G	C	A	A	T	A	A	G	A	G	A	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	
701	A	A																											

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

a992.pep

1	M	F	R	R	H	R	L	K	N	M	Q	I	K	K	I	M	K	W	L	P	V	A	L	S	L	L	G	A
51	G	A	A	G	D	A	G	S	D	A	P	A	R	R	R	A	S	A	K	S	G	H	R	Y	T	G	T	V
101	M	A	Y	I	D	A	P	E	M	K	Q	A	Y	G	T	R	S	R	D	N	L	R	A	A	A	E	G	
151	K	T	D	L	N	L	M	Q	V	Q	D	G	A	A	W	H	Y	K	S	Y	A	K	E	Q	Q	D	K	
201	K	N	P	Q	A	P	W	A	Y	R	A	G	R	S	G	G	G	N	K	D	W	M	D	A	V	G		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992.pep	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
m992	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
m992	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180

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```

a992.pep      LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
               |||
m992          LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
               130      140      150      160      170      180

               190      200      210      220      230
a992.pep      ADYADAQIQAERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDDAVGEWLGIX
               |||
m992          ADYADAQIQAERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDDAVGEWLGIX
               190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1   CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATTCCG ATGGTGGAAG
101 TTACCGGGCA GTATCTGCAC TATATTGCC AAATGGAAGC CTATCAGTTT
151 GATTGGCGG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGCG TTGCCTACGA GCAATGAAA
301 CTGCGCGCGC AGGGTTTGA CGCGCTGCCG CGTGCGGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCGAGG
401 TTTACATCGC CGATTGATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCCTT CCGTGC CGCGC
501 GCAATGACG GCAATCCTGC GCCGTTTGA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTACAGACG CATTTTCGGC ACACGGGGCG GGC CGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1   LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVEITGOYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTEAVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLVRAQMT AILRRLNEHG ICRFHALFNP EQGAAYVIVN
201 FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1   TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTACT GGATATTCCG ATGGTGGAAG
101 TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGCG TGGCTTACGA ACAGATGAAG
301 CTGCGCGCGC AGGGTTTGA CGCGCTGCCG CGAGCCGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCAAA GAAACCATCT CCGTGC CGCGC
501 GCAATGACG GCAATCCTGC GCCGTTTGA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCTGCAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTACAGACG CATTTTCGGC ACACGAGGCG GGC CGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1   LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MKVITEQYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNGHG ICRFHDLFNP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

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m993/g993 93.1% identity in 248 aa overlap

	10	20	30	40	50	60
m993.pep	LKVVLSFGQPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQIETYQ	FDLAAEYLLMA			
g993	LKVVLSFGQPLDLLLYLIRKQNI	DVLDIPMVEITGQYLHYIAQMEAYQ	FDLAAEYLLMA			
	10	20	30	40	50	60
	70	80	90	100	110	120
m993.pep	AMLIEIKSRLLLPRTETVEDEEADPRAELV	RRLAYEQMKLAAQGLDALPRAGRDFAWAY				
g993	AMLIEIKSRLLLPRTAEVEDEEADPRAELV	RRLAYEQMKLAAQGLDALPRAGRDFAWAY				
	70	80	90	100	110	120
	130	140	150	160	170	180
m993.pep	LPLEIAVEAKLPEVYITDLTQAWLGILSR	AKHTRSHEVIKETISVRAQMTAILRRLNKG				
g993	LPLEIAAETKLPEVYIADLMQAWLGILSR	AKHTRSHEVIQETLSVRAQMTAILRRLNEHG				
	130	140	150	160	170	180
	190	200	210	220	230	240
m993.pep	ICRFHDLFNPQGAAYVVVNFIALLELAKE	GLVRIVQEDGFGEIRISLNHEGAHSDGISG				
g993	ICRFHALFNPQGAAYVIVVNFIALLELAKE	GLVGIVQEDGFGEIRISLNHEGAHSDGIFG				
	190	200	210	220	230	240
	249					
m993.pep	TRGGRDVF					
g993	TRGGRDVF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

1	CTGAAAGTCG	TATTGAGCAG	TTTCAAGGC	CCTTTGGATC	TGCTGCTCTA
51	CCTTATCCGC	AAGCAGAACA	TCGATGTTCT	CGATATTCCG	ATGGTGAAGA
101	TTACCGAACA	GTATCTGCAC	TACATCGCCC	AAATAGAAAC	CTATCAGTTT
151	GATTTGGCGG	CGGAATATCT	TTGATGGCA	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCCTG	CTGCTGCCGC	GTACCGAAAC	CGTCGAAGAC	GAAGAAGCCG
251	ACCCGCGTGC	CGAGTTGGTG	CGCCGCCTGC	TGGCTTACGA	GCAGATGAAG
301	CTGGCGGCAC	AAGGGTTGGA	TGCGCTTCCT	CGTGGCGGCC	GGGATTTCGC
351	ATGGGCATAC	CTGCCACTGG	AAATTGCCGT	CGAAGCCAAG	CTGCCCGAAG
401	TCTATATTAC	CGACTTGACG	CAGGCGTGGC	TGAGTATTTT	GTCTCGGGCA
451	AAACATACGC	GCAGCCACGA	AGTTATCAAA	GAAACCATCT	CCGTGCGCGC
501	GCAAATGACG	GCAATCCTGC	GCCGTTTGAA	CAAACACGGG	ATATGCAGGT
551	TTACAGACCT	GTTCAATCCC	GAACAGGGCG	CGGCTTACGT	GGTCGTCAAC
601	TTCATCGCAC	TGTTGGAGCT	TGCCAAAGAA	GGTTGGTTCG	GAATCGTACA
651	GGAAAGTCGGT	TTCGGAGAAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCGC
701	ATTACAGACG	CATTCCGGC	ACACGGGGCG	GGCGCGATGT	GTTCTAA

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

1	LKVVLSFQGLDLLLYLIR	QNI	DVLDIP	MVKITEQYLH	YIAQIETYQF
51	DLAAEYLLMA	AMLIEIKSRL	LLPRTETVED	EEADPRAELV	RRLAYEQMK
101	LAAQGLDALP	RAGRDFAWAY	LPLEIAVEAK	LPEVYITDLT	QAWLSILSRA
151	KHTRSHEVIK	ETISVRAQMT	AILRRLNKHG	ICRFHDLFNP	EQGAAYVVVN
201	FI	ALLELAKE	GLVGIVQEVG	FGEIRISLNH	EGAHSDGISG

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

	10	20	30	40	50	60
a993.pep	LKVVLSFQGLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQIETYQ	FDLAAEYLLMA			
m993	LKVVLSFQGLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQIETYQ	FDLAAEYLLMA			

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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
m993	70	80	90	100	110	120
a993.pep	130	140	150	160	170	180
m993	130	140	150	160	170	180
a993.pep	190	200	210	220	230	240
m993	190	200	210	220	230	240
a993.pep	249					
m993	249					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1   ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGGTTGC TTCTTACCGC
51  CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTGCTTGC CTTGGGCGAT TCGCTCACCT TCGGCTACGG AGCAAACCCC
151 GCGGAATCCT ACCCGCGCA ACTGCAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACGTCCGC GCAAGCCCTA TCGGCGCTGC
251 CCGCGCTGTT GGCACGCAAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCCAAAGT TCCCGAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AAAAGGAAA CATTCGCCG GTCTCGTCG
401 GCGTGCCGCA CATCACA CTG GCGCGTTGT TCGGGCATT GAGCGACCAT
451 CCGCTGTATG AGGATTTGTC CGAGGAATAC GGCATTCCGT TGTTCGGCGG
501 CCGGTGGGCG GAAATTTTGG GCAATAATA TCTGAAATCC GACCAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTCG CCGAAATTT GAATCAATTT
601 TTGAGAAAAC ATGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1   MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51  GESYPALQK LTGWNIVNGG VSGDTSQAAL SRLPALLARK PKLVIVGIGG
101 NDFLRKVP EE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
151 PLYEDLSEY GIPLEGGAWA EILGNLNLKS DQIHANGKGY RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1   ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGGTTGC TGCTTACCGC
51  CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCCCT
151 GCGGAATCCT ACCCGCGCA ACTGCAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCTGC CCAAGCCCTG TCGGCGCTGC
251 CCGCGCTGTT GGCACGCAAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCCAAAGT TCCCAAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AGAAGGAAA CATCCCGGCC GTCTCGTCG
401 GCGTGCCGCA CATCACA CTG GGTGCGTTGT TCGGGCATT GAGCGATCAT
451 CCGCTGTATG AGGATTTGTC CGAGGAATAC GGCATTCCGC TGTTCGGCGG
501 CCGGTGGGCG GAAATTTTGG GCGATAATA TCTGAAATCC GACCAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTTG CCGAAGATT GAATCAATTT
601 TTGAGAAAAC AGGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1   MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51  GESYPALQK LTGWNIVNGG VSGDTSQAAL SRLPALLARK PKLVIVGIGG

```

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101 ND~~FL~~RKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLS~~SDH~~
 151 PL~~YED~~LSE~~EY~~ GIP~~LF~~GGAWA EILGDN~~N~~LKS DQIHANGKGY RKFAEDLNQF
 201 L~~RK~~Q~~GFR~~

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

	10	20	30	40	50	60
m996.pep	MNRRTFLLGAGALLLTACGRKSART HAKI PEGSTVLALGDSLTFGYGANPGESYP AQLQK					
g996	MNRRTFLLGAGALLLTACGRKSART HAKI PEGSTVLALGDSLTFGYGANPGESYP AQLQK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m996.pep	LTGWNIVNGGVSGD TS SAQALSRLPALLARKPKLVIVGIGGND FL RKVPKEQTRANI AKII					
g996	LTGWNIVNGGVSGD TS SAQALSRLPALLARKPKLVIVGIGGND FL RKVPKEQTRANI AKII					
	70	80	90	100	110	120
	130	140	150	160	170	180
m996.pep	ETVQKENIPAVLVGVPHITL GAL FGHLS SDH PLYEDLSE EY GIP LF GGAWAEILGD NN LKS					
g996	ETVQKENIPAVLVGVPHITL GAL FGHLS SDH PLYEDLSE EY GIP LF GGAWAEILGD NN LKS					
	130	140	150	160	170	180
	190	200				
m996.pep	DQIHANGKGYRKFAEDLNQFL RK Q GFR					
g996	DQIHANGKGYRKFAEDLNQFL RK Q GFR					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq
 1 ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGTC TCCTTACCGC
 51 CTGCGGCAGA AAATCCGCC CAAATTCCTT CAAATTCCTT CAAATTCCTT
 101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCCC
 151 GGCGAATCCT ACCCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
 201 CAACGGCGGC GTATCGGGCG ATACATCCGC CCAAGCCCTG TCGCGCCTGC
 251 CCGCGCTGTT GGCACGCAAA CCAAGCTTG TGATTGTCGG CATAGCGCGC
 301 AACGACTTTC TCGCGAAAGT TCCCAAGGAG CAGACCCGCG CCAATATCGC
 351 GAAATCATC GAAACCGTGC AGAAGGAAA CATCCCCGCC GTCCTCGTCG
 401 GCGTGCCGCA CATTACCTTG GCGCGTTGT TCGGGCATTT GAGCGATCAT
 451 CCGCTGTATG AGGATTGTC CGAGGAATAC GGCATTCCGC TGTTCGGCGG
 501 CGCGTGGCG GAAATTTTGG GCGATAATA TCTGAAATCC GACCAATCC
 551 ACGCCAACGG CAAAGGCTAT CGGAAATTG CCGAAGATT GAATCAATT
 601 TTGAGAAAC AGGGTTTAG ATAA

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep
 1 MNRRTFLLGA GALLLTACGR KSART~~HAKI~~P EGSTVLALGD SLTFGYGANP
 51 GESYP~~AQLQK~~ LTGWNIVNGG VSGD~~TS~~SAQAL SRLPALLARK PKLVIVGIGG
 101 ND~~FL~~RKVPKE QTRANI~~AKII~~ ETVQKENIPA VLVGVPHITL GALFGHLS~~SDH~~
 151 PL~~YED~~LSE~~EY~~ GIP~~LF~~GGAWA EILGDN~~N~~LKS DQIHANGKGY RKFAEDLNQF
 201 L~~RK~~Q~~GFR~~*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

	10	20	30	40	50	60
a996.pep	MNRRTFLLGAGALLLTACGRKSART HAKI PEGSTVLALGDSLTFGYGANPGESYP AQLQK					

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```

|||||
m996  MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFYGANPGESYPALQK
      10      20      30      40      50      60
      70      80      90      100     110     120
a996.pep LTGWNIVNGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
      |||||
m996  LTGWNIVNGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
      70      80      90      100     110     120
      130     140     150     160     170     180
a996.pep ETVQKENIPAVLVGVPHITLGALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGDNNLKS
      |||||
m996  ETVQKENIPAVLVGVPHITLGALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGDNNLKS
      130     140     150     160     170     180
      190     200
a996.pep DQIHANGKGYRKFAEDLNQFLRKQGF
      |||||
m996  DQIHANGKGYRKFAEDLNQFLRKQGF
      190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGCGC TTGTCCGCCG CCGTCACCTT GCGCGGCAC GCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GAAGGCGCG CACACTGGCC
151 GGAATACCG ACGTTTCGG TTTTGTGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGTGT TGCCTGAT GAAACCATC GGTTCAGACC
251 CCCGTGCCGC CTTTGTGCG GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CTGCGCGCG CCGCTGCATA TTTGGGCGG
351 CGTGCTGCTT GCCCGCGCG TACCGTCCG ATTCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCCGGTG CCGCGTAAT
501 GCAGTTTGG CAGCCCTTGG TCTGGGCGC GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTT TGTCCGACG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCGGAA CCGCCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAACC GCGCGTATG CGTCTGAACA CCCTCCGGA CGGAAAAGTC
751 CTCGTCAACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCGGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCTGCG CCGCCCGCTG ACCGGCATtg CCGAcggcAC
951 ggcaCaatg CTGCTTTgcc cgGGGcAGGc tccggactgc CcccaaAacg
1001 aagTCTCCGc cGTcAttagc GTTTCGgAcc GCGTcggcgC Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MMNTPHPRPK IAVIGAGWAG LSAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILLGAY RGVLRMLKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLQPDIT
151 TVAQWLKQRN VPRRAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKS GSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGAGGA CTGTCCGCCG CCGTCACCTT GCGCGGCAC GCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGCGCG CACACTGGCC
151 GGAATACCG ACGTTTCGG TTTTGTGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGTGT TGCCTGAT GAAACCATC GGTTCGGATC
251 CCCGTGCCGC CTTTGTGCG GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CTGCGCGCG CCGCTGCATA TTTGGGCGG
351 CGTGCTGCTT GCCCGCGGTG CACCGACTGC ATTCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCCGGTG CCGCGTAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGCGC GCTCAACACG CCTTTGGAAA

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1417

```

551 CC GCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AA AAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
651 CG TCGCCGAA CCCGCCCTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GC CTCGAAAC GCGCGTATGC CGTCTGAACA CCTTCCCGGA CGGGAAAGTG
751 CT CGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCCGCCA CCGCGCCCTA
801 CC ACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCAGACAC GTTCAGACGG
851 CA TATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GC CGAACCCG TCCGCCCTGCC CGCCCCGCTG ACCGGCCTTG CCGACGGCAC
951 GG TGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAAACGAAG
1001 TG TCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GC GTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GG GCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAACGC GCCACAACCG
1151 CA GCCGATGC CCGCCGCCG GACTTGTCGT GGTGACCG GCACCGCATC
1201 TT CCCCCTCG GCGACTACCT CCACCCGAC TACCCGCCA CGCTCGAAGC
1251 CG CCGTACAA TCAGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GC GATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

m997.pep

```

1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GN TDGFGFLD NGQHILGAY RGVRLMKT I GSDPRAAFLR VPLHWHMHGG
101 LQ FRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLO KSARLGQPD
151 TV AQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVL
201 KK SGSDYLLP KQDLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LV NGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLR
301 AE PVRLPAPL TGLADGTQVQW LLCRGLGLP ENEVSAVISV SDRVGAFA
351 AW ADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRRH
401 FP AGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

	10	20	30	40	50	60
g997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGFLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGFLD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g997.pep	NGQHILGAYRGVRLMKTIGSDPRAAFLRVPLHWHMHGGLOFRALPLPAPLHILGGVLL					
m997	NGQHILGAYRGVRLMKTIGSDPRAAFLRVPLHWHMHGGLOFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g997.pep	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC					
m997	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC					
	190	200	210	220	230	240
	250	260	270	280	290	300
g997.pep	RLNTLPDGKVLVNGEAFDAAILATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLR					
m997	RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLR					
	250	260	270	280	290	300
	310	320	330	340	350	
g997.pep	AEPVRLPAPLTGIADGTAQWLLCPGQAPDCPQNEVSAVISVSDRVGAFANR					
m997	AEPVRLPAPLTGLADGTQWLLCRGRL-GLPENEVSAVISVSDRVGAFANRAWADKAHAD					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGGCG TTGTCCGCGG CCGTTACCTT GCGCGGCAC GCCGACGTTA
101 CCC TGTTTGA AGCCGCGCGG CAGGCGGGCG GCAGGGCGCG CGCACTGGCC
151 GGA AATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGG CGCATAC CGGGGCGTGT TCGCCCTGAT GAAAACCATC GTTTCAGACC
251 CCC ATGCGCG CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTG CAGTTCC GCGCCCTCCC CCTGCCCGCG CCCCTGCATA TTTTGGGCGG
351 CGT GCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAACGTGCTTG
401 CCG ATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACA GTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCA GTTTTGG CAGCCCTTGG TTTGGGGCGC GCTCAACACG CCTTTGGAAG
551 CCG CAAGCTT GCGCGTGTG TGCAACGTTT TGTCGACGG CGTGCTGACG
601 AAA AATACCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGT CGCCGAA CCCGCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCC TCGAAAC GCGCATATGC CGTCTGAACA CCCTCCCGGA CGGGAAGTG
751 CTC GTCAACG GCGAACCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CCA CGCCGCG GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CAT ATCAAAA CCTTCGCTAT CAGGCCATCA CCACCGTCTA TCTGCGCTAT
901 GCC GAACCCG TCCGCTTGCC TGCCCGCGTG ACCGGACTTG CCGACGGCAC
951 GGT GCAATGG CTGCTTTGCC GGGGCAAGCT CGGACTGCCT GAAAACGAAG
1001 TGT CCGCCGT CATCAGCGT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCG TGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCCGCATT
1101 GGG CGAACCC GAAGCCGTC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAG CCGATGC CCGCCGCGG GATTGTGCT GGTTCACCG GCACCGCATC
1201 TTC CCCGCGG GCGACTACCT CCACCCAGAC TACCCGCGCA CGCTCGAAGC
1251 CGC CGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCG ATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVRLRMKTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVL
201 KKS GSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEFPDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQVW LLCRGRGLP ENEVSAVISV SDRVGAFANR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPP DLSQLHRHRI
401 FPGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

```
a997/m997 98.2% identity in 437 aa overlap

      10      20      30      40      50      60
a997.pep MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD
          |||
m997      MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD
          |||

      70      80      90     100     110     120
a997.pep NGQHILLGAYRGVRLRMKTIGSDPHAAFLRVPLHWHMHGGGLQFRALPLPAPLHILGGVLL
          |||
m997      NGQHILLGAYRGVRLRMKTIGSDPRAAFLRVPLHWHMHGGGLQFRALPLPAPLHILGGVLL
          |||

     130     140     150     160     170     180
a997.pep ARRVPFAFKA KLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT
          |||
m997      ARRAPTAFKA KLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT
          |||

     190     200     210     220     230     240
a997.pep PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRIC
          |||
```

1419

```

m997      PLETASLRVLCNVLS DGVLT KKS GSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

a997.pep      RLNTLPDGKVLVNGEPFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           250      260      270      280      290      300
           |||
m997      RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           250      260      270      280      290      300

a997.pep      AEPVRLPAPLTGLADGTQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKVVHADL
           310      320      330      340      350      360
           |||
m997      AEPVRLPAPLTGLADGTQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

a997.pep      KRILPHLGEPEAVRVITEKRATTAADAPPPDL SWLHRHRI FPAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420
           |||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDL SWLHRHRI FPAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

a997.pep      SGFASAEACLQSLSDAVX
           430
           |||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTTCAA TTGTTTTATC
51  AGCCTGCAAC CAACAATCAA AAACGGCACA AGCCGAAGAA CCTGTCCAAA
101 GTATCCAGGC TGCTGATTGT ACCGCCCCAA TGGACATCAC AGTTGAACAA
151 TATCTCATCA ATTTGGAGCA AGCATTTAAA ACTCAGAACG TCTCAACAAA
201 AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT
251 TGGTAATGGA TTTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
301 ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
351 ACAAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAGGCAG
401 TTCTGTCTTT AACTACCACA GACAAATTGG GCGAATCGGA AGCAGGAAAA
451 CAACCTTTTA CAGCTTTAAC CGAAGTCGTC AAAGAATCCA ATCAGACAGG
501 AGCAACAGCG CAAAAGACG TTCCGGCAGA TGGTATTTTA TATAGCGTTG
551 TTTTGAAGA AGAAACAAAC ACCATTGCAA TAATCGGCAG AAAACAACCC
601 TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI CVSIVLSACN QSKTAQAE PVQSIQAADC TAPMDITVEQ
51  YLINLEQAFK TQNVSTKIHN KNIVKDCGY DLTLMDFGA IALKLDEQOK
101 IRAISVGYIL KTDGEKGQNL VNNAINGLHS IQAVLSLT TT DKLGESEAGK
151 QLFTALTEVV KESNOTGATA QKDVFPADGIL YSVVFEKETN TIAIIGRKQP

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

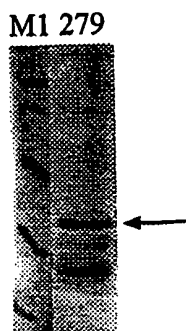
17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

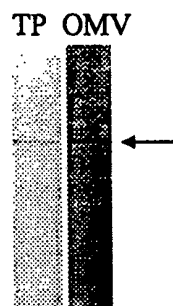
Fig. 2

279 (10.5 kDa)

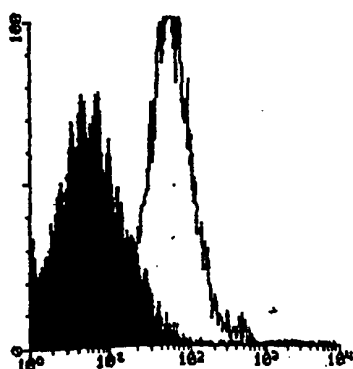
A) PURIFICATION



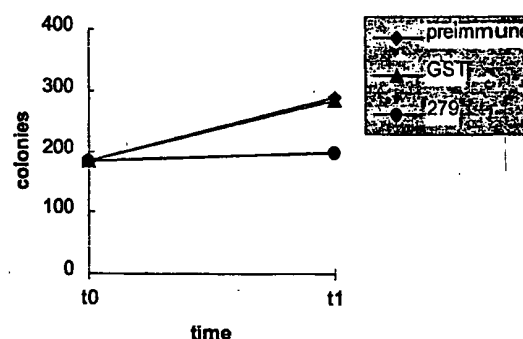
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay: positive

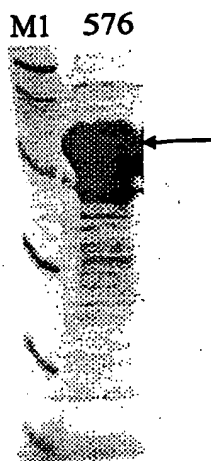
279

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

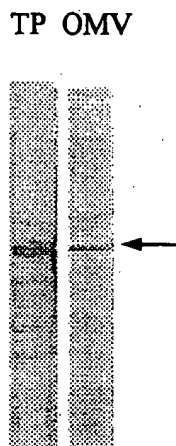
Fig. 3

576 (27.8 kDa)

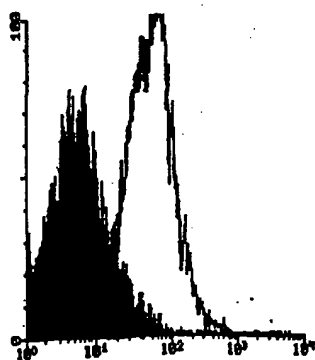
A) PURIFICATION



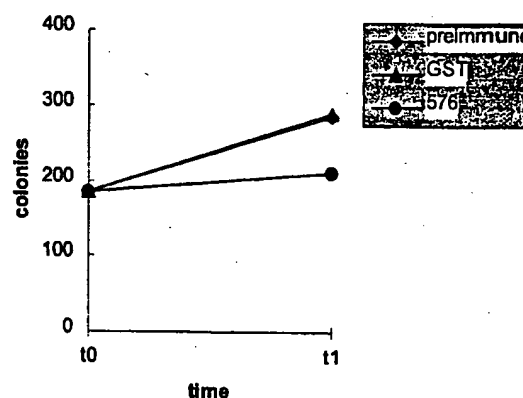
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay: positive

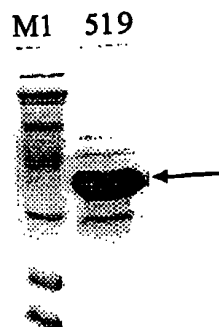
576

The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 4

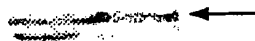
519 (33 kDa)

A) PURIFICATION

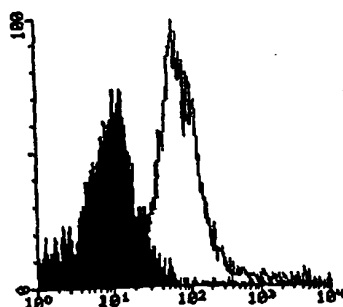


B) WESTERN BLOT

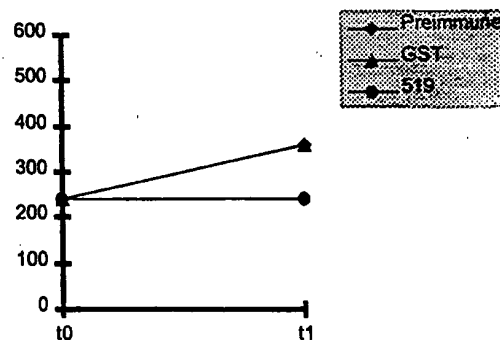
TP OMV



C) FACS

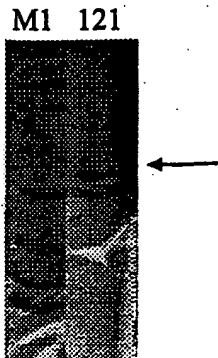
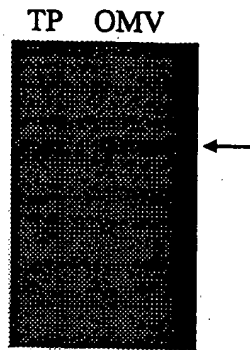
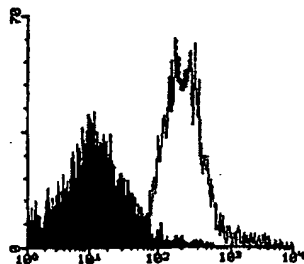
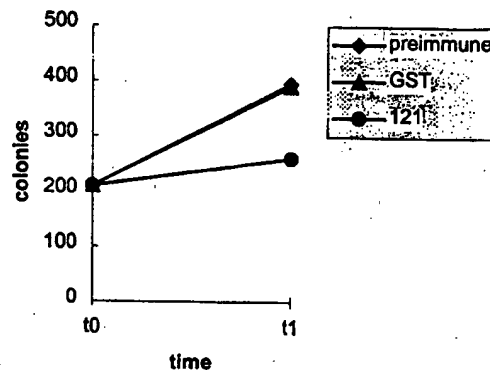


D) BACTERICIDAL ASSAY

E) ELISA assay: positive

519

The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

121 (40 kDa)**A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

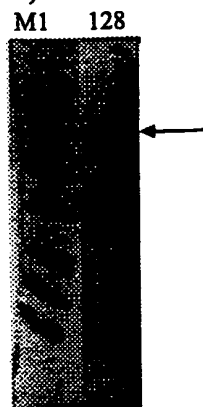
The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 5

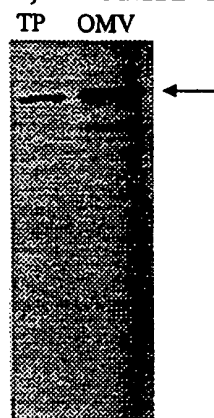
128 (101 kDa)

Fig. 6

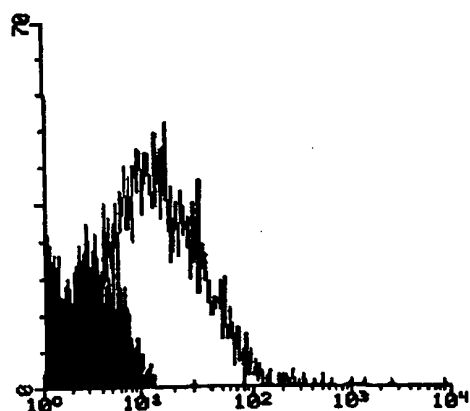
A) PURIFICATION



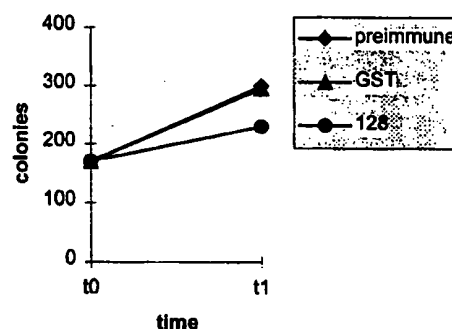
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY



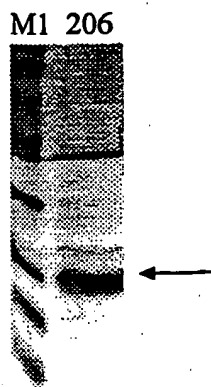
E) ELISA assay: positive

128

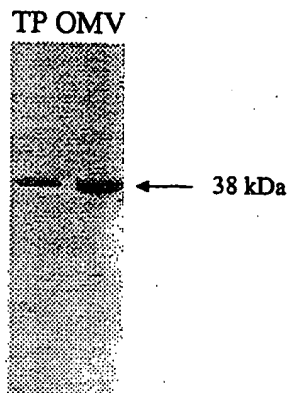
The predicted gene 128 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

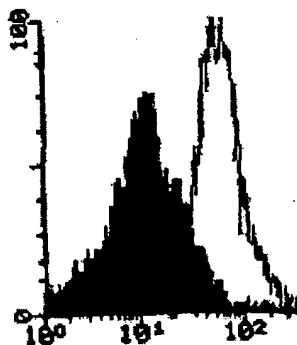
A) PURIFICATION



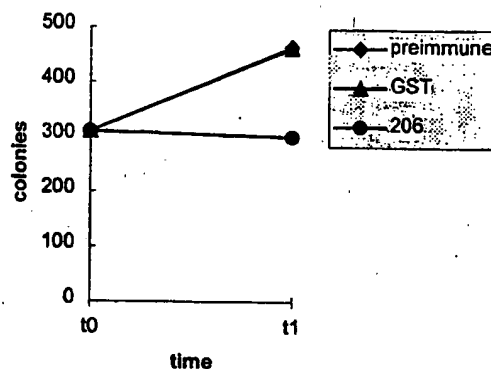
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY



E) ELISA assay: positive

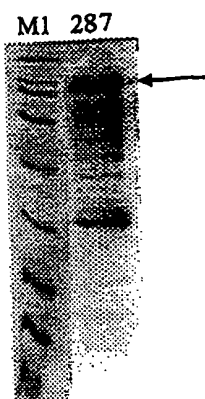
206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worth noting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a reactive band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C) is shown the FACS analysis, in panel D) the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

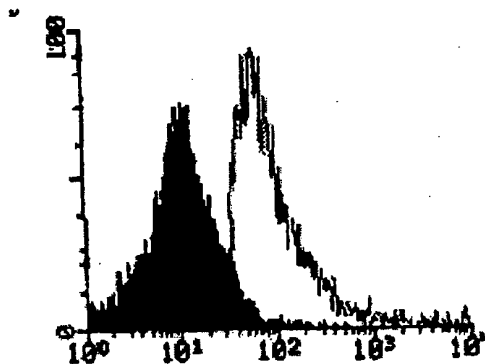
287 (78 kDa)

Fig. 8

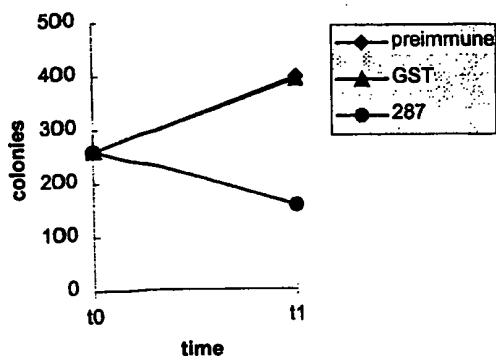
A) PURIFICATION



B) FACS



C) BACTERICIDAL ASSAY

D) ELISA assay : positive

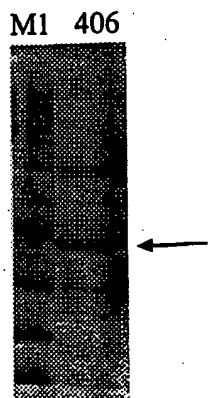
287

The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

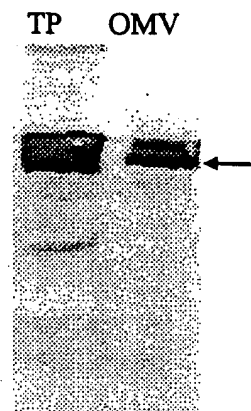
406 (33 kDa)

Fig. 9

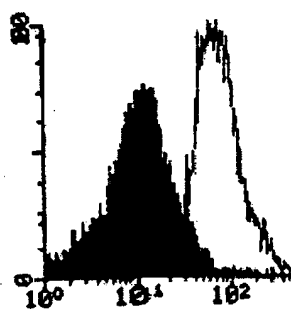
A) PURIFICATION



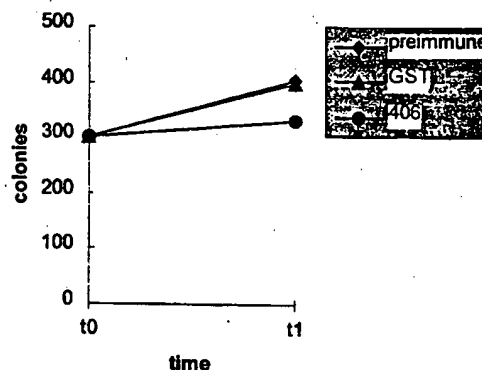
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay : positive

406

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

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919

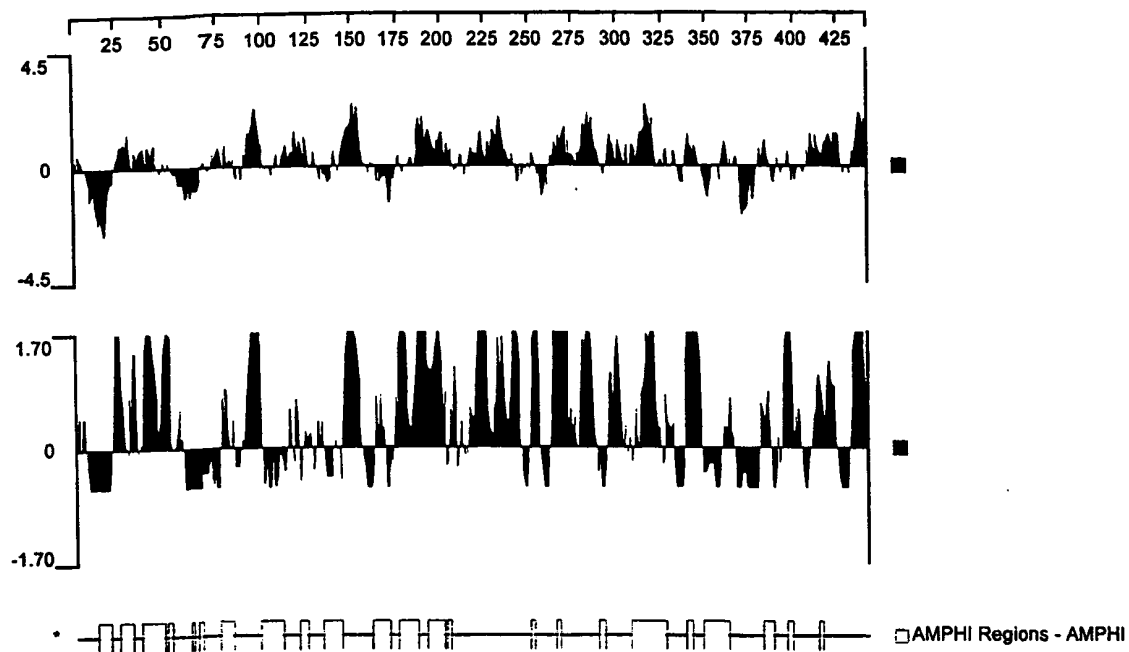
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

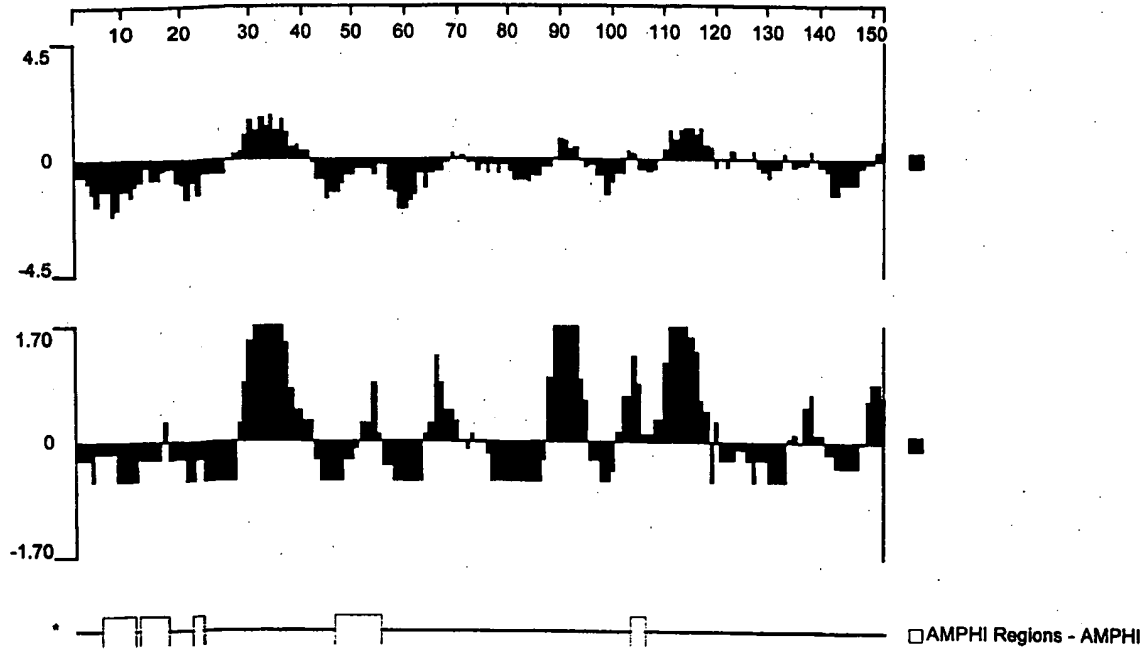
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11

11/30

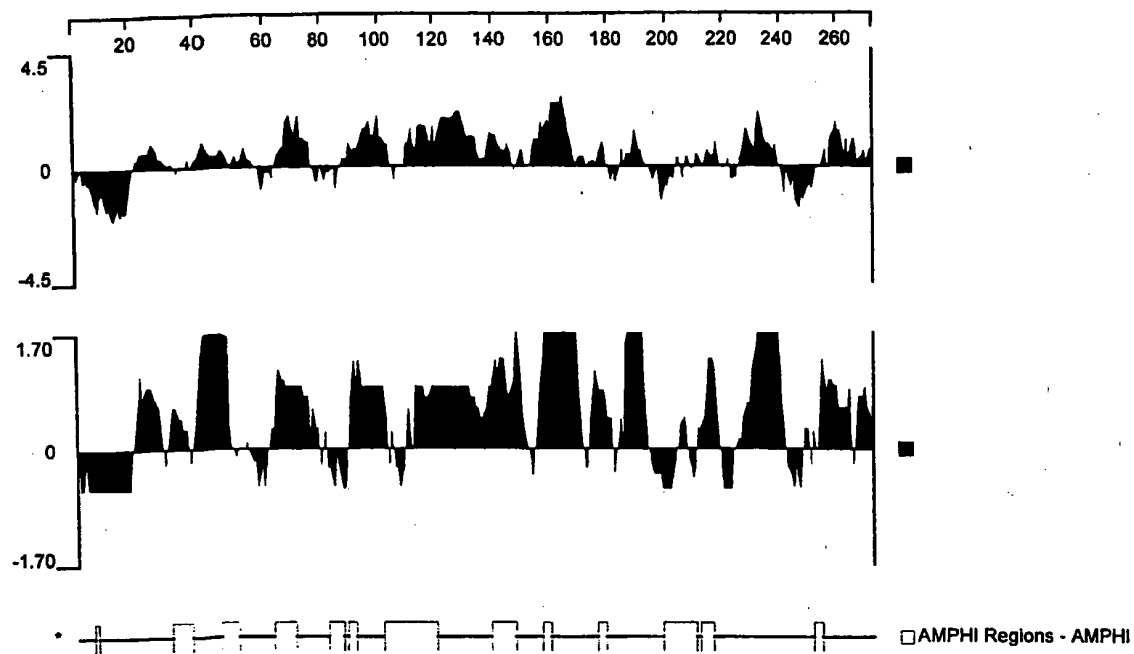
576-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

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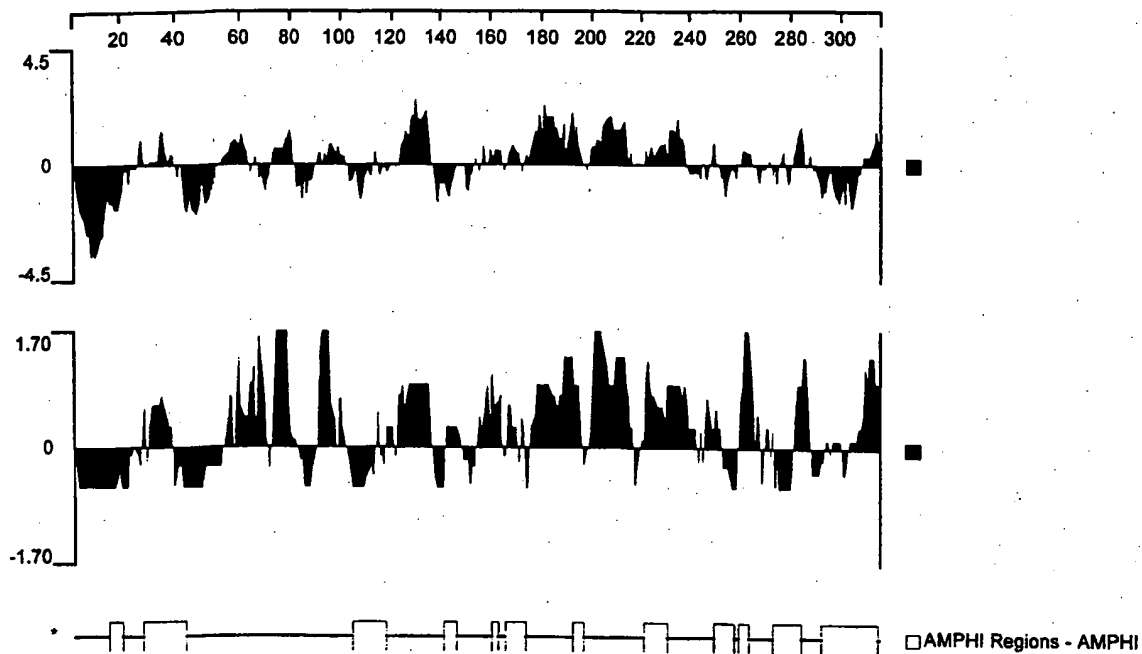
519-1Hy drophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 13

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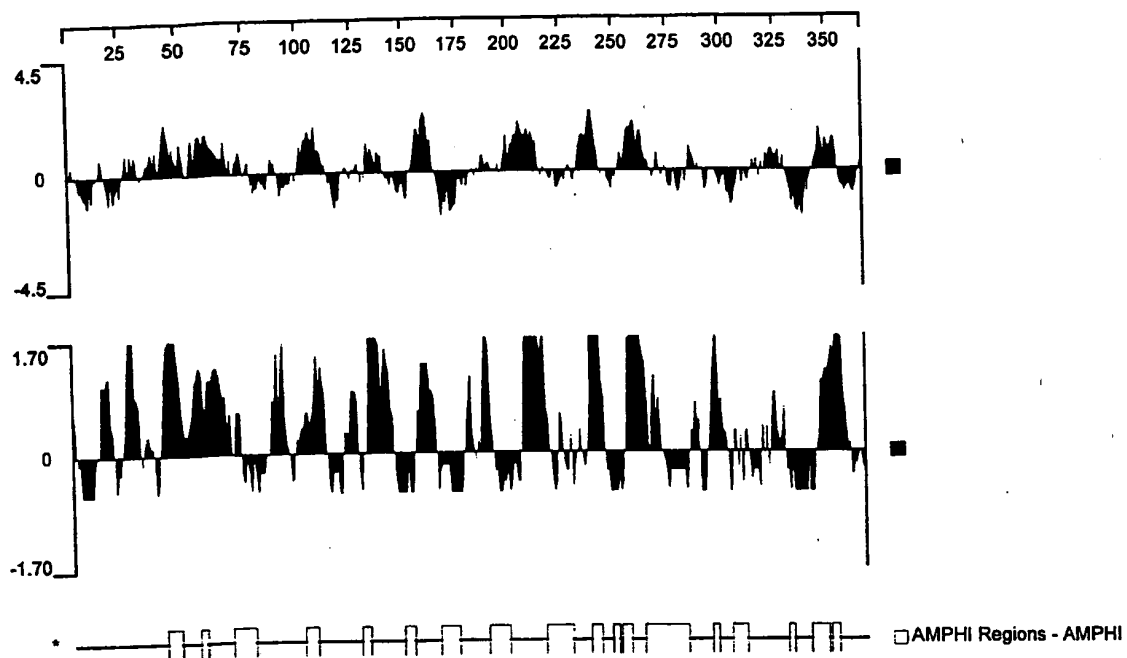
121-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 14

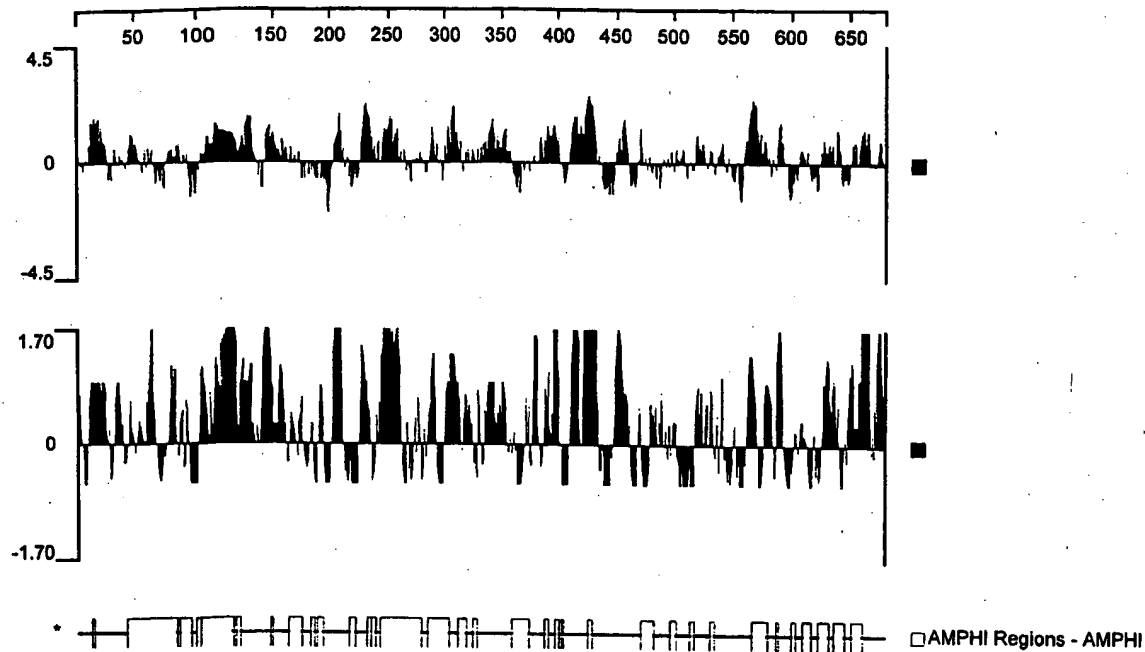
128-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 15

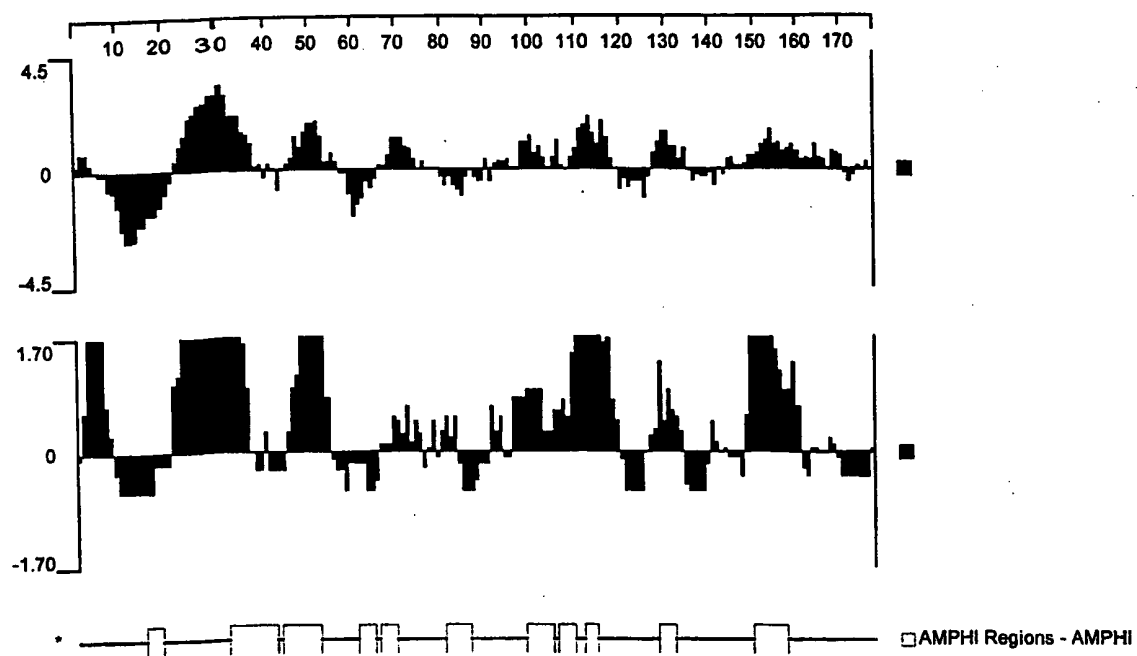
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 16

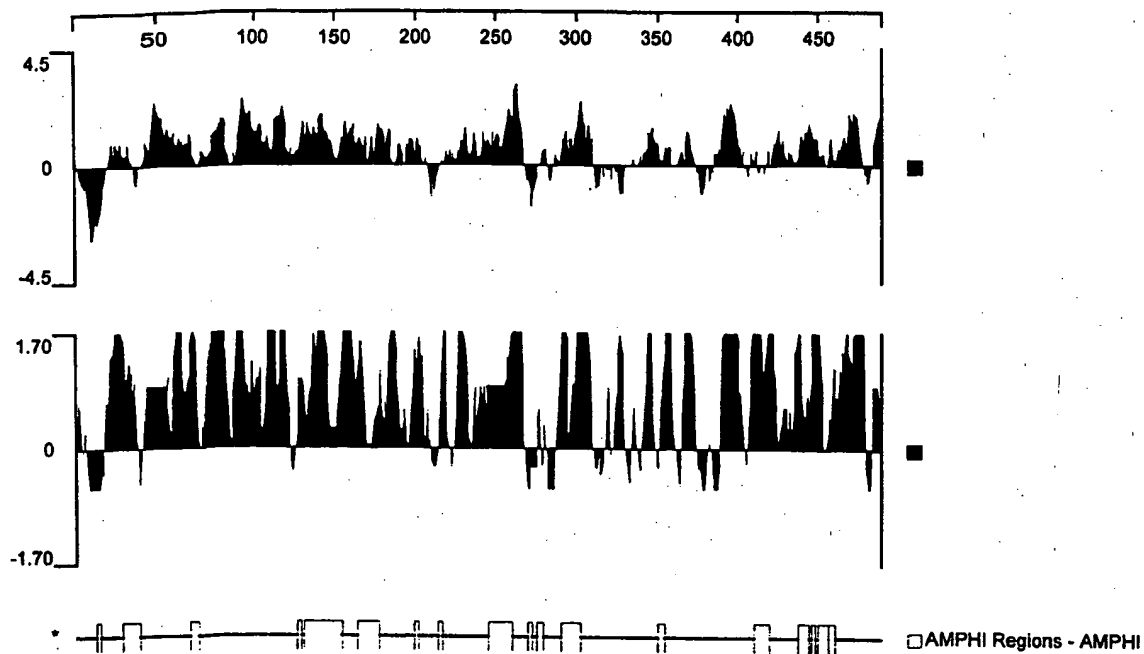
287Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

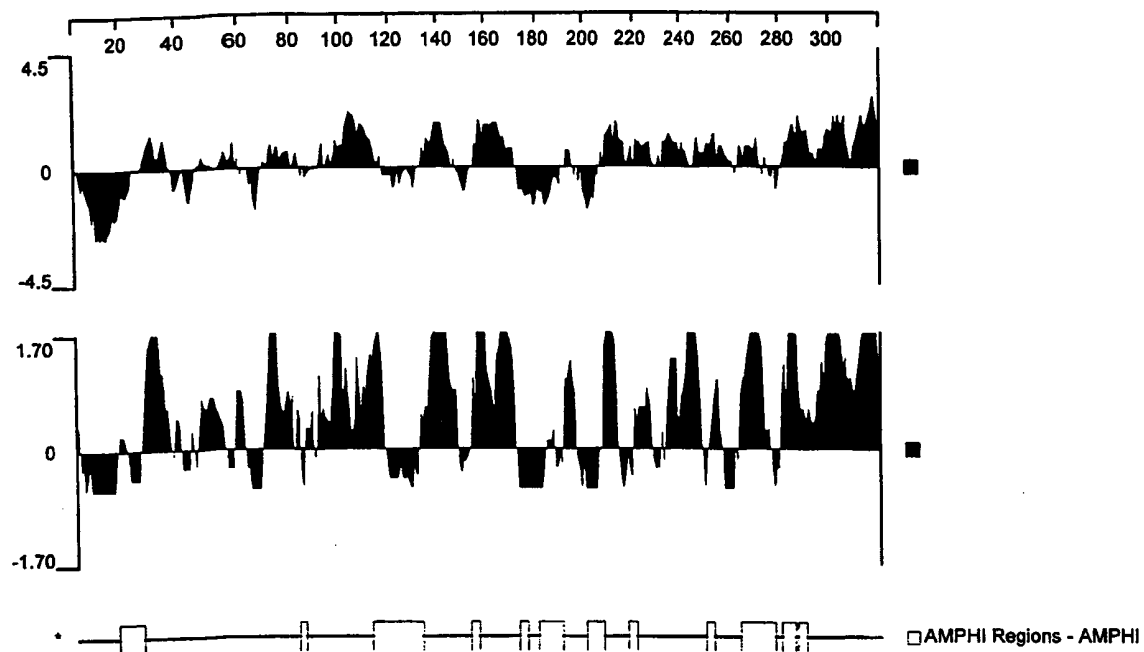
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

zo05_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo08_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
z2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo11_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo20_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo09_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo22_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo23_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo24_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo25_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo26_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo04_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo06_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo07_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo10_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo14_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo16_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo17_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo18_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo19_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo21_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo27_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo28_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo29_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo13_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Fig. 19C


```

287_14 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV...KETE
287_2 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV...KETE
287_21 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV...KETE
z2491 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV...KETE
287_9 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV...KETE
fa1090 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV...KETE

287_14 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT
287_2 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT
287_21 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT
z2491 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT
287_9 61 VSGAPQAD...QDATAGKGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT
fa1090 61 AGGAPQAD...QDATAGKGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT

287_14 110 DSLTPNHTPASNMPAGNMEQAQDAGESEOPANQPDMANADGMQGGDDPSAGGENAGNTA
287_2 110 DSLTPNHTPASNMPAGNMEQAQDAGESEOPANQPDMANADGMQGGDDPSAGGENAGNTA
287_21 110 DSLTPNHTPASNMPAGNMEQAQDAGESEOPANQPDMANADGMQGGDDPSAGGENAGNTA
z2491 110 DSLTPNHTPASNMPAGNMEQAQDAGESEOPANQPDMANADGMQGGDDPSAGGENAGNTA
287_9 119 DSLTPNHTPASNMPAGNMEQAQDAGESEOPANQPDMANADGMQGGDDPSAGGENAGNTA
fa1090 117 .....

287_14 170 AQTNOAENNOTAGSQNPASSINPSATNSGGDEGRITNNGNSVVIDGPSQNTILTHCKGDS
287_2 170 AQTNOAENNOTAGSQNPASSINPSATNSGGDEGRITNNGNSVVIDGPSQNTILTHCKGDS
287_21 170 AQTNOAENNOTAGSQNPASSINPSATNSGGDEGRITNNGNSVVIDGPSQNTILTHCKGDS
z2491 170 AQTNOAENNOTAGSQNPASSINPSATNSGGDEGRITNNGNSVVIDGPSQNTILTHCKGDS
287_9 178 DQANOAEENNOVGGSONPASSINPSATNSGGDEGRITNNGNSVVIDGPSQNTILTHCKGDS
fa1090 117 .ESANOTGNNOPAGSSDSAPAENPAPANGSDEGRITNNGNSVVIDGPSQNTILTHCKGDS

287_14 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNDKFGVLVADSVMQKGINQYII
287_2 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNDKFGVLVADSVMQKGINQYII
287_21 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNDKFGVLVADSVMQKGINQYII
z2491 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNDKFGVLVADSVMQKGINQYII
287_9 238 CORDFLDEEAPPKSEFEKLSDAKISNYKKDGKNDGKNDKFGVLVADSVMQKGINQYII
fa1090 176 CNGNDLDEEAPSSEFEKLSDAKISNYKKDGKNDGKNDKFGVLVADSVMQKGINQYII

287_14 290 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_2 290 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_21 286 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
z2491 286 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_9 293 IYKDKSASSTSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
fa1090 232 FYTDKPT.....RSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG

287_14 348 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPLRGRFAA
287_2 348 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPLRGRFAA
287_21 344 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPLRGRFAA
z2491 344 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPLRGRFAA
287_9 353 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPLRGRFAA
fa1090 285 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPLRGRFAA

287_14 408 KVDFGSKSVDCIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_2 408 KVDFGSKSVDCIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_21 404 KVDFGSKSVDCIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
z2491 404 KVDFGSKSVDCIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_9 413 KVDFGSKSVDCIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
fa1090 345 KVDFGSKSVDCIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA

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FIG. 21A

287_14	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_2	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_21	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
z2491	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_9	473	GKYSYRPTDAEKGGFGVFAGKKEQD*
fa1090	405	GKYSYRPTDAEKGGFGVFAGKKEQD*

FIG. 21B

z2491_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv26_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
z222_519ass	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
fa1090_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv32_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv11_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv28_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv96_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv02_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv03_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv04_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv05_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv01_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv07_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv12_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv18_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv19_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv21_519ass	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv27_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv20_519ass	121	RMELDKTFEERDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv06_519ass	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv29_519ass	121	RMELDKTFEERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE

FIG. 22A

```

z2491_519      181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass    181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519     181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass    181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519       181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass    181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass    181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass    181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR

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z2491_519      241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv26_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv22_519ass    241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
fa1090_519     241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv32_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv11_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv28_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv96_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv02_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv03_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv04_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv05_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv01_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv07_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv12_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv18_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv19_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv21_519ass    241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv27_519       241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv20_519ass    241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv06_519ass    241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv29_519ass    241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL

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z2491_519      301 ISAGMKIIDSSKTA*
zv26_519       301 ISAGMKIIDSSKTA*
zv22_519ass    301 ISAGMKIIDSSKTA*
fa1090_519     301 ISAGMKIIDSSKTA*
zv32_519       301 ISAGMKIIDSSKTA*
zv11_519       301 ISAGMKIIDSSKTA*
zv28_519       301 ISAGMKIIDSSKTA*
zv96_519       301 ISAGMKIIDSSKTA*
zv02_519       301 ISAGMKIIDSSKTA*
zv03_519       301 ISAGMKIIDSSKTA*
zv04_519       301 ISAGMKIIDSSKTA*
zv05_519       301 ISAGMKIIDSSKTA*
zv01_519       301 ISAGMKIIDSSKTA*
zv07_519       301 ISAGMKIIDSSKTA*
zv12_519       301 ISAGMKIIDSSKTA*
zv18_519       301 ISAGMKIIDSSKTA*
zv19_519       301 ISAGMKIIDSSKTA*
zv21_519ass    301 ISAGMKIIDSSKTA*
zv27_519       301 ISAGMKIIDSSKTA*
zv20_519ass    301 ISAGMKIIDSSKTA*
zv06_519ass    301 ISAGMKIIDSSKTA*
zv29_519ass    301 ISAGMKIIDSSKTA*

```

Fig. 22B

Fig. 23A

Fig. 23B

fa1090	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm33asbc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm32asbc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm23asbc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm27bc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm09	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm10	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm24	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm25	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm14	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm04	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm11asbc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm08n	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm96	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm01	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm02	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm03	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm07	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm12	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm18	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm19	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm20	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm21	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm06	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm17	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm13	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm05	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
z2491	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm22	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm26	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm28	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm29asbc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm16	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm15	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm31asbc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
fa1090	421	QKTTGYVWQLLPNGMKPEYRP*
zm33asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm32asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm23asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm27bc	421	QKTTGYVWQLLPNGMKPEYRP*
zm09	421	QKTTGYVWQLLPNGMKPEYRP*
zm10	421	QKTTGYVWQLLPNGMKPEYRP*
zm24	421	QKTTGYVWQLLPNGMKPEYRP*
zm25	421	QKTTGYVWQLLPNGMKPEYRP*
zm14	421	QKTTGYVWQLLPNGMKPEYRP*
zm04	421	QKTTGYVWQLLPNGMKPEYRP*
zm11asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm08n	421	QKTTGYVWQLLPNGMKPEYRP*
zm96	421	QKTTGYVWQLLPNGMKPEYRP*
zm01	421	QKTTGYVWQLLPNGMKPEYRP*
zm02	421	QKTTGYVWQLLPNGMKPEYRP*
zm03	421	QKTTGYVWQLLPNGMKPEYRP*
zm07	421	QKTTGYVWQLLPNGMKPEYRP*
zm12	421	QKTTGYVWQLLPNGMKPEYRP*
zm18	421	QKTTGYVWQLLPNGMKPEYRP*
zm19	421	QKTTGYVWQLLPNGMKPEYRP*
zm20	421	QKTTGYVWQLLPNGMKPEYRP*
zm21	421	QKTTGYVWQLLPNGMKPEYRP*
zm06	421	QKTTGYVWQLLPNGMKPEYRP*
zm17	421	QKTTGYVWQLLPNGMKPEYRP*
zm13	421	QKTTGYVWQLLPNGMKPEYRP*
zm05	421	QKTTGYVWQLLPNGMKPEYRP*
z2491	421	QKTTGYVWQLLPNGMKPEYRP*
zm22	421	QKTTGYVWQLLPNGMKPEYRP*
zm26	421	QKTTGYVWQLLPNGMKPEYRP*
zm28	421	QKTTGYVWQLLPNGMKPEYRP*
zm29asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm16	421	QKTTGYVWQLLPNGMKPEYRP*
zm15	421	QKTTGYVWQLLPNGMKPEYRP*
zm31asbc	421	QKTTGYVWQLLPNGMKPEYRP*

Fig. 23D

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